OS PROTOCOL AND PROCEDURE: DMP – DATA MANAGEMENT

PREPARED BY	ORGANIZATION	DATE
Tera Del Priore	SCI	02/12/2026
Cody Flagg	SCI	04/02/2019
Courtney Meier	SCI	01/02/2018
Sarah C. Elmendorf	DPS	01/05/2015
Kate Thibault	SCI	01/05/2015

APPROVALS	ORGANIZATION	APPROVAL DATE
Kate Thibault	SCI	02/12/2026

RELEASED BY	ORGANIZATION	RELEASE DATE
Tanisha Waters	CM	02/12/2026

See configuration management system for approval history.

The National Ecological Observatory Network is a project solely funded by the National Science Foundation and managed under cooperative agreement by Battelle. Any opinions, findings, and conclusions or recommendations expressed in this material are those of the author(s) and do not necessarily reflect the views of the National Science Foundation.

Change Record

REVISION	DATE	ECO #	DESCRIPTION OF CHANGE
A	05/30/2014	ECO-01835	Initial release
B	01/05/2015	ECO-02633	Added information regarding recent developments of web interfaces and mobile applications for data entry
C	04/04/2016	ECO-03640	• Updated formatting to latest Protocol/SOP template (previous version did not have SOP sections) • Added more text to Background section • Added clarifying steps for data entry QA procedures • Updated acronyms in Table 2 • Section 8.2 – updates to best practices section
D	03/09/2018	ECO-05383	• Changed title from “Manual Data Transcription” to “Data Management” to better reflect the contents • Added text in Background section to address mobile data collection with no paper datasheets • Expanded Method section that provides more rationale and language describing data quality concepts • Updated definitions to better match digital data collection concepts • Previous Table 1 was deleted as it was no longer relevant. • Deleted old Table 2, no longer relevant • Added Table 4, Field Sampling Completeness table for Process Quality review • Added Table 5, Protocol Sampling Completeness table for Process Quality review • Replaced Figures 1 with a more up to date version of the data ingest process. • Added Figure 2, workflow diagram from field data collection to data quality review. • Re-arranged SOPs to emphasize the mobile/digital elements of data collection (SOPs originally started with paper datasheet collection workflow) • Added SOP A: general overview of data collection and data quality review process

REVISION	DATE	ECO #	DESCRIPTION OF CHANGE
			• Added SOP B: data quality methods for detecting duplicate records • Added SOP C: data quality methods for assessing process quality (complete record sets) • Removed old Appendix A “Best Practices for Data Entry and Data Quality Management” • Removed old Appendix B “NEON Specific Guidelines and Tips for Taxonomy related Data Entry” • Old Appendix C, “Data entry training checklist” is now Appendix A • Added Appendix B “QA/QC for Digital Hemispherical Photos” • Added Appendix C “Vegetation Structure QA/QC”
E	04/16/2019	ECO-06020	• Section 3.1.2: Added paragraph about how checklists should be developed and used for QA/QC • Section 3.1.3: Added a new table as “Table 1” – general description of parser validation rules. • Section 3.1.3: Added more descriptive text about the data ingest process. • SOP E: New SOP outlining how to create and use QC checklists, and when they should be implemented. • Removed Appendix B “QA/QC for Digital Hemispherical Photos”, this should go into the new protocol specific QC checklists that are being developed. • Removed Appendix C “Vegetation Structure QA/QC”, this should go into the new protocol specific QC checklists that are being developed. • Added Appendix B “How to Export Fulcrum Data”
F	03/20/2023	ECO-06963	• Migrated content into newest protocol template Rev L • Re-organized SOP’s order • Added SOP A.4: Review Remarks • Added SOP D: Quality Control Shiny Applications • Added SOP E: How to Use the Magpie Data Viewer Application • Added SOP H: Parser Error Resolution • Added Appendix B: How to Filter and View Fulcrum Data in the WebUI • Expanded Appendix C to include how to download full Fulcrum version history • Added Appendix D: Supplemental Parser Error Resolution Workflows
G	05/05/2023	ECO-07012	• Updated Table 2 • Updated the title of SOP H.2

REVISION	DATE	ECO #	DESCRIPTION OF CHANGE
H	02/12/2026	ECO-07172	• Migrated to protocol template rev M • Minor text edits throughout for clarity • Modified definition for MDR (now mobile device) and DEA (now application) in the Definitions section – these were confusing and dated • Updated SOP A – removed reference to mobile data recorder in tile, added sub-section describing proper mobile devices for data entry, added sub-section describing proper procedure for using the Personnel-List Fulcrum app and obtaining OrcidIDs, added description for use of inventory app • Removed sub-section in SOP B to scan field datasheets • Added section in SOP B – how to access datasheet scans on the Google Cloud • Moved content from formerly SOP C.3 – Data entry procedures to SOP A • Updated SOP E – added more details regarding when to use each request type in Magpie • Updated SOP E – added directions for new ‘Taxonomic Change request’ option in Magpie app • Updated SOP E – shipping app requests are available on all four subsystem tabs • Updated language in SOP H – multiple places where inaccurate text was found • Added new SOP I – how to correct manifest errors for shipments to external labs • Updated language for Canary throughout – now a shiny app, no longer a Google spreadsheet • Added mention of Clorkwork Shiny App

TABLE OF CONTENTS

LIST OF TABLES AND FIGURES

1 OVERVIEW

1.1 Background

This document provides a cross-protocol set of data management instructions for the NEON Terrestrial and Aquatic Observation Systems. It includes a framework for data quality control and assurance measures that should be applied before, during, and after data collection, best practices for data collected on mobile devices, guidelines for transcription and storage when field and lab data are recorded with paper datasheets, a reference for how to troubleshoot, correct, and report data that fail to load into the NEON database, and finally, a reference for how to correct shipping record errors made during shipping.

Data management is the application of a "…consistent methodology that ensures the deployment of timely and trusted data" (Fisher 2009). There are two primary goals that staff should understand before engaging in the data management process. The first goal is to ensure that high quality data are collected, maintained, and delivered to end users by preventing or identifying data quality issues. *Data quality* issues can be defined as any condition that is an obstacle to the data consumer's use of those data (Sebastian-Coleman 2013). Data management in this context is the process by which we prevent, remove, or reduce obstacles to the effective use of data. The second goal of data management is therefore to establish a responsive process that identifies, measures, tracks, and resolves data quality issues.

The aim of quality control (QC) during data management is to prevent the introduction of errors throughout all stages of data collection, transcription (where relevant), and storage. The purpose of quality assurance (QA) is to detect and correct errors and prevent future data quality issues. Identifying and resolving data quality issues early in data collection processes is particularly important to NEON's strategic goal of providing standardized, long-term data sets to the ecological community. It is critical that personnel understand the data quality process and their role in it at NEON.

This document is formatted such that the individual standard operating procedures (**Section 7**) can and should be referenced frequently before, during, and after data collection by field staff to ensure data quality control and assurance is performed correctly and any issues are communicated via the proper mechanisms.

1.2 Scope

This document provides a change-controlled version of Observatory protocols and procedures. Documentation of content changes (i.e. changes in particular tasks or safety practices) will occur via this change-controlled document, not through field manuals or training materials.

1.2.1 NEON Science Requirements and Data Products

This protocol fulfills Observatory science requirements that reside in NEON's Dynamic Object-Oriented Requirements System (DOORS). Copies of approved science requirements have been exported from DOORS and are available in NEON's document repository, or upon request.

Execution of this protocol procures samples and/or generates raw data satisfying NEON Observatory scientific requirements. These data and samples are used to create NEON data products and are documented in the NEON Scientific Data Products Catalog (RD[03]).

1.3 Acknowledgments

N/A

2 RELATED DOCUMENTS AND ACRONYMS

2.1 Applicable Documents

Applicable documents contain higher-level information that is implemented in the current document. Examples include designs, plans, or standards.

AD[01]	NEON.DOC.004300	EHS Safety Policy and Program Manual
AD[02]	NEON.DOC.004316	Operations Field Safety and Security Plan
AD[03]	NEON.DOC.050005	Field Operations Job Instruction Training Plan
AD[04]	NEON.DOC.004104	NEON Science Data Quality Plan
AD[05]	NEON.DOC.014051	Field Audit Plan

2.2 Reference Documents

Reference documents contain information that supports or complements the current document. Examples include related protocols, datasheets, or general-information references.

RD[01]	NEON.DOC.000008	NEON Acronym List
RD[02]	NEON.DOC.000243	NEON Glossary of Terms
RD[03]	NEON.DOC.002652	NEON Data Products Catalog

2.3 Acronyms

Acronym	Definition
AOS	Aquatic Observation System
FSCI	Field Science
HQ	Headquarters
PDR	Processed data repository
QA	Quality assurance
QC	Quality control
SCI	Science team
SSL	Sampling Support Library
TOS	Terrestrial Observation System

2.4 Definitions

Common terms used throughout this document are defined here, in alphabetical order.

Application: An electronic, protocol-specific, user interface managed by NEON Science to provide controlled data entry that can be accessed through mobile devices or desktop/laptop computers. Currently, NEON applications are created and deployed via the Fulcrum platform. These applications are used by NEON field staff to submit data to the NEON Processed Data Repository (PDR).

Aviary: Internal NEON website with links to applications for data QAQC and reporting.

Canary: A NEON created and managed Shiny app that holds and updates current parser errors for Fulcrum records that fail ingest into the NEON database.

CERT: Certification Fulcrum applications used for training and practice; data entered into CERT apps will never be published to the NEON data portal.

Child record: In data entry applications, the nested form/screen where sub-sample data or multiple observations are recorded; child records inherit metadata from the parent record. The paper datasheet analog would be the rows where sample, trap, or observation specific data are recorded.

Data quality dimension: Characteristics of data that can be measured through which data quality can be described and quantified.

Data quality context: The description of when and where data quality tasks are conducted within a workflow.

Data quality focus: The combination of data quality dimensions that build towards organizational data quality goals (example: a process quality focus is the assessment of both sampling completeness and timeliness).

Downstream application: An application that receives metadata from another application.

Field datasheet: A pdf document to be printed and filled out by hand in the field or the lab; datasheets are typically used when digital applications are not available.

Fulcrum: Software platform used to create and deploy NEON electronic data entry applications.

Ingest workbook: A spreadsheet that outlines all the validation rules for a particular data product and is read by the parser upon an ingest attempt to validate data against the rules outlined.

L0 data: Level zero data – i.e., raw data collected in Fulcrum applications and loaded via the parser.

L1 data: Published and processed L0 data that are made publicly available on the NEON Data Portal.

Load Delay: The application/protocol specific number of days before records in Fulcrum are ingested and evaluated by the parser. The number of days are counted from the date of record creation. Records that successfully "pass" the parser validation rules are set to a read-only state; rejected records remain editable in Fulcrum.

Load Group: The set of applications whose data are ingested at the same time. Applications related to the same protocol are generally within the same load group (e.g., Litter: Trap Deployment, Litter: Field Sampling, and Litter: Lab Mass Data).

LOV: A ‘List of Values’ is a list of constrained values accepted by the parser for a particular field in a data product.

Magpie: A NEON created and managed Shiny app used to view and perform QA/QC on data collected in Fulcrum applications, and to request deletions of records or updates to loaded, read-only records.

Metadata: Information that describes where observations or samples were collected, when those data were collected, who collected them, and other observations about the data.

Mobile device: Handheld, field-portable equipment that runs protocol-specific data entry applications created by NEON Science.

NEON Data Portal: The public interfacing website to access NEON data as well as other resources and information regarding the observatory, found here**:** https://data.neonscience.org/

Orphan Record: A record whose unique identifier (e.g., sampleID, individualID, etc.) is not logically traceable to an upstream record. Field data are often related to downstream domain lab and/or external lab generated data. An example orphan record would be a lab sample whose sampleID does not match metadata for a field collection event (e.g., a Soil Moisture sample “GRSM_006-O-11.5-34-20180409-sm” *should* match an upstream Soil Core Collection sample “GRSM_006-O-11.5-34-20180409”; if it does not, the Soil Moisture record is an orphan).

Parent record: In data entry applications, the first form/screen where metadata are recorded; parent records are often linked to child records. The paper datasheet analog would be the “header” section where sampling location, sampling date, and field personnel information is recorded.

Parser: NEON data validation software that evaluates Fulcrum records against protocol-specific rules during the ingest process. The parser either “passes” and locks records that successfully pass validation and moves data on for web publication, or “rejects” records that fail validation from the publication process resulting in parser errors.

Parser Errors: Records that fail the front-end validation (Parser) and are rejected and not ingested into the database and will result in an error with an accompanied error message that is viewable within the Canary shiny app. Parser errors alert NEON staff to 'bad data' that have been prevented from loading into the publication database.

Processed Data Repository (PDR): Database that manages information for data processing and publishing.

PROD: Production Fulcrum applications used for real data entry; data will be loaded and published to the NEON data portal.

Quality Assurance: Methods for detecting and correcting errors, and for preventing future data quality issues, abbreviated as ‘QA’.

Quality Control: Methods for preventing the introduction of errors throughout all stages of data collection, transcription, and storage, abbreviated as 'QC'.

Record: The collection of data values that describe a sampling entity or event. If data are viewed in a spreadsheet or tabular format, each row is a record, and each column is an attribute of that entity or event.

Recorder: The person who enters the data.

Sampling Support Library (SSL): A webpage housed on the NEON Sharepoint site which provides links to access all current documents and resources for OS protocols, IS instruments, plus field and lab equipment found at each domain support facility.

ServiceNow: Software tool used for problem/incident tracking and resolution.

Sharepoint: Microsoft's customizable Cloud-based content collaboration and management platform that allows organizations to store, organize, share, and access information.

Shiny App: Shiny is a web application framework that enables developers to build an interactive interface for data viewing and analysis.

Syncing/synchronization: The process of transferring digital records from an application to a cloud database for long-term storage. On mobile devices, this specifically refers to the act of pressing the "sync" button, when connected to Wi-Fi. On laptop or desktop computers, syncing occurs as soon as a record is saved.

Upstream application: An application that is the *source* of metadata such as plotID, collectDate, sampleID, etc. These are typically *field* applications such as BET: Field Sampling.

UUID: A Universally Unique Identifier value used to identify information in a system. The NEON database creates a UUID for every data record ingested.

3 METHOD

This protocol provides Standard Operating Procedures (SOPs) for all aspects of data management that are relevant to field staff.

- **SOP A:** General Data Collection and Data Quality Workflow for all Protocols – describes how data and/or samples collected should be managed and reviewed
- **SOP B:** Paper Datasheet Quality Checking – addresses management and review of data collected on paper datasheets
- **SOP C:** Using Checklists for Quality Control – describes checklists available to field staff to use to perform data quality checks
- **SOP D:** Quality Control Shiny Applications – describes tools available to field staff to perform data quality checks
- **SOP E:** How to Use the Magpie Data Viewer Application – describes the Magpie data viewer application and how and when to use it
- **SOP F:** Referential Integrity Data Quality Review – describes how to perform data integrity quality checks
- **SOP G:** Detecting Process Quality Issues – describes how to perform data process quality checks
- **SOP H:** Parser Error Resolution – describes the workflow to resolve data errors
- **SOP I:** Shipping Manifest Error Correction Workflow – describes the workflow to resolve errors in shipping manifests

In addition, each protocol may contain instructions under the "Data Entry and Verification" SOP, which supplement procedures listed here.

3.1 Data Quality Framework

Data quality can be defined as the degree to which data meet the expectations of data consumers per the intended use of those data (Sebastian-Coleman 2013). More specifically, the proposed framework helps to clarify answering what (data quality dimensions), where and when (data quality context), and why (data quality focus) of the entire data quality process. While these expectations are not objective and can vary widely among the broad range of potential NEON data users, there are dozens of data quality attributes that can be measured, reported, and assessed by users. These attributes can be directly measured by NEON staff as well, and are summarized as **data quality dimensions** (from Sebastian-Coleman 2013):

1. **Completeness**: the expected data exist and are complete according to pre-defined characteristics (e.g., all relevant attributes are measured, and the amount of data collected meets the expectations articulated in NEON Science Design documents).

2. **Timeliness**: data are collected, processed, and delivered at the expected time according to a set schedule or when an event occurs.
3. **Validity** (may also be referred to as Plausibility in some NEON documents): data conform to the expected syntax, allowable type (string, integer, date etc.), ranges, or other pre-defined rules.
4. **Consistency**: the absence of variance or change in comparison to some pre-defined expectation.
5. **Integrity**: data contain all relevant relationship linkages (e.g., no orphans or missing child records).

Where and when data quality is controlled and assessed is just as important to consider as *how* to measure quality and is referred to as the **data quality context**. At NEON, the following contexts should be familiar to experienced staff:

- **Pre-Collection QA/QC**: activities that take place prior to data collection, aimed at maximizing data collection consistency – e.g., protocol training, calibration for field staff collecting data, etc. For example, field staff may calibrate phenophase evaluation or estimating percent cover.
- **Collection QA/QC** (or “field QA/QC”): activities that take place during or immediately after data collection, but before leaving a field site, aimed at maximizing data validity and completeness.
- **Post-Collection QA/QC** (or “office QA/QC”): activities that generally take place after field collection, and are designed to maintain data completeness, sampling timeliness, data validity, and between bout observation consistency.

Measuring multiple data quality dimensions simultaneously is important in assessing the quality of underlying processes of data collection within an organization. These are referred to as a **data quality focus**, of which the OS subsystem is primarily interested in or focused on:

- **Referential Integrity (validity and integrity)**: the absence of duplicate, orphaned, and/or ‘childless’ records from datasets.
- **Process Quality (completeness and timeliness):** the presence of all expected data and/or samples within a well-defined time interval.
- **Data Plausibility (validity and consistency):** a qualitative assessment of whether data are “reasonable” or not. Data Plausibility issues and methods are NOT addressed in this document, but should be documented within protocols as a “Data QA/QC Checklist” (as indicated in **SOP D**).

3.2 Data Quality Review Workflow

Mobile applications are the preferred mechanism for data collection and entry. The first stage of the process is to review critical field metadata values soon after collection, preferably before leaving a field site. Critical metadata values, such as plotID and collection date, are important data that cannot be easily inferred and/or corrected after staff leave a field site, and include data that pass application validation rules but could be ***inaccurate*** or ***incorrect*** in some way (e.g., the wrong plotID was accidentally selected; see **Box 1** and **SOP A.3** for specifics).

It is recommended that field staff use digital tools such as Shiny applications created and managed by Field Science and Headquarters staff scientists to detect, report, and correct issues. However, note that Shiny applications complement but do not replace protocol-specific QAQC Checklists. If a Shiny QAQC application does not exist for a given data product, it is recommended to consult the QAQC Checklist and to analyze data with filters and Pivot Tables in Microsoft Excel to summarize patterns in large datasets. Viewing raw data can be useful but is the least desirable option because it's easy to overlook errors when faced with hundreds of data values.

Referential quality checks are concerned with maintaining the "referential integrity" of datasets by ensuring that ingested records are free of potentially misleading data (e.g., duplicate records with slightly different data values are confusing to end users) and have concrete relations to relevant records (e.g., records have all necessary metadata). Duplicate records are a major concern as even a single duplicate record will cause an entire batch of data to fail upload for many NEON data products. Duplicate records can be identified as the presence of two or more records in a data set with the exact same sample identifier.

Ideally, field staff review data for referential quality (e.g., duplicates) once an entire bout's worth of data have been entered into (or collected with) a protocol-specific application. The exception is for bouts that extend for long periods (i.e., bouts longer than 2 weeks), in which case data reviews should occur before the bout is completed. At a minimum, data should be reviewed before the load delay is reached for a data product, as this simplifies the data editing and record deletion process; see **Section 3.3** below *Timing ("load delays")* for more details regarding load delays. Technicians use the Magpie data viewer application to conduct QA/QC tasks that are standard across multiple OS protocols. Magpie can be accessed via the Data Management page of the Sampling Support Library (SSL), or via the NEON Aviary, and contains instructions on how to use the interface, see **SOP E**. Technicians assess the results of each query conducted with Magpie, then determine whether corrective action needs to be taken, such as submitting record deletion requests or correcting data, see **SOP F** and **SOP G**.

Identifying process quality issues allows NEON to improve data collection procedures over time while also ensuring that all expected data/samples are collected and published. Incomplete data sets can be particularly detrimental to scientific end users as fewer samples or data points decrease the ability to detect significant ecological changes or trends. Analyzing process quality includes assessing whether domains and field staff are correctly implementing NEON protocols and encompasses 'bout-level' metrics such as sampling completeness and sampling timeliness, as prescribed by protocols. Quantitatively analyzing data for process quality issues means checking that:

- Expected number of field records are present per site and protocol ("Field Sampling Completeness")

  - You should always have the expected number of field records even if sampling was cancelled or incomplete if **samplingImpractical** records were created as required.

- Expected number of records are present for all SOPs in a protocol per sampling location, bout, and protocol ("Protocol Sampling Completeness").

Technicians should use the Clockwork Shiny application, found in the NEON Aviary, as a final check of field and lab sampling completeness. Clockwork generates a high-level summary of all records created for the selected domain and protocol within a given time-frame and is typically used during the monthly schedule status update process. For most protocols, Clockwork groups Fulcrum records by eventID to allow for a quick check that all expected records are present. Clockwork summaries can reveal tablet sync failures, mis-entered plotIDs or eventIDs, and missing field, lab, or sampling impractical records. Details on using the Clockwork application can be found in the OS Monthly Activity Status Tracking SOP (linked via the 'About' tab in the Clockwork app).

Finally, domain staff should use existing QA/QC checklists for assessing protocol-specific data quality criteria. Most all sampling protocols have a companion QA/QC checklist document detailing key data attributes to review before data are ingested. These checklists can be found on the landing page for the respective protocol on the SSL. Many checklist items describe important aspects of a data product's quality that are not, and may never be, detected by either the OS Parser or protocol-specific Shiny QAQC applications. For example, the Parser cannot inspect the photographic quality of images collected for the measurement of Leaf Area Index, thus the QA/QC checklist highlights the following checks:

- Are images in focus?
- Are images over/under exposed? If exposure is acceptable, are ISO and f/stop values in acceptable ranges?
- Are NEON staff visible within images?

Checklists should be used by staff at all levels throughout the data review process, and are intended to ensure consistency, to convey best practices, to help avoid poor decision making, and to sustain patterns of success.

3.3 Data Validation and Ingest Process

Validations

Field staff must understand the process and timing of how data are transferred, or "ingested", from data entry applications to the NEON Data Portal, as digital records are only directly editable for a limited time frame. Automated data validation checks are documented in a data product's "Ingest Workbook", which details a two-stage process. The first round of data validation occurs directly within Fulcrum applications. Data that do not meet the expectations of these rules are generally prevented from being saved and synchronized with the Fulcrum cloud database.

Given that the first round of validations within Fulcrum applications occurs in the field and without internet connection, the Fulcrum validation rules are limited to checking data within a single parent record, and if applicable, to child record(s) within that parent record, thus rarely checking for referential integrity issues. For example, without internet connection these validation rules cannot check for duplicate sampleID or barcode values across multiple parent or child records.

A piece of software known as the "OS Parser" (or "parser" for short) carries out the second round of validations and makes up for some of the limitations of the Fulcrum rules. The parser executes several referential integrity checks to prevent duplicates and orphaned data from entering the database, in addition to checking the Fulcrum rules again (**Table 1**). This second check of Fulcrum rules is done to ensure that the applications have been designed and implemented correctly by application developers.

Table 1. OS Parser Data Validation rules and associated error messages when incoming data do not meet requirements.

Method	Checks for…	Error Message
Geographic Range Constraint (integrity, validity)	Valid plotID names for a specific protocol are selected. Sampling cannot occur at certain types of plots or transects.	NAMED_LOCATION_TYPE
Sample Identifier Check (integrity)	Whether sample identifiers are unique within the system and/or whether downstream sample identifiers correctly match upstream identifiers e.g. checks for duplicate and orphan records. • 'ReferenceCount' indicates duplicates within the batch of records being ingested. • 'Sample already exists' indicates a record attempting to ingest is a duplicate of a record already ingested. • 'Sample does not exist' typically indicates a required upstream record is missing.	'ReferenceCount' 'Sample already exists' 'Samples does not exist'
Barcode Check (integrity)	Whether scanned barcodes are unique, whether a barcode has been associated with more than one sample type (e.g., a barcode scanned in ALG and again in CFC would fail validation)	'Has different tags' 'Has different barcodes' 'Configuration error changing tag'
Taxonomic Value Constraint (validity)	Only animal or plant taxa that have been identified to exist within a domain's geographic boundaries are selected.	ELEMENT_OF
Required Fields (completeness)	Whether required fields have been filled out; conditionally dependent on data entered, whether certain fields have been left blank. Fields are usually required as a way of delivering a minimum usable data product for end users (e.g., many data are unusable if collection dates are missing).	REQUIRE, REQUIRE_NULL

Method	Checks for…	Error Message
List of Values Constraint (validity)	Whether selected data values match against a pre-specified list. More of a check on the application's design because end users cannot enter custom values.	LOV
Numeric Range Constraint (validity)	Whether entered values fall within a specified range.	GREATER_THAN, LESS_THAN

Timing ("load delays")

Every record entered into an application is "stamped" with a creation date (**Figure 1**). Once a record is synchronized with the cloud database, a "load delay" countdown begins that starts from the record creation date. The load delay defines how long a record can be edited by field staff. Load delays vary from 14 to 365 days, and protocol-specific load delays are available to view per application via the Magpie Shiny application. The Magpie application link, like links to all OS Data QAQC Shiny applications, is available from The Aviary (https://aviary.gcp.neoninternal.org/).

Once the difference between a record's create date and the current date exceeds the load delay, the OS Parser attempts to ingest the data. Records that "pass" parser validation are then locked, and the data eventually appear on the NEON Data Portal. Records that "fail" validation generate error messages that are collated across protocols and distributed to FSCI and HQ staff by the Canary Shiny app (see **SOP H.3**).

Field staff can view, but not directly edit, records that are locked and properly synched. However, if there is a version of a locked record on a tablet that wasn't properly synched after creation and re-opened on that tablet, the Fulcrum application can revert the record's load status back to NONE when the tablet is synched. If a record's load status reverts back to NONE after already loading, parser errors will result as there will be duplicate load attempts by the parser.

The same error messages for data issues are provided until they are addressed. Failed records are usually corrected by field staff; however, there are some failures that require HQ staff to correct. Changes to locked and loaded data records may be necessary if field staff determine the need for updates (e.g., a valid taxonID was selected, but is known to be the incorrect sub-species for a particular site), or if field staff detect data errors not caught by the parser (e.g., a valid but incorrect collection date was entered). These updates must be requested by Field Science staff via the Magpie application (i.e., "Update Requests") and are handled by HQ staff.

Difficulties

One major feature of the OS data ingest system is that records are not ingested individually; instead, records are ingested in 'batches' or 'sets' referred to as 'load groups'. Load groups contain all the records from a suite of related applications for a given domain. This means that a single record fail results in all related records within and across applications failing at the same time (all records will also receive a load_status of "PARSE_FAIL", which can be misleading for troubleshooting). All related records are rejected as there may be duplicate records present that need to be resolved or deleted before the data can be ingested.

OS data are sometimes heavily interrelated across field, domain lab, external lab, and shipping applications. Since metadata are inherited/passed across these applications, errors in one application may cause the Parser to flag records in other linked applications. This inter-application complexity can make resolving parser errors difficult if one does not understand what the Parser is checking for or how metadata are related across applications. This is why it is important to have fully trained staff members perform data QA/QC activities. Experienced staff understand the data structure and know where to obtain the resources to effectively and efficiently correct data issues.

Finally, post-parser "Update Requests" can be very time consuming and difficult to work through because records can no longer be edited through Fulcrum applications. It is easier to complete QC and make updates to data before the load delay expires!

As a rule of thumb, experienced Field Science staff should spend no more than 1 hour trying to determine the root cause of any given parser error (or set of related parser errors). If the root cause and required steps to resolve the error(s) remain unclear after 1 h of due diligence, submit an Incident via ServiceNow and engage the Science team for assistance.

Standard Operating Procedures (SOPs), in **Section 7** of this document, provide detailed step-by-step directions, resources, and best practices for implementing this procedure.

The value of NEON data hinges on consistent implementation of this protocol across all NEON domains, for the life of the project. It is therefore essential that field personnel carry out this protocol as outlined in this document. In the event that local conditions create uncertainty about carrying out these steps, it is critical that technicians document the problem and enter it in NEON's problem tracking system.

Quality assurance is performed on data collected via these procedures according to the NEON Science Data Quality Plan (AD[04]).

4 SCHEDULE

4.1 Data Entry and Review

It is preferable to use mobile devices and NEON data entry applications to capture data electronically in real-time whenever possible. Data collected on a mobile device should be synchronized **as soon as possible.**

Data collected on **paper datasheets should be entered within 14 days of collection** for protocols with long bouts (e.g., Vegetation Structure) *or* within 14 days of the end of a bout for protocols with short bouts (e.g., Mosquitoes).

All digital records, whether originally recorded with a mobile device or paper datasheet, must be reviewed and edited **before** the load delay occurs. Load delays per protocol are defined on the "About" page of the Magpie application: https://fulcrum-qa.gcp.neoninternal.org/

The following tasks should be completed in descending order of priority **within 14 days of collection or the end of a bout**:

- Field datasheets and data entry application records should be quickly reviewed for critical errors by technicians on a daily basis (**SOP A.4**, step 2). Critical errors are incorrectly recorded sampling locations and sampling dates that cannot be accurately corrected after leaving the field.
- Sync mobile device data when a web/data connection is available (**SOP A.5**)

The following review tasks should be completed in descending order of priority and completed within the **load delay period**:

- Perform referential integrity reviews (i.e., check for duplicates) for a given protocol before data are ingested and locked (**SOP F**).
- Perform a process quality review for a given protocol at the end of a sampling bout and field season (**SOP G**).
- Perform additional quality control procedures outlined in protocol specific "Data QA/QC" checklists (**SOP C**).
- Manually enter paper data (where applicable), starting with the earliest collection date. *Every paper data entry bout should include paper datasheet data quality checking* (**SOP B.3**).

Scheduling considerations

Effective completion of data QA/QC tasks can take significant time; therefore, it is important to schedule for and allow ample time to complete these tasks. It is important to set aside time:

1. At the end of the field day to QC data, and
2. After the bout/end of the week/after lab processing/etc to QA the data.

Time is scheduled for data QC/QA activities after each scheduled field or lab sampling activity per protocol and can be found on the master schedule on the NEON Sharepoint.

5 SAFETY

This document identifies procedure-specific safety hazards and associated safety requirements. It does not describe general safety practices or site-specific safety practices.

Personnel working at a NEON site must be compliant with safe field work practices as outlined in the EHS Safety Policy and Program Manual (AD[01]) and Operations Field Safety and Security Plan (AD[02]). Additional safety issues associated with this field procedure are outlined below. If an employee witnesses any unsafe conditions or uncontrolled hazards that present an imminent danger, they should immediately take action to stop work and report such conditions to their manager. Employees must also report all workplace injuries, illnesses, incidents, or releases to the environment as soon as possible, regardless of the severity.

6 PERSONNEL

Technicians entering data should familiarize themselves with the protocol, the mobile application(s) in which data will be entered, and with the backup paper datasheets. Lead field staff should take a guiding role in directing all data management activities, from ensuring mobile applications are used properly, to paper datasheet data entry and data quality checking (DQC), and to data quality review.

6.1 Training Requirements

All technicians must complete protocol-specific training as required in the Field Operations Job Instruction Training Plan (AD[03]). Additional protocol-specific required skills and safety training are described here.

Field staff should have basic knowledge of the software used to host data entry applications and should have familiarized themselves with the relevant data ingest sheets and protocol-specific applications involved in their work.

6.2 Specialized Skills

Prior experience viewing, sorting, filtering, and manipulating data in spreadsheet software such as Microsoft Excel is desirable but not required.

7 STANDARD OPERATING PROCEDURES

SOP Overview

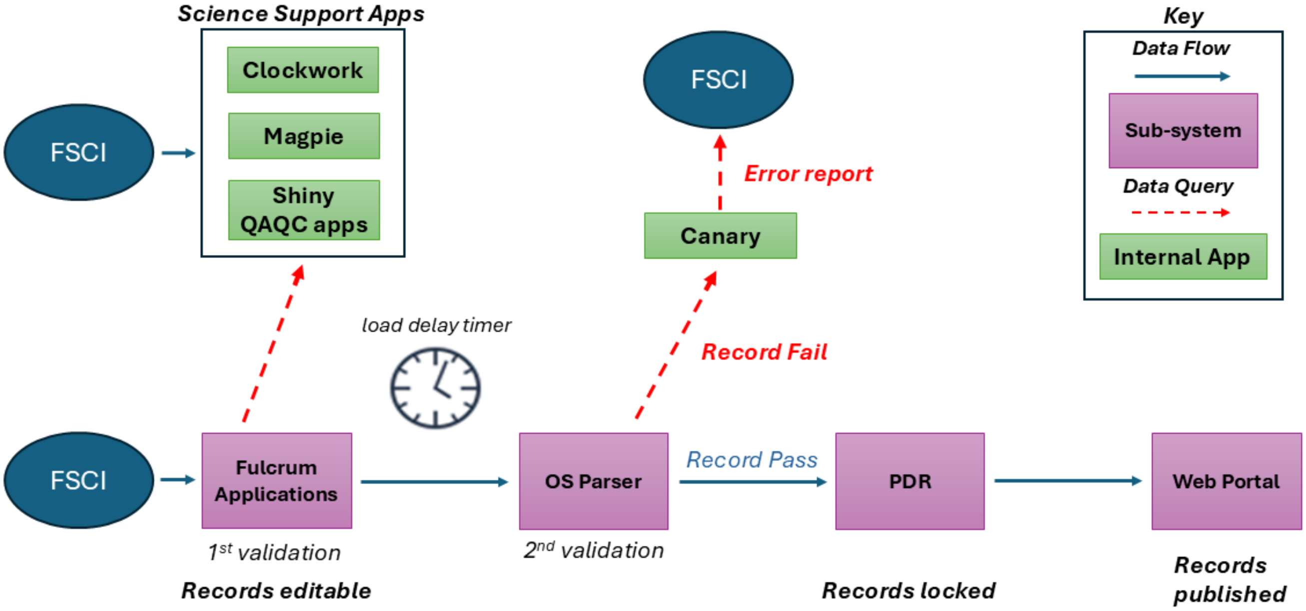


Figure 1. Observatory System data ingest process. Records begin moving through the ingest process once the "load delay", or number of days since record creation, is exceeded. Data are automatically validated twice in the process, before being stored in the Processed Data Repository (PDR) and accessed via the NEON Data Portal. Data for specific protocols are manually validated with various "Science Support Applications". The Canary Shiny app analyzes and distributes error messages to Field Science and HQ staff when records fail to pass through the OS Parser.

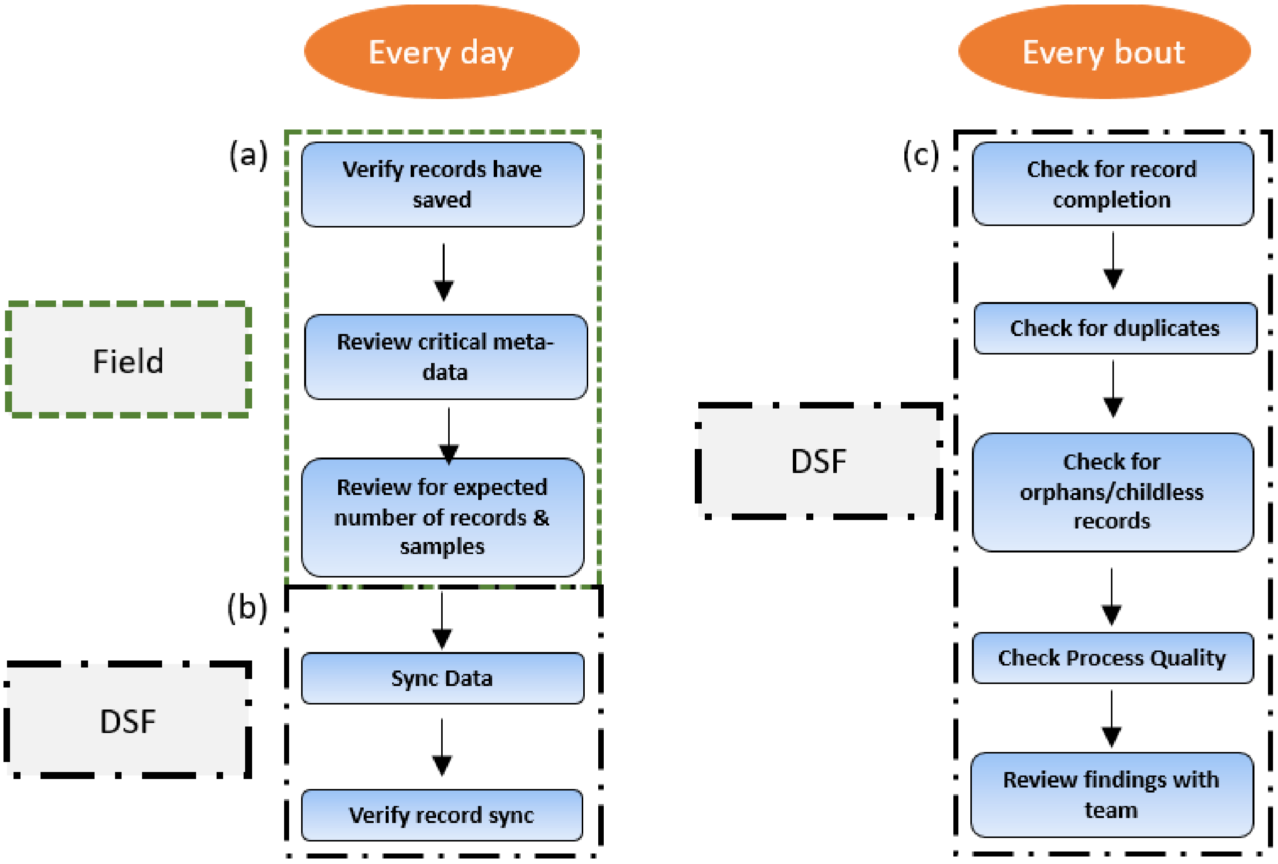


Figure 2. Workflow diagram for reviewing data quality per day and per bout. Dashed boxes represent *where* data should be reviewed, orange circles represent *when* in the workflow review steps should happen.

- **SOP A**: General Data Collection and Data Quality Workflow for all Protocols
- **SOP B:** Paper Datasheet Quality Checking
- **SOP C:** Using Checklists for Quality Control
- **SOP D:** Quality Control Shiny Applications
- **SOP E:** How to Use the Magpie Data Viewer Application
- **SOP F:** Referential Integrity Data Quality Review
- **SOP G:** Detecting Process Quality Issues
- **SOP H:** Parser Error Resolution
- **SOP I:** Shipping Manifest Error Correction Workflow

SOP A General Data Collection and Data Quality Workflow for all Protocols

Ensure that the person conducting data entry has read through the training materials associated with the protocol-specific data entry application, and that they have practiced entering data using the *Training* version of that application – i.e., the [CERT] version. A training checklist for data entry is provided in **Appendix A**. Staff entering data for the first time should work through the checklist, in combination with reading the SOPs below, to ensure an understanding of the NEON OS Data Quality Workflow.

A.1 Mobile Device for Data Entry

Data entry in the field should only be done with a tablet. Collecting data on field iPhones is not supported for several important reasons.

Reasons field iPhones are not used for data collection:

1. **Development Environment:** The Fulcrum application developers on the Science team develop and test all Fulcrum applications on iPads running iPadOS. Fulcrum applications are not tested on field iPhones running iOS.
2. **Troubleshooting Limitations:** Fulcrum Developers do not have access to iPhones for troubleshooting purposes, which limits the ability to address issues effectively.
3. **Testing Environment Challenges:** Creating a true testing environment or process is challenging due to the variety of phone versions that may exist for FSCI at any given time.
4. **Safety Concerns:** NEON Fulcrum applications are designed to run in airplane mode, which is not conducive when using Fulcrum on an iPhone. The iPhones are provided for communication and safety and always need to be online.
5. **Data Synchronization Issues:** NEON Fulcrum apps are designed and tested with the fundamental assumption that the application is on an iPad and the internet is not available; internet availability affects the timing of certain events within the application structure.

DO NOT use NEON Fulcrum applications on personal devices or iPhones. Instead, use the field iPhones only as a backup alternative to paper data sheets, in case an iPad fails.

Additional Resources:

If there are concerns about not having enough tablets for certain protocols, work with IT in advance to obtain additional tablets.

A.2 Personnel-List Fulcrum Application Procedures

The Personnel-List Fulcrum application houses important metadata for any employee at NEON who records and/or measures data collected for the project. It is important this information is always accurate and up to date for new and existing NEON employees. The application incorporates an ORCiD, a unique, 16-digit personal identifier that is connected to an individual.

To create an ORCiD go to: https://orcid.org/register, then create an account using your Battelle Ecology email and preferred first and last name.

To create a new Personnel-List Fulcrum application record:

- Create a new record and record the following:
    - domainID
    - Preferred name
    - Email address
    - 16-digit ORCiD

This record is constrained by domainID, and feeds into the "measured by" and "recorded by" fields in other applications.

Occasionally, employees are sent to work in other domains and/or may help process or ship other domain's samples. When this occurs, it is necessary to *create a new record* in the Personnel-List Application for the employee, using the domainID where you/they are helping.

- Once work has been complete, be sure to set the record to 'inactive.'

NOTE: The data collection apps filter to available personnel based on domainID and 'active' status.

A.3 Fulcrum Data Entry WebUI Training Procedures

1. It is best practice to connect to the NEON network (use of VPN may be necessary at remote sites) when working on NEON job duties. Use only supported web browsers for data entry – i.e., Google Chrome, Mozilla Firefox, or Microsoft EDGE. Using an unsupported browser may result in lost data. Supported browsers may change in the future.
2. Login to https://www.fulcrumapp.com/ and navigate to the appropriate, protocol-specific application. Links and application names can be found on the protocol-specific pages of the Sampling Support Library.
3. The person conducting data entry must have practiced entering data using the *Training* [CERT] version of that application.
    a. **Training Applications (CERT)**
        i. NEON provides a copy of each Fulcrum data entry application for the sole purpose of training. These are labeled with the application name plus "CERT" for "certification". Technicians should use CERT applications in concert with app-specific Fulcrum Manuals

to enter test data for training purposes, as the data from these apps are not ingested into the NEON data repository.

ii. New technicians must read the Fulcrum Manual and practice data entry in CERT applications *for each protocol where they plan to enter data*. Domains should consider generating test data that highlight common local data entry issues to assist with training.

iii. Entered training data should be exported as a .CSV and reviewed by experienced field staff.

4. Once training requirements are met for that application/protocol, data can be entered into the protocol-specific *Production* (PROD) version of the data entry application.

    a. **Production Application (PROD)**

        i. NEON provides Fulcrum PROD data entry applications for all field and lab data entry. Data entered into PROD apps are ingested into the NEON data repository and published on the NEON data portal.

        ii. It is difficult to locate and fix incorrectly entered data once they have been locked and transitioned to the NEON PDR. *Extra time and effort should thus be devoted to careful data entry and data review before the load delay expires*.

5. Data entry applications are customized for each individual protocol. Detailed training for each protocol interface is available in the 'Supporting Documents' section of the protocol page in the SSL, but here are some general rules:

    a. Sync mobile devices often in order to ensure that up-to-date versions of all applications are available.

    b. Remember that most of the applications have a 'nested' structure, meaning that some of the higher-level information (plotID) is entered once but applies to a group of samples.

    c. Data entry through a data entry application is a multi-step process:

        i. The 'Create' button (+) will allow you to create a new record.

        ii. Once all required information about that record has been entered, use the '**Save**' button (✓) to save the data and store it locally.

    NOTE: Once records are created, saved, and synced, they cannot be deleted without submitting a request to NEON HQ. Nested child records may be deleted if they have not synced.

        iii. The data entry application will allow you to review and edit data you have recorded until the load delay expires and the data are ingested into the NEON data repository. Review can be accomplished by clicking on the 'Quick View' option for a specific record, while editing can be accomplished using 'Edit.'

   iv. Use the **Status** column to identify records that have been flagged as needing further attention – they will be highlighted in red, orange, or other colors.

A.4 Every Day: Before Leaving a Field Site

Context: Collection QA/QC

The component of the Quality Workflow that is implemented daily before leaving the field site is shown in **Figure 2a**. Steps include:

1. Verify that entered data have been saved on the mobile device.
   a. For parent-child records, be sure to save the **parent** record. Saving child records does NOT mean that a parent record has been saved.

NOTE: It is a common misunderstanding that the data entry application will automatically save any entered data. A person who is not the data recorder should double-check that the recorder has properly saved all data before leaving a field site. All too often, data are entered and then discarded by accident only for the data loss to be recognized after leaving a field site.

WARNING: Records can be saved in a temporary state called a "draft" when one or more required fields are left blank (appears as a yellow pencil icon on mobile devices). ***Draft records are never synced to the cloud*** and should be completed as soon as possible to prevent data loss – i.e., the draft record will only exist on the device used to collect data.

2. Review critical metadata fields for accuracy and completeness. This step is important to prevent incorrect, but technically valid data from being entered (**Box 1**).
   a. Check for valid and correct *sampling location* values (e.g., siteID, plotID, clipCellNumber, trapID, etc.)
   b. Check for valid *sampling date and time* values (e.g., setDate, collectDate, setTime, collectTime, etc.)

   NOTE: If a field is edited on the parent page of a record, the change will not automatically propagate to the child records. Child records need to be re-opened and saved to receive the update.

   c. Check for valid *event identifier* values (e.g., weekBoutBegan, yearBoutBegan, eventID, etc.)
   d. Check that the expected number of records has been created and saved on the mobile device.

   Examples:

   - For many data entry applications, one parent record is often created per sampling location.
     - If the field crew is expected to sample 10 mosquito traps in one day, there should be 10 mosquito records on the mobile device.

- In other data entry applications, one parent record represents a single sampling location, and the child records represent sub-samples within that same location.
    - If a field crew is visiting three plots to take digital hemispherical photos there should be:
        - Three parent records (one per plot).
        - Either 12 or 24 child records per parent record (12 or 24 photos taken per plot).

Box 1. Inaccurate but technically valid data.

Definition: Inaccurate but technically valid data are entered data values that pass application validation rules but are mis-recorded or factually incorrect. Inaccurate data records are particularly troublesome because while they can often be identified as incorrect, how to correct the data is not always obvious or possible. Delaying the data review process leads to the loss of useful information from field staff that might help rectify errors.

- ***Example***: Data recorded for plot "X" when observations are actually from plot "Y".
    - Actual plotID = "CPER_012"; recorded plotID = "CPER_014"
    - *Results in*…a data set with fewer records than expected AND duplicate records; lower process quality and spatio-temporal data gaps that reduce statistical power.

- ***Example***: A recorded tree diameter that is within range but an order of magnitude off from the actual measurement.
    - Actual Tree Diameter = "12 cm"; Recorded Tree Diameter = "120 cm" (min value = 1 cm, max value = 400 cm)
    - *Results in*…a data set with more outliers; reduced confidence in the plausibility of the data; inaccurate plot-level biomass and productivity estimates.

3. If field samples were collected:
    a. Check that the number of samples matches the number of digital records created.
    b. Check a subset of sample labels and/or barcodes for accuracy.
    c. At a minimum, check 10% of the total samples or 10 samples (whichever is greater).
        - For samples with barcodes, the barcodes can be scanned with the mobile device via the "Search" function or using a handheld barcode scanner.
            - Records with a matching barcode will appear in the record list *if they exist.*
            - **If no records** are returned after scanning a barcode, this means the barcode wasn't initially scanned correctly or at all, and you should find the appropriate record and ensure that the barcode is scanned with that record.
            - **For records that appear** after scanning, verify that the record's metadata match the human readable information on the sample.

  - ○ **If more than one record appears** after scanning, a barcode has likely been scanned more than once and associated with different unique samples. This is considered a duplicate record error and should be resolved before data are loaded.
- For non-barcoded samples, the information on the sample should match the metadata in the record.

A.5 Every Day: Returning to the Domain Support Facility or Field House

Context: Post-Collection QA/QC

The component of the Quality Workflow that is implemented daily upon returning to the domain support facility or Field House is shown in **Figure 2b**. Steps include:

1. Sync the mobile device's data.
   a. Be sure that the device is connected to a secure Wi-Fi network or has a data connection before attempting to sync.
   b. The synchronization mechanism can fail for multiple reasons, meaning that data are not fully transferred from the mobile device to the cloud database.

NOTE: Un-synced draft records are isolated to the device on which they were collected. They will not appear on another device or in a web browser because the data have not been properly transferred.

⚠ **IMPORTANT**: In isolated cases, if a LOADED record is re-opened on a tablet that was not synced properly after creation, then the Fulcrum application can roll back the record to have a load status of NONE and thus the parser will attempt to re-load the record resulting in a duplicate record!

2. Verify that all mobile device data have been synced: Use a web browser to check that records have transferred from the mobile device to the cloud.
   a. Navigate to the appropriate application (application names are identical on both the mobile device and the web browser).
   b. Sort the data table by the "Created date" column (this is the date and time a record was created) by selecting "Sort Dec -> Jan".
   c. The most recently created records will appear at the top of the table.
   d. Locate and identify the records that should have been synced from the mobile device.
   e. If all expected records do not appear in the table, double-check the mobile device to see if the syncing process failed and try to sync the device again.
3. If physical specimens were collected:
   a. Transfer samples to the appropriate storage containers and locations.

4. Record this information in a sample inventory (see SOP A.6 below for more information).
    a. Verify that the number of samples stored matches the expected number of records.

A.6 Every Bout: Data Quality Assurance

Context: Post-Collection QA/QC

This section gives a brief overview of the rest of the data quality review process, the components of which are shown in **Figure 2c**. Expanded step-by-step details are provided below in **SOP E** and **SOP F**.

1. Check that all entered records have been completed.
    a. All data entered into each record:

       NOTE: To align with optimal field workflows, certain applications allow users to save records without entering key metadata. These data values should always be recorded as soon as possible even if they are not specifically required in the application, else records may be rejected by the ingest system.

       Example: Mosquito Collection ("MOS") application records can be saved without a **collectDate** or **collectTime**, however records ingested without these values will be rejected by the OS Parser.

    b. All related records have been entered (for protocols with multiple SOPs and data entry applications).

       Example: Herbaceous Biomass and Productivity clip harvest sampling ("HBP") has two primary applications: Field and Lab. One Lab record should exist for each Field record where targetTaxaPresent = "Yes".

    c. Follow additional protocol-specific instructions from the "Data Entry and Verification" SOP within each protocol and the protocol-specific QC Checklist linked via the SSL.
    d. Check for duplicate records: Use the Magpie application or the protocol-specific Shiny QAQC application to find and resolve duplicate records (**SOP F.1**).
    e. Prevent orphan records from being created: The parser will detect and reject orphan records.
        - Some Shiny QAQC applications can help detect orphan records; however, this capability does not exist for all protocols. In this context, field staff should implement procedures that prevent creation of orphan records (**SOP F.2**).
2. Perform quantitative process quality review:
    a. Check that all expected digital records for a given protocol and bout exist.
    b. Check that all expected sampling locations for a given protocol and bout have been visited.

3. If physical samples were collected:
    a. Ensure that samples are organized and stored in appropriate locations.
    b. Verify that any human-readable sample labels exactly match the corresponding sampleIDs in Fulcrum.
    c. Enter sample information into a sample inventory.
    d. If samples are to be stored long-term or shipped to an external lab, using the Domain Support Inventory Fulcrum application is recommended for creating sample inventories. This app collects sample metadata from scans of sample barcodes to create inventory records for samples stored at the domain support facility for longer than 7 days.
    e. The Domain Support Inventory app doubles as a QC of sample labels and Fulcrum records:
        - A sample barcode must be properly entered in the upstream Fulcrum record for it to load into a Domain Support Inventory app record.
        - Inventory app records can be easily checked against upstream Fulcrum records to ensure that all expected samples are accounted for, and that barcodes, sample types, and sampleIDs in Fulcrum match the physical samples.
    f. If a storage container barcode is used, Inventory app records link directly to the Shipping: Shipment Creation Fulcrum app to generate shipping manifests.
    g. For additional details on using the Inventory app, consult the “Manual for Fulcrum Applications: Domain Support Inventory” linked in the Shipping section of the SSL.

    NOTE: As with other linked Fulcrum applications, if sample data are updated or changed in the upstream Fulcrum record, those changes will not transfer automatically to the Domain Support Inventory application record. <u>The inventory app child record for an updated sample needs to be deleted and re-entered</u>.

4. Perform additional quality control review outlined in protocol specific “Data QA/QC” checklists (**SOP D**).
    a. Check dataset attributes that are not detected by the parser or by protocol-specific Shiny QAQC applications.

A.7 Every Bout: Review Remarks

A 'Remarks' field is usually present in the data recording applications to allow Field Science staff to comment for end users about a particular circumstance regarding the collection of field or laboratory data. Because remarks are published to the end user, the remarks field should be written professionally and only used to communicate pertinent information to an end user that isn't captured elsewhere within the data record. Remarks should not be used for internal information such as placeholders, reminders, or notes for field staff, unless a separate "internal remarks" field exists in the app. **Table 2** outlines some examples of useful remarks that should be included in a record and those that are not useful and should be omitted.

Table 2. Example remarks, both relevant and non-relevant for end users from various protocols.

Subsystem	Protocol	Remark	Useful (Y/N)	Explanation
AOS	INV	Partial sample collected with small sieve	N	Unclear – not enough detail
AOS	INV	Sediment in 19.5m tow. Tow taken at 19m instead	Y	Informs end user depth is different than expected
AOS	APL	Crispy brown morphospecies	N	Redundant – recorded in morphospecies app
TOS	MAM	Bad door	N	Internal note – irrelevant to end user
TOS	MAM	Nontarget: amphibian	Y	Provides end user data not available elsewhere
TOS	MOS	Catch cup found on ground	N	Redundant – recorded in CatchCupStatus
TOS	MOS	Parasitic mites present on mosquitoes within catch cup	Y	Provides end user data not available elsewhere

SOP B Paper Datasheet Procedures

Paper datasheets can be used as a backup data recording method in cases of adverse field conditions, equipment failure, or missing equipment. However, it is best practice to enter data into a mobile device. Data recorded on paper should be entered within 14 days of collection.

B.1 Every Day: Review Field Datasheets before Leaving the Field

1. Review the field datasheets for completeness:
   a. Check BOTH sides of the datasheets for extra taxa or notes.
   b. Be sure to clarify and annotate any shorthand notes on the datasheet; don't assume the shorthand will be meaningful to staff in the future.
   c. Finally, check that all required fields/columns have been filled out.
2. Protocol leads should review critical metadata values on datasheets at the end of the sampling day, similar to steps 1 and 2 outlined in **SOP A.4**. Critical metadata fields should be reviewed for accuracy and completeness (see **Box 1**):
   a. Check for valid and correct *sampling location* values (e.g., siteID, plotID, clipCellNumber, trapID, etc.).
   b. Check for valid *sampling date and time* values (e.g., setDate, collectDate, setTime, collectTime, etc.).
   c. Check for valid *event identifier* values (e.g., weekBoutBegan, yearBoutBegan, eventID, etc.).
   d. Check that the expected number of rows has been recorded.
3. If physical specimens were collected:
   a. Check that the number of samples matches the number of rows on the datasheet.
   b. Check all sample labels for accuracy.

B.2 Every Bout: Data Entry Procedures

Enter data captured on paper datasheets into the applicable Fulcrum application(s) using the procedure outlined in **SOP A**.

All bouts of data entry must be accompanied by the Paper Datasheet Data Quality Checking procedure, outlined below. <u>This procedure must be conducted before the data entry bout is considered complete.</u>

B.3 Every Bout: Paper Datasheet Quality Checking

1. Field technicians should quality check a minimum of 10% of the entered data records or 10 records, whichever is higher. These targets are either on a per sampling/data entry bout or per

SOP level (clarified below). Data quality control is accomplished by comparing entered values to the original paper datasheet values.

   a. **Per sampling or data entry bout**: Data quality checks should be carried out for each field sampling/data entry bout during a field season. This is done so that errors in data entry and problematic data entry habits can be detected and corrected.

   b. **Per SOP**: the number of records reviewed should be considered per protocol SOP rather than all protocol records totaled together.

      ***Example**:* After a sampling/data entry bout, a domain has 40 records from Litterfall SOP C (Field Sampling) and 390 records from Litterfall SOP D (Lab Processing – Dry Mass) for bout 3 of the season. Staff should therefore review 10 records from SOP C (because 10% of 40 is only 4 records) and 39 records from SOP D (because 10% of 390 is 39).

2. After a dataset is transcribed, it can be checked in one of two ways – either by exporting as a spreadsheet directly from the application or using the NEON custom data viewer "Magpie" (linked via the Aviary). Both options will provide relatively fast ways to compare entered data to paper datasheet values.

   a. If choosing to export data as a spreadsheet from the application, refer to **Appendix B**.

3. If using the Magpie data viewer, use the instructions provided in the 'About this application' tab to select and filter the records relevant to the bout. Once selected and filtered, the records can be exported in spreadsheet form using the 'Download Query' button. From there, they can be further filtered as described above to facilitate data quality review.

4. Using the filtered data, compare the entered data values of each field to the original paper datasheet with one of the following procedures:

   a. **Read Aloud Review**: Data checking conducted by two technicians: one technician should read the values on the original paper sheet aloud, while the other visually checks against the electronically entered values.

   b. **Independent Data Review**: If it is not possible for two technicians to conduct data quality review together, then a technician who did not enter the data should perform the review.

   c. **Redundant Data Review**: If a separate technician cannot conduct data quality review, then the technician who entered the data should also visually re-check the data.

      i. It is strongly recommended that technicians employ the Read Aloud Review or Independent Data Review procedures over Redundant Data Review.

5. For any records that have errors, navigate to the relevant data entry application and correct them.

B.4 Discard Paper Datasheets

Once the procedures described in **SOP B.1** through **SOP B.3** have been complete, physical paper datasheets may be discarded/recycled as appropriate.

There is no need to store either physically or digitally.

NOTE: This does not apply to in-house tracker type datasheets that do not correspond to a Fulcrum application. Continue to follow your domain's workflow for storage of these types of datasheets.

B.5 How to Access Legacy Digital Datasheets in Google Cloud Storage

All digital scans of legacy paper datasheets have been migrated to Google Cloud Storage (GCS) for long-term storage and have been removed from domain N-drives. The directions below describe how field science staff can access the files for viewing and downloading purposes.

General notes about GCS storage access

- NEON users should use their personal username@battelleecology.org ECO domain credentials to authenticate and access GCS.
- Google provides an extensive cloud console, the GCP console, to interact with their cloud platform. All NEON users have access to the GCP console, and the console is the recommended GUI tool for browsing and downloading archived data sheets.
- The GCP console is highly suited to browsing GCS buckets and downloading individual objects. It supports folder uploads but only supports downloading individual objects. Tools that can be used to download multiple objects are detailed at the end of this SOP.

How to navigate the Google Cloud Console to access the 'neon-paper-datasheets' bucket

1. Open Google Chrome and sign into Chrome with your NEON ECO credentials – i.e., username@BattelleEcology.org (click the icon in the upper-right corner of the Chrome browser).
    a. You will be prompted to authenticate.
    b. *If you are already logged into Google Chrome with a different profile*, you will need to log out or use a new Chrome window to which you are signed in with your ECO credentials.
2. Use Google Chrome to access the GCS 'neon-paper-datasheets' bucket (GCS Paper Datasheet Bucket).
    a. You should now find yourself within the 'neon-paper-datasheets' *bucket* within the 'neon-prod-longtermstorage' *project.*
    b. The bucket is organized by **domainID**.

3. Navigate to your domain folder, and then to the file you wish to view/download and click on it. That will take you to an informational page on the file. To view or download the file, either click on 'Authenticated URL' or the 'DOWNLOAD' button and it will open in another window.

4. See below for instructions on accessing the console with other tools (useful if you need to bulk download).

NOTE: Alternatively, you can access the console here: https://console.cloud.google.com/. Once in the GCP console you can access the project and bucket by selecting the hamburger menu in the top-left, select 'Cloud storage' and then 'Browser'. Then at the top of the page, select the project 'neon-prod-longtermstorage'. Finally, scroll through the alphabetical list to find 'neon-paper-datasheets' to access the bucket.

Google Cloud Command Line Interface (gcloud CLI)

Google provides an extensive CLI toolset, the gcloud CLI, to interact with their cloud platform. All NEON users can use the gcloud CLI. Gcloud (gsutil) CLI is the recommended tool for interacting with GCP from a command line.

Locally install the Gcloud command line tool (which includes gsutil)

1. Install the gcloud CLI, which is also known as the Gcloud SDK, by following the instructions on this page. https://cloud.google.com/sdk/docs/install
2. The Google Cloud command "gcloud init" will be run at the end of the installer. This will open a web browser. Log in with your ECO credentials via Okta to authorize the Google Cloud SDK Shell.
3. Return to the gcloud init command and select the project you want to use by default – i.e., neon-prod-longtermstorage.
4. You can now use gcloud and gsutil commands.
5. Note that you should periodically run "gcloud components update" to ensure you are using current versions of the tools.

- Quick start on gcloud PowerShell: https://cloud.google.com/tools/powershell/docs/quickstart
- The gsutil command line tool that is included with the gclould CLI is highly suited to interacting with GCP from a command line.
    - The syntax of the commands are very similar to many Unix command line file system tools – e.g., ls, cp, du, rm, etc.
    - It supports uploading and downloading multiple files and folders, and supports wildcarding, filtering, etc.

Cyberduck

Cyberduck is a free Windows and macOS remote file system browser with a GUI that is compatible with multiple protocols, including Google Cloud Storage. Cyberduck is the recommended GUI tool for performing bulk downloads from GCS.

Configure Cyberduck to access GCS storage

1. Install Cyberduck https://cyberduck.io/download/
2. Once the installation is completed, run the Cyberduck application.
3. Click the "+" button on the bottom left to add a bookmark or click on the "Open Connection" button at the top of the screen to connect without bookmarking the connection.
4. Select "Google Cloud Storage" in the top dropdown. Enter the project ID of the project that contains the GCS bucket from which you want to download.
    a. In most cases this will be "**neon-prod-longtermstorage".**
    b. Optionally enter the bucket name under More Options → Path.
    c. Click **Connect.**
5. Cyberduck will open a web browser to authenticate GCP. **Log in** with your username@BattelleEcology.org credentials and click "**Allow**" to allow Cyberduck to authenticate. **Copy the authentication code** from the webpage to Cyberduck and click **Continue.**

Note that Cyberduck does not support authenticating to GCS using a service account, only user account authentication is supported.

SOP C Using Checklists for Quality Control

Incorporating checklists into routine procedures has been shown to reduce the number of serious errors committed in both the aviation and healthcare industries (Clay-Williams and Colligan 2015). Checklists are best suited to situations where performance requires standardization (e.g., reviewing data quality), time is not critical, tasks may be forgotten or skipped, and the number of tasks may be too great to accurately memorize. Checklists are not just a memory aide but should also be considered a tool for discussing important aspects of a procedure with other staff members.

Research indicates that checklists are more likely to be effective and adopted into workflows when teams are actively engaged in the process of developing and adapting them to their particular contexts or work environments (Gillespie and Marshall 2015). As such, NEON protocol authors have not specified uniformly formatted, “one size fits all” data quality checklists for each protocol. Rather, protocol authors identify: (1) tasks that define the minimum standard for delivering high quality data; and (2) effective guidance that supports consistent decision making when minimum data quality standards are not met. In general, minimum data review standards:

- Clearly define the frequency of data review.
- Stipulate when data review must occur during a bout.
- Generate binary outcomes (i.e., pass/fail, yes/no), and
- Provide guidance when expected outcomes are not met.

Each field office should use the minimum data review standards and decision-making guidelines as a starting point for implementing checklists, while also acknowledging and incorporating data quality conditions unique to a domain (e.g., biological soil crust cover estimates are only carried out in D14 and D15).

C.1 Checklist Preparation

1. Consult the protocol’s Data Entry and Verification SOP for key items that have been identified as critical to check.
    a. The protocol specific “Data QA/QC Checklist” is described within the SOP and where it is located on the Sampling Support Library (SSL) is typically linked.
    b. The minimum data standards specified by the document should be effective for each bout unless otherwise specified.
    c. Any additional checks NOT specified in the “Data QA/QC Checklist” are entirely optional.
2. Two documents are provided for each protocol’s data quality review process:
    a. A Word document that lists specific details on how to conduct data review, referred to as the “**checklist**”.

    - The checklist provides step-by-step instructions on how to review data and lists only the key procedures that need to be carried out.
    - Anything not listed on the checklist is not considered to be critical to the data product.
  b. An Excel spreadsheet that contains abbreviated checklist items referred to as the "**worksheet**".
    - The QC worksheet is intended for domain staff to track and communicate where data are in the review process, when review occurred, and who carried out review.
    - QC worksheet documents ***can be modified*** by Field Staff as needed but ***must still contain the QC items listed in the Word document checklist.***

3. Review the various checklist worksheet templates provided and adapt as appropriate for your domain's workflow.
   a. There is not a single right or wrong way to format a checklist.
   b. These templates are examples of the different ways a checklist can be implemented.
4. Create a checklist for your domain by combining the items listed in a protocol's Quick Reference section (or Knowledge Base article) and information from the QC Checklist with a worksheet template.
5. Review the content of your checklist worksheets and implementation strategy with fellow domain staff.
6. Store the digital version of the domain-specific QC Worksheet in a well-known, easy to find location.
   a. Save QC Worksheets to the SharePoint All Collaboration Library and set the Category to 'QC Checklists' to enable easy discovery and retrieval.
   b. Alternatively, save worksheets in an appropriate Microsoft Teams channel using the following naming convention: "moduleAbbreviation_DXX_QCChecklist_YYYYMMDD"
7. Incorporate use of QC Checklists into training for all protocols.

SOP D Quality Control Shiny Applications

Many internal web applications (Shiny apps) have been developed to aid Field Science staff with quality control processes. These QC applications help to automate specific data quality checks, have enhanced data viewing features built in to identify potential data quality issues, and can save time.

The Aviary houses these applications, direct link here: NEON Aviary. In addition to QC specific applications, the Aviary also hosts various other data viewing applications such as Magpie and the Canary Shiny apps, which are discussed in **SOP E/SOP F** and **SOP H** respectively.

> **REMINDER**: The NEON Aviary will not load if you are working outside of the Battelle network and are not connected to the VPN.

Refer to an individual protocol for more information regarding how and when to use a particular QC application. These applications are subject to change as some may be decommissioned, new ones added over time, or changes or enhancements are made to existing applications. ***Note that Shiny QC applications typically cannot perform all of the QC checks defined in the protocol-specific QC Checklist so it is important to always refer to the QC Checklist before concluding that QC is complete.***

Refer to the “OS Standard Operating Procedure: Monthly Activity Status Tracking” for more information about how and when to use the Clockwork application for generating summaries of Fulcrum field and lab records and assessing protocol completeness.

SOP E How to Use the Magpie Data Viewer Application

The Magpie Shiny application is an online interface to view NEON data pulled from the NEON Fulcrum data recording applications. Magpie is used for the following tasks:

1. Viewing load delays for a given application suite and data product (loadGroup).
2. Submitting requests to HQ Science staff for data deletions of UNLOADED records or data updates/deletions when Fulcrum records have passed the load delay and are LOADED and locked.
3. Conducting data QA/QC (see **SOP F**).

The three types of requests that may be submitted are:

1. Deletion Request
    - Use this to request deletion of an UNLOADED record with an issue. Do not wait to complete this step! An unloaded record is simple to delete from Fulcrum. After a record has loaded, it requires more work to delete the record in both Fulcrum and the NEON database.
2. Update Request
    - Use this to request a change in a record's metadata (any field) *except for taxonomy* (see below).
    - Use this to request deletion of a LOADED record with issues.
3. Taxonomic Change Request
    - Use this to request an update in a record's *taxonomy.*
    - **NOTE**: NEON data products that include taxonomic information are now providing 'identificationHistory' tables to alert data users to cases when the published taxonomic determination for a record has changed. The identificationHistory tables retain the old taxonomic determination information and include the evidence gathered to support the deprecation of the old determination.

Magpie can be accessed via the Data Management page of the Sampling Support Library (SSL) or via the NEON Aviary, located here within the Aviary: Magpie: Fulcrum Data Viewer.

The application itself has detailed descriptions of terms and instructions on how to use the interface in the 'About this application' tab, and Magpie training is included in the training plan for this protocol.

E.1 Workflow for How and When to Use Magpie

The Magpie application has two tabs, the 'About this application' and 'QA Data' tabs.

About this application tab:

- Orient yourself to this page before using the application for the first time. There is pertinent information about general data checks as well as instructions about how to use the application itself.
- The 'Data Delivery Deadlines' section outlines timelines between when data are entered into Fulcrum and when the parser attempts to load.
    - The load delay for all Fulcrum applications is listed under the **daysBeforeLocked** column and can be queried per application. Reference this section of the app to confirm how many days after a record is *created* you have to QC the data before there is a load attempt by the parser.
    - Remember that the parser ingests data per **loadGroup**, meaning it is possible data from more than one application will be pulled by the parser for a load attempt. For example, the Herbaceous Biomass loadGroup includes both the *HBP: Field Sampling* and the *HBP: Lab Masses* applications.
    - The **daysBeforeDeleted** column lists how long records in a given load group are kept in Fulcrum following creation before they are deleted. Applications that produce samples that are shipped to external facilities for analysis or archive have a long period before deletion to ensure field staff have shipped the samples and the receiving institution has received them without any problems.

NOTE: Fulcrum record deletion is a manual process performed by HQ staff after a series of checks have been performed to ensure data have been successfully ingested into the NEON database, and any samples have been shipped and properly received by external facilities. Fulcrum records are deleted to ensure the applications run smoothly and do not get slowed down by old records. Deleted Fulcrum records are no longer visible in the Fulcrum application; however, these records can be found in the NEON L0 database or the NEON Data Portal.

QA Data tab:

This tab is used for two purposes:

- To QC data for duplicates in a dataset as part of the standard quality control workflow outlined in **SOP F.1**.
- To report records for either deletion or modification that have known issues, either discovered during the QC process or from ingest failures:

To perform data QA:

1. Enter your **NEON email address**.
2. Choose a **subsystem**.
3. Constrain your dates – i.e., **Start and End dates.** These dates should bound the dates the records were created in Fulcrum and do not *necessarily* correspond with the field collection date(s).

4. Select your **domain**, **site**, and **application.**
    a. If the application has child records, a box will pop up prompting selection of a subtask – select either Parent-Only or Child records.

    NOTE: The Shipping: Shipment Review app is available to select under all four subsystems.

5. **Select a Query Type** – should be 'Raw Data' for putting in a request for a known issue.
6. After these parameters have been set, a table will populate with any pertinent records.
    a. Find the record(s) of interest and select by clicking anywhere along the line. Multiple records may be selected at the same time, and a selected record will become highlighted in blue.
7. Clicking the '**Edit Record**' (loadStatus=NONE) or the '**View Loaded Record**' (loadStatus=LOADED) button will open the record in another Fulcrum browser window.

TIP: The search bar at the top right is useful for querying records via **fulcrumID**, **loadStatus**, or another attribute.

8. For **Report Records?** – Select either **Deletion Request**, **Update Request**, or **Taxonomic Change Request**.
    a. **Deletion Request** – Request to completely delete a load_status = "NONE" record from the Fulcrum application. Note that Field Science staff can delete child records from a parent record with load_status = "NONE" without further assistance.
        i. Select a **Reason for Deletion.**
        ii. The **Deletion Explanation** field can be used to further clarify the reason for deletion.
        iii. Click the **Report Fulcrum Records for Deletion** button.
        iv. A message pop-up box will say either "Deletion Request Completed" for success, or if you accidentally requested deletion of a LOADED record it will fail and say, "Deletion Request >REJECTED<"
    b. **Update Request** – Request to modify or delete a load_status = "LOADED" record in the NEON database and possibly in the Fulcrum application if necessary.
        i. Select the field that is errant in **Which column is in error?**
        ii. Type in the **Corrected Value** – best practice is to copy/paste to avoid possible transcription errors.
        iii. The **Reason for Update** field lists several choices for record modification, choose the best option.
            1) DELETE RECORD means you want to delete a LOADED record already ingested to the NEON database, not just in Fulcrum.

iv. Add any **Additional Remarks** in free-form text that the HQ staff member may need to know to better understand and process your request. Please include any relevant ServiceNow Incident or Request numbers if applicable.

v. The **Fulcrum Record Update Required?** field auto-populates to 'No' (Most Common) but can be modified if the record does need updating for other reasons.

   1) In most cases, updating the Fulcrum record is NOT necessary, as edited data can be viewed in the NEON L0 database.

   <u>**NOTE**</u>: This *IS* necessary and should be 'Yes' when an updated sampleID is needed for creating shipping records or downstream processing of records, or the record is within a permanent application.

vi. Click the **Report Fulcrum Records for Deletion** button.

vii. A message pop-up box will say either "Update Request Completed" for success, or if you accidentally requested an update or deletion of an UNLOADED record (and could therefore be edited in Fulcrum), it will fail and say, "Update Request >REJECTED<".

c. **Taxonomic Change Request** – Request to modify a load_status = "LOADED" record's taxonomy in the NEON database and possibly in the Fulcrum application if necessary.

i. Select the new/corrected identification from the **Updated Taxon ID** dropdown. These lists are constrained by the associated Fulcrum taxa application(s) that is used by the chosen app.

ii. Choose an **Identification Qualifier** if needed.

iii. Choose the **Reason for Update**. Options include "Data Entry Error", "Missing Choice Value", and "Taxon Misidentification".

   1) If the reason is either "Missing Choice Value" or "Taxon Misidentification", the additional 'Evidence for Change' field will become visible.

iv. **Linked Data** – used to specify if other records will also require requests related to this change.

   1) Select "Linkages may be present" if an individual is a recapture or samples exist in other tables or data products.

   2) If unsure, select "Unknown".

v. **Evidence for Change** (if visible) – Select the most relevant reason from the drop-down list, if additional reasons should be noted, describe in the **remarks** field.

vi. Select the **Identification Reference** used to support identification. If specific reference is not listed, please update relevant Fulcrum AOS/TOS ID Reference application.

vii. Select the **Identified By** name. List is constrained by Domain personnel.

viii. Add any **Additional Remarks** in free-form text that the HQ staff member may need to know to better understand and process your request. Include any relevant ServiceNow Incident or Request numbers if applicable.

ix. The **Fulcrum Record Update Required?** field auto-populates to "No" (Most Common) but can be modified if the record does need updating, for example, if the sample will eventually be shipped.

x. Click the **Report Taxon Id Update in Loaded Data** button.

xi. A message pop-up box will say either "Taxonomic Change Request Completed" for success, or if you accidentally requested an update of an UNLOADED record (and could therefore be edited in Fulcrum), it will fail and say, "Taxonomic Change Request >REJECTED<".

E.2 How to View and Edit Submitted Magpie Requests Within the Magpie Fulcrum Applications

After a Magpie request has been submitted it will create a Fulcrum record in either the **Magpie Deletion Requests** application (for Deletion Requests of UNLOADED records), the **Magpie Update Requests** application (for Update Requests to LOADED records), or the **Magpie Taxonomic Change Requests** application (for Taxonomic Requests to LOADED records). Field Science staff can use the Fulcrum applications to view their requests. It is best practice to review Magpie requests after submitting to ensure accuracy.

1. To view either of your request types (deletion or update), navigate to the appropriate Fulcrum application.
   a. The **Status** field defaults to 'In Review' for newly submitted records.
      i. If a record has been processed – i.e., Resolved = "Y", the status will automatically set to "Processed by HQ".
      ii. If a record was submitted for deletion by mistake, or if there is another type of problem with the request, Field Science staff can manually set the status to "Ignore Request".
         1) Additional notes can be written to HQ staff members in the 'Field Notes' section to communicate why a record should be ignored.
      iii. When changing the status of a record to "Ignore Request" it will automatically set the Resolved status to "NA". The following text is displayed in the application itself:

   ***<u>NOTE</u>**: Changing this record's status to "Ignore Request" will update the "resolved" value to "NA". HQ will not process your request. If you need to reverse an "Ignore Request" edit, change the record status to "Edited by FS". This will change "resolved" to "N", and HQ will then proceed with processing the record.*

   b. The **Resolved** field defaults to "N" for newly submitted records.

    i. A status of “NA” will be ignored and not processed.
    ii. A status of “Y” means the request has been processed.

c. The **HQ Remarks** field is a free form text field for HQ staff to include links to data edits or write notes etc.

<u>NOTE</u>: Most Magpie Update Requests will not result in an updated Fulcrum record unless explicitly requested. This does not mean your request has not been fulfilled! If the Resolved status = “Y”, assume the request has been processed.

SOP F Referential Integrity Data Quality Review

Context: Post-Collection QA/QC

F.1 Analyze Data for Duplicate Records

Sample identifier fields are commonly named “sampleID”, but also include a number of variations that all end with the suffix “ID” as described in the relevant protocols – e.g., individualID, subsampleID, fieldSampleID, massSampleID, moistureSampleID, archiveID, etc. Sample identifiers are composed of human-readable unique ***metadata*** from each record, such as:

- plotID
- date
- sub-location, and
- sometimes a suffix or prefix related to the protocol (e.g., “***hbp***.CPER057163”).

To analyze data for duplicate records:

1. Navigate to the Magpie: Fulcrum Data Viewer in a web browser (the link can be found in the NEON Aviary). Review more detailed instructions for using the Magpie application in **SOP E**.
2. Enter the appropriate search parameters for the data set you are checking – e.g., **subsystem**, **date range**, **domainID**, **siteID**, **application**, and **subtask** (**SOP** (if applicable)).
    a. For **Query Type**, select “Duplicates by Sample Identifier”.
    b. **Choose Identifier Field to check** will automatically populate with the correct identifier if there is only one option, otherwise choose the appropriate identifier for the sample type.
    c. For **Report Records?**, select “Deletion Request”.
    d. If there are multiple sample identifiers (e.g., sampleID and subsampleID), an additional field will appear for you to indicate which value you’d like to check against.
3. **If there are any duplicates**, the application will return a set of records on the screen.
    a. Sort the records by the sample identifier field so that duplicate records are ordered together.
    b. You must now determine which record is the erroneous record that should be **fixed** (i.e., ***edited***) or ***discarded*** (i.e., ***reported for deletion***).
    c. ***Records can be discarded or reported for deletion***:
        - If every single column value is identical across the duplicate records set (excluding fulcrum_id or created_at date), you can simply report all but one record for deletion.

- If the duplicate record in question is a ***child***, you can simply delete it yourself without using Magpie:
  a. Navigate to the record in Fulcrum.
  b. Click the 'edit' icon (pencil) on the top right of the list.
    i. In a web browser, click on the "x" symbol to the left of the child record's title.
      1) Select "yes" when prompted to confirm the record deletion.
    ii. On an iPad, swipe left on the record and press 'delete'.
    iii. On a tablet, long pressing on a child record will bring up a "context menu".
      1) Select the trash bin symbol.
      2) Select "yes" when prompted to delete the record.

NOTE: This can be reversed if you discard the changes to the record before saving.

- If the duplicate record in question is a ***parent***:
  a. Select the duplicate record(s) in Magpie.
  b. Select an appropriate **Reason for Deletion** from the drop-down menu options.
  c. The **Deletion Explanation** field is a free-form text box to add more details to the request for HQ staff.
  d. Tap the blue "**Report Fulcrum Records for Deletion**" button.
  e. HQ staff will process the deletion request.
- ***Records can be fixed*** if all column values are *not* identical.
  - If this is the case, you must determine whether the recorder accidentally selected or entered a metadata value that created the duplicate sample identifier (e.g., plotID, collectDate, coordinates, etc.).
    - For example, an incorrect (but valid) plotID was selected for a record on the same date as another duplicate record with the sample plotID value.
    - Or an incorrect but technically valid date was selected for a record from the same plotID.
  - Edit the erroneous records so that the sample identifier is not a duplicate value of another record's sample identifier.

NOTE: Records upstream or downstream that are linked to the record that was fixed will not automatically be updated with the fix and should be edited to match the newly fixed record (see next section, **SOP F.2**).

F.2 Prevent Creation of Orphan Records

For protocols with linked applications, where metadata are referenced across applications (e.g., a lab record references a field sampling event), changes or corrections to metadata that make up the unique identifier fields in upstream applications can result in “orphaned” records. Orphaned records are a data quality issue because data in “downstream” applications cannot be accurately traced to an “upstream” record. Changes to sampling locations (e.g., plotID, clipCellNumber, soil coordinates) and/or sampling dates (e.g., setDate, collectDate) are the most common source of orphan records, as these values are almost always used to construct a unique sample identifier and data edits are never automatically propagated across applications.

Upstream applications are usually the first place where important metadata are recorded by field staff (plotID, subplotID, sampling date, soil coordinate, clip cell number, sample type etc.). Many protocols generate a unique identifier, typically named “sampleID”, that is used to link data across multiple data tables. Identifiers that are not **exact matches** across applications result in “orphan” and “childless” records.

Downstream applications “inherit” metadata from upstream applications, most importantly the sample identifier. Data that were already entered in an upstream application are generally un-editable. This is to prevent users from entering the same metadata values multiple times in different locations, which results in difficult to resolve transcription errors.

Follow these steps to prevent an orphan record in a downstream application when making edits to a record in an upstream application:

1. Have the application user manual on hand (Fulcrum Manuals are currently linked via each protocol page on the SSL).
2. **For each edit to a sampling location or sampling date** in an upstream record (**Table 3**), write down the original sample identifier.
    a. Using the original sample identifier, locate the downstream record.
    b. Open the downstream record and update the metadata following instructions from the application’s user manual.

Table 3. List of protocols that have linked applications. Applications to the left of a table cell are "upstream"; applications to the right are "downstream". Records in downstream applications can have orphan records if corresponding sample information in upstream records is altered. *(p-c) = application has a parent-child structure, child records inherit metadata from the parent, and each child must be updated if sample identifier information in the parent is changed.

Upstream ←---→ Downstream

Protocol	**App 1**	**App 2**	**App 3**	**App 4**
Algae – Periphyton and Phytoplankton Sampling	(AOS) Algae - Field (p-c)	(AOS) Algae - Lab (p-c)		
Aquatic Plant, Bryophyte, Lichen, and Macroalgae Sampling	(AOS) Plant Biomass - Field	(AOS) Plants - Lab		
Plant Belowground Biomass Sampling	BBC: Field Sampling (p-c)	BBC: Lab Weighing (p-c)	BBC: Grind and Pool (p-c)	
Plant Belowground Biomass Sampling	BBC: Field Sampling (p-c)	BBC: Lab Dilution (p-c)		
Canopy Foliage Sampling	CFC: Field Sampling (p-c)	CFC: LMA		
Canopy Foliage Sampling	CFC: Field Sampling (p-c)	CFC: Chemistry Subsampling		
Coarse Downed Wood	CDW: Field Bulk Density (p-c)	CDW: Lab Bulk Density (p-c)		
Ground Beetle Sampling	BET: Field Sampling (p-c)	BET: Lab Processing (p-c)		
Fish Sampling	(AOS) Fish (p-c)	(AOS) Fsh Summary (p-c)		
Fish Sampling	(AOS) fsh_nonTargetSpecies	(AOS) Fish (p-c)		
Fish Sampling	(AOS) Fsh Morphospecies List	(AOS) Fish (p-c)		
Fish Sampling	(AOS) Fish (p-c)	DNA: Sample Processing (p-c)		
Measurement of Herbaceous Biomass	HBP: Field Sampling	HBP: Lab Masses (p-c)		
Litterfall and Fine Woody Debris	LTR: Trap Deployment (links to TOS Clip List)	LTR: Field Sampling (p-c)	LTR: Lab Mass Data (p-c)	LTR: BGC Sub-Sampling
Plant Phenology	PHE: Field Setup (p-c)	PHE: Phenophase Observations (p-c)		

Protocol	**App 1**	**App 2**	**App 3**	**App 4**
Plant Phenology	PHE: Field Setup (p-c)	PHE: Annual Measurements (p-c)		
Shipping	SCS: Shipment Creation	SCS: Shipment Review		
Small Mammal Sampling	MAM: Trap Setting	MAM: Trap Collection (p-c)		
Small Mammal Sampling	MAM: Trap Collection (p-c)	DNA: Sample Processing (p-c)		
Soil Biogeochemical and Microbial sampling	SLS: Field Sampling (p-c)	SLS: pH		
Soil Biogeochemical and Microbial sampling	SLS: Field Sampling (p-c)	SLS: Moisture		
Soil Biogeochemical and Microbial sampling	SLS: Field Sampling (p-c)	SLS: Metagenomic Pooling (p-c)		
Soil Biogeochemical and Microbial sampling	SLS: Field Sampling (p-c)	SLS: BGC Sub-Sampling		
Soil Biogeochemical and Microbial sampling	SLS: Field Sampling (p-c)	SLS: Nitrogen Transformations (p-c)		
Measurement of Vegetation Structure	VST: Plot Meta-data	VST: Mapping and Tagging	VST: Apparent Individuals (p-c)	
Measurement of Vegetation Structure	VST: Plot Meta-data	VST: Shrub Groups (p-c)		
Wet Deposition	(TIS_AIS) Wet Deposition SET	(TIS_AIS) Wet Deposition COLLECT		

SOP G Detecting Process Quality Issues

Context: *Collection QA/QC* (for protocols with bouts that are longer than 2 weeks) or *Post-Collection QA/QC* (***before*** the next bout begins).

NOTE: The tables referenced in this SOP, **Table 4 - Proc Qual Field** and **Table 5 - Proc Qal Lab**, are housed here: Data Management Spreadsheet (linked on the Data management SSL page). These are dynamic tables maintained by science staff, and not directly located in any protocol.

- Tables 4 and 5 are maintained by Science staff and provide the expected number of records for field and lab activities per bout.
    - These activities are divided by sub-system and protocol and are to be used as a reference during quality control activities as described below.

G.1 Analyze Process Quality: Field Sampling Completeness

The goal of checking data for “Field Sampling Completeness” is to ensure that all data have been collected from the field *and* are present in the cloud database. Refer to **Box 2** for a more detailed walk-through.

1. From the Fulcrum application dashboard on a web browser:
    a. Click “View Data” for the application you are checking; you should be taken to a table-like view of the application’s data.
    b. If a table does not appear, click “Table Mode” in the top-right corner of the screen (next to the “+” add record button).
2. If “Clear All Filters” appears in blue text at the top of the table, click the “X” to remove filtering.
3. Most protocols have an “event” identifier (e.g., weekBoutBegan, boutType, eventID, yearBoutBegan, etc.)
    a. If it is not visible, click on the “Column Setup” (three vertical lines) button and search for an event field; check it to make the column appear.
    b. For protocols with no event identifier, filter by collectDate, setDate, etc.
4. Filter the visible rows to the sampling bout/event you are reviewing.
    a. Click the down arrow of the event column, a window appears.
    b. Click “Select Specific Values”, search for and select an event identifier.
    c. Be sure to filter data by a single siteID, as this simplifies record counts and will match the information in **Table 4 (companion spreadsheet, tab 1).**

TIP: You can also filter via the main search bar by typing in any field value (e.g., “eventID”) because it searches through all fields except for “Record ID”.

5. Only records with the specified event identifier will now appear in the web browser table.
6. **Evaluate the record count:**
   a. For a given bout, if **the application does not have child or grandchild records**:
      - The total number of records will appear at the top-left above the table.
      - **Compare this number to what is expected in Table 4, columns E-H**, based on information in the relevant protocol and SOPs listed.
        - **Column E** contains rules describing how many digital parent records should appear per sampling location.
        - Columns F and G only need to be referenced if an application has nested child and/or grandchild records (see below).
        - **Column H is the total expected number of parent records that should appear in the web browser.**
      - If your counts are **BELOW** the expectation, you may be missing records from the bout, missing physical samples from the field, missing samplingImpractical records, or have incorrectly entered metadata that goes into the event identifier (e.g., yearBoutBegan, siteID, soil coordinate, etc.)

      <u>NOTE</u>: You may be able to discover if records have incorrect metadata by sorting records based on the “created date”. Records collected in sequence and/or in the same time interval should be adjacent when sorted this way.

      - If your counts are **ABOVE** the expectation, there may be duplicate records in the dataset and/or too many samples were collected in the field.

   b. For a given bout, if **the application has child or grandchild records**:
      - The total number of **parent records** will appear at the top-left above the table. **This number should equal the number in Column H** (**Table 4**)
      - For each parent record, open the record and view the number of child and grandchild records present.
        - **View the number of child records** (**Table 4, Column F**).
        - **If present, tally the number of grandchild records per child record** (**Table 4, Column G**).
      - If your counts are **BELOW** the expectation, you may be missing records from the bout and/or missing physical samples from the field.
      - If your counts are **ABOVE** the expectation, there may be duplicate records in the dataset and/or too many samples were collected in the field.

G.2 Analyze Process Quality: Protocol Sampling Completeness

The goal of checking for “Protocol Sampling Completeness” is to ensure that all post-field sampling data have been collected, entered, and align with field sampling data. These checks only need to occur if protocols require additional data collection generated from lab procedures. Refer to **Box 2** for a more detailed example.

1. From the Fulcrum application dashboard on a web browser:
    a. Click “View Data” for the application you are checking; you should be taken to a table-like view of the application’s data.
        - If a table does not appear, click “Table Mode” in the top-right corner of the screen (next to the “+” add record button).

    NOTE: *This tab will be referred to as the “**upstream**” application (e.g., Field Sampling).*
2. Open another tab in the web browser and locate the second application you will be checking.

    NOTE: *This tab will be referred to as the “**downstream**” application (e.g., Lab Mass).*
3. Select “Clear All Filters” for both open tabs.
4. Filter the visible rows to the sampling bout/event you are reviewing in ***both tabs:***
    a. Click the down arrow of the event column, a window appears.
    b. Click “Select Specific Values”, search for and select an event identifier.
    c. Be sure to filter data by a single siteID, as this simplifies record counts and will match the information in **Table 4.**

TIP: You can also filter via the main search bar by typing in any field value (e.g., “eventID”) because it searches through all fields except for “Record ID”.

5. For a given bout:
    a. Note the number of upstream records there are after filtering.
    b. Note the number of downstream records there are after filtering.
6. Evaluate the record counts:
    a. **Table 5** (**companion spreadsheet, tab 2**) describes rules for how to count downstream records.
        - These are rules rather than specific numeric values because not all sampling events result in a downstream record but are instead based on various conditions defined in a protocol (e.g., Lab Mass records are not created if no field sample was collected).
        - Applications and protocols not listed in **Table 5** do not need to have Process Quality checks performed.

b. In most cases, **the number of parent records in the downstream application should equal the number of parent records in the upstream application.**

- If your counts are **BELOW** the expectation, you may be missing records in the downstream app that should be present.
    - Potential reasons for this include:
        i. Data have been collected, but a device was not fully synced.
        ii. Data have been collected but were recorded on paper and not entered.
        iii. Critical upstream metadata may have been changed, causing a mismatch (e.g., siteID or an event identifier were changed in some way).
        iv. Data have not been collected, recorded, or entered.
- If your counts are ABOVE the expectation, there may be duplicate records present in the upstream or downstream app, or event identifiers may be incorrect (e.g., weekBoutBegan was manually adjusted improperly).
- Workflows that deviate from these general guidelines are listed below. See **Table 5** for more details.
    - Canopy Foliar Sampling (CFC).
    - Soil Biogeochemistry and Microbe Sampling (SLS).

Box 2. Detailed example of conducting all Process Quality checks with Litterfall data in Fulcrum (Field and Lab data).

1. Open the "**LTR: Field Sampling**" data table in a web browser.
2. Open the "**LTR: Lab Mass**" data table in another web browser window.
   <u>TIP</u>: The 'Save View' button can be used to save a particular filter set for quick viewing next time. Give your custom view a meaningful title and click 'Confirm'.
   - Your saved view will be displayed in the application bar at the top of the screen underneath the application name titled 'Views'.
3. To assess ***Field Sampling Completeness*** (**SOP G.1**)
   a. **<u>Organize data</u>**:
      i. In "*Column Setup*" the first four columns are re-arranged as siteID, weekBoutBegan, setDate, and trapID.
      ii. The rows are sorted by trapID so that duplicates can be spotted.
   b. **<u>Filter data</u>:**
      i. In the **siteID** column: select one site, "**UNDE**"
      ii. The event identifier is **"eventID"**, select a single value in the **eventID** column.
   c. **<u>Assess results:</u>**
      i. UNDE is a forested site that uses 1600 m^2 plots, and **Table 4** of the Data Management Protocol suggests that there should be two parent records per plotID and 40 records total (two traps per plot in two random subplots)
      ii. The web browser shows 40 records:
         1) Are there any duplicate records inflating the count?
            a. Click on the trapID column options, then "*Select Specific Values*".
            b. This shows a count of the number of rows with the same trapID value.
            c. All counts equal "1", so there are no duplicates present.
            d. The correct number of records has been collected and synced.
4. To assess ***Protocol Sampling Completeness*** (**SOP G.2**)
   a. **Table 4** of the Data Management Protocol suggests that LTR: Lab Mass records should appear if a Field Sampling record has a **trapCondition** of "OK" or "PF"
      i. **<u>Organize data:</u>**
         1) In the "Column Setup" of the "**LTR: Lab Mass**" application, the first three columns are re-arranged as siteID, eventID, and setDate
      ii. **<u>Filter data:</u>**
         1) In the "**LTR: Field Sampling**" window, limit the visible records by the trapCondition column to those with "OK" or "PF"
         2) In the "**LTR: Lab Mass**" window, filter data to the same site and eventID as is visible in "**LTR: Field Sampling**"
      iii. **<u>Compare results across applications:</u>**
         1) There are 40 records visible in the "**LTR: Field Sampling**" window.
         2) There are 41 records visible in the "**LTR: Lab Mass**" window.
         3) All expected records appear to be present from the Field and Lab portions, however there is one more record in the Lab app…
      iv. **<u>Evaluate discrepancy:</u>**
         1) There are more records in the "**LTR: Lab Mass**" app, start there.
         2) Clicking on the **trapID** column options and "*Select Specific Values*" shows there is a single **trapID** with two entries, checking the box on this trapID filters rows down to these two records.
         3) Further inspection of the records shows that one parent record has qaDrymass values and is a duplicate of the other record.
         4) One record should be reported for deletion.

SOP H Parser Error Resolution

It is inevitable that some data records will fail to pass the parser given the sheer volume of human-collected data NEON ingests. Fortunately, there are multiple systems in place to catch those errors before they are published on the NEON Data Portal. As discussed in Section 3.3 of this document, the Fulcrum applications have built in checks and validation requirements, and once data are set to load, the parser provides another round of validation requirements before data are ingested.

This SOP describes the Field Science staff role with regard to parser error resolution. These tasks comprise the final opportunity for Field Science to ensure data are complete and accurate.

H.1 Data Ingest Process and Statuses

On a nightly basis, the OS parser attempts to load Fulcrum application records that have passed the load delay timeframe. The system communicates whether records were loaded successfully by updating the record's 'load_status' field in Fulcrum.

1. LOAD_STATUS states:
    a. **PARSE_FAIL** = set by Parser; indicates a record failed ingest.
    b. **LOADED** = set by Parser; indicates a record passed ingest and was loaded into the NEON database.
    c. **SKIP** = set by apps or has not been finalized by field science staff; indicates the parser will ignore the record and it will not be pulled for ingest.
    d. **NONE** = set by apps; generally means the record has not hit the load delay and has yet to be evaluated by the parser.

<u>**NOTE**</u>: HQ staff members can set a record to have any load status and may need to do so to resolve certain parser errors.

2. Record Status:
    - **Complete** = set by app upon finalization or set by user.
    - **RECORD_ERROR**/**recordError** = set by app or user.

<u>**NOTE**</u>: After a record error has been fixed, the Record status may not automatically re-set to "Complete." This means a successfully loaded record can have a record status of "RECORD_ERROR". Field Science staff have control over the record status field and can change it from "RECORD_ERROR" to "complete" if desired.

H.2 Efficient Workflow for Addressing Parser Errors

The parser errors listed in the Canary Shiny app (see below section **H.3**) can sometimes be overwhelming, and although all parser errors must eventually be resolved, it can be unclear where to start. Records can sometimes be flagged erroneously due to problems with linked records in *upstream* applications. For example, a **sampleID** error in a Field record will cause a "Sample does not exist" error in the related Lab record and potentially in the shipping review record if the sample shipped.

Identifying and fixing 'high priority' errors first should be the standard workflow. Remember that Fulcrum records are loaded per load group, ***so one error within one application for a load group may be holding up data from a completely different application***.

The following order of operations is suggested when tackling parser errors:

1. Resolve all errors ***within a load group*** at the same time.
2. Within a load group, identify and prioritize resolving errors ***for the data from one Fulcrum app at a time*** (if more than one error per record or sample identifier).

NOTE: See **Table 5** below for definitions of ingest workbook validations.

3. In linked applications, ***resolve sampleID errors in upstream applications first (see Table 3).***
4. Resolve errors associated with ***samples sent to an external lab*** for analysis or an external facility for taxonomic identification, these are typically sampleID or barcode issues.

IMPORTANT: Errors should not persist for weeks and months on end. Create an Incident in ServiceNow and seek help if necessary if an error persists for longer than one month.

H.3 Canary Shiny App – NEON Parser Errors

The Canary Shiny app holds and updates current parser errors daily at 10 AM (MST). The Canary system sends out a weekly email to domain staff on Monday at 10 AM (MST) as well. If there are no errors within a *domain*, an email will still be sent to confirm no errors exist.

To access the Canary Shiny app go here: NEON Aviary.

There are three tabs in the Canary app: Canary Output, Summary Report, and About This App.

H.3.1 Canary Output

The "Canary Output" tab displays important data for record failures, and its content matches what is sent weekly in the emailed report. The Canary Output tab should be the first place Field Science staff go to correct errors. The following fields are displayed, filterable, and should be used to narrow down pertinent errors:

- **Domain ID**
- **App Name** – name of the Fulcrum application.
- **Load Group** – name of the data product according to the OS Parser.
- **Error Message** – details describing what type of failure occurred, what sample identifiers were involved (if applicable), and the applicable Fulcrum Record ID.

- **Error Field** – the field in the Fulcrum application with the issue.
- **Error Value** – the value causing the error – e.g., a sample identifier.
- **Fix** – more detailed instruction regarding what the *Error Message* means and how to correct it.
- **Fulcrum RecordID** – a direct link to the Fulcrum record triggering the issue.
- **Original Error Date** – this is the date the error was first reported.
- **Error Duration (days)** – how many days the record has failed ingest. This field dictates the color scheme for the entire row, depending on the duration of the error:
    - Error duration < 14 days → no color
    - Error duration ≥ 14 days and < 28 days → yellow
    - Error duration ≥ 28 days and < 35 days → orange
    - Error duration ≥ 35 days → red
- **Ingest Table** – the NEON database table into which the record will load once it passes the OS parser.
- **Focus** – who is responsible for correcting the record, either Field Science or the Science Load Group Manager.
    - *If the error is assigned the "Science/App developer" focus, then an HQ staff member is responsible for correcting the error*.

TIP: There is also an option to download the report to a .csv or a .xlsx spreadsheet to view record failures in Excel instead of the Shiny app interface.

IMPORTANT: One single issue can cause multiple error messages in the Canary Shiny app, and thus, multiple lines with different error messages can correspond to the same problem in one record.

For example (**Table 4**): A *MAM: Trap Collection [PROD]* record is causing an error because a single barcode is associated with more than one sampleID. The Canary Shiny app lists this single error in three different ways! Note that the Error Value is the same for all three.

Table 4. Example error values and error messages from the Canary Shiny app. The same error is reported three different ways.

Error Value	Error Message
D00000082539	Changing Tag from HARV.20220622.R6812.B to HARV.20220623.R6812.B not allowed for Sample[[tag=HARV.20220622.R6812.B,barcode=D00000082539,sampleClass=mam_pertrapnight_in.bloodSampleID]].

D00000082539	ReferenceCount is greater than one: [tag=HARV.20220623.R6812.B,barcode=D00000082539,sampleClass=mam_pertrapnight_in.bloodSampleID]. Fulcrum ID=8ed907c4-2d3a-4788-ab6a-a94c1c95bdb7.
D00000082539	Uploaded sample with barcode 'D00000082539' has different tags. (HARV.20220623.R6812.B, HARV.20220622.R6812.B).

Do not let this confuse you. Consolidating these messages so they are all together may be useful (such as how they appear above). Choose whichever error message makes the most sense for you to digest and go from there.

H.3.2 Summary Report

The "Summary Report" tab displays four different figures that track the quantity and types of parser errors through time.

- **Figure 1** displays the number of errors reported by the parser through time for TOS (the date range can be modified by selecting the 'Select Date Range' feature at the top).
- **Figure 2** displays the number of errors reported by the parser through time for AOS (the date range can be modified by selecting the 'Select Date Range' feature at the top).
- **Figure 3** displays the number of errors by Domain and the loadGroups in which errors exist (this is a Plotly figure and can be manipulated by the viewer or exported as a .png).
- **Figure 4** displays the most common error type reported and the related loadGroups (this is a Plotly figure and can be manipulated by the viewer or exported as a .png).

H.3.3 About This App

The "About This App" tab offers a ReadMe of the Canary app and its features.

H.4 General Workflow for Resolving Parser Errors

There are many resources for resolving parser errors, and as such, there may be more than one avenue to resolve a parser error given the different levels of experience and familiarity with these types of issues amongst Field Science staff. This protocol should serve as a resource along with knowledge base articles, domain specific training, staff meetings, word-of-mouth, weekly meetings, asking for assistance via ServiceNow from HQ Science staff, etc.

The following table lists the type of error messages that may be found within the Canary Shiny app and weekly emailed reports and disseminates what they mean in more literal terms for field staff to resolve. Note some messages may be something only HQ Science staff can resolve, but you may still be notified of the issue via Canary.

REMINDER: A record UUID is a universally unique identifier value used to identify information in a system. The NEON database creates a UUID for every data record ingested, so if an error message contains a UUID that means the associated record has loaded into the NEON database and is causing failure of a record that has not loaded.

Table 5. Description of parser error message language, what it means in simpler terms, and how to resolve. Note, reference to sample tag is synonymous with sampleID.

Generic Error Message	Example message	Issue
ACTIVITY_END_DATE_VALIDATION	Validation failed for field 'collectDate' in function ACTIVITY_END_DATE_VALIDATION. The end date (2021-07-05T10:20-05:00[US/Central]) for the record is before the start date (2021-07-05T22:00-05:00[US/Central]).	The date entered does not clear the validation rule for start/end time. Typically the result of an incorrect date entry but may be an app error that HQ Science staff will fix.
Changing Barcode	Changing Barcode from B00000153375 to A00000358651 not allowed for Sample[[uuid=4d486a7e-fc12-4d59-9b5b-c74276778a16, tag=LIRO.W2.20220606.RAW,barcode=B00000153375,sampleClass=swc_fieldData_in.rawSampleIDgwc]].	Duplicate sampleID where both duplicates are in the current data upload: same sample tag, different barcodes
Changing SampleClass	Changing SampleClass from apl_domainLab_in.herbariumSampleID to apc_voucher_in.herbariumSubsampleID not allowed for Sample[[uuid=f409145d-2ca2-415b-bc72-e86fa48f23aa,tag=BARC.20220629.AP2.P3.H,barcode=A00000173431,sampleClass=apl_domainLab_in.herbariumSampleID]].	Indicates the sampleClass ingested by the parser and what is acceptable in the ingest workbook differs from what is in the record. These are most common in shipment records and can arise when a sampleClass changes and was not propagated downstream.
Changing Tag	Changing Tag from TOOK.INFLOW.20220516.FIL to TOOK.IN.20220516.FIL not allowed for Sample[[uuid=3d0e81a7-c00d-4ea3-bd34-98859024c506, tag=TOOK.INFLOW.20220516.FIL,barcode=A00000302356,sampleClass=swc_fieldData_in.filtSampleID]].	Changing tag from SAMPLE.TAG.X to SAMPLE.TAG.Y and sampleClass from sampleClassA to sampleClassB not allowed for sample with uuid ### and barcode ###
CONVERT_TO_UTC	Validation failed for field 'collectDate' in function CONVERT_TO_UTC. The incoming value '-0-0T' expected to be a date but instead is a 'StringC' type.	HQ Science staff must address this error.
DERIVE_FROM_SAMPLE_TREE	Validation failed for field 'collectDate' in function ACTIVITY_END_DATE_VALIDATION. The incoming value '' expected to be a date but instead is a 'VoidC' type.	The voidC failure for dates can mean blank, or it can also mean a date in an unreadable format such as in Excel with "PM" in the time column. HQ Science must address this error.

Generic Error Message	Example message	Issue
GREATER_THAN	Validation failed for field 'height' in function GREATER_THAN. Comparison failed (0 > 0).	The value in this field does not fulfill the validation that the number for the field in question needs to be greater than a specified value.
Has different tags	Uploaded sample with barcode 'D00000012729' has different tags. (FSH.CARI.01.20180904.2.0001.DNA, FSH.TOOK.09.20220629.5.0001).	Duplicate barcode where both duplicates are in the current data upload: Same barcode, different sample tags.
LESS_THAN	Validation failed for field 'vdBaseBreakHeight' in function LESS_THAN. Comparison failed (2.4 < 2.4).	The value in this field does not fulfill the validation that the number for the field in question needs to be less than a specified value.
LOV	Validation failed for field 'samplingProtocolVersion' in function LOV. LOV value 'NEON.DOC.014049vM' could not be validated due to missing activity end date.	Invalid LOV value – i.e., the value entered doesn't match one of the constrained list of values the parser is expecting. Typically HQ Science Staff must address this error.
NAMED_LOCATION_TYPE	Validation failed for field 'plotID' in function NAMED_LOCATION_TYPE. Named location KONZ with type 'OS Plot - bet' is not allowed	HQ Science staff must address this error.
ReferenceCount	ReferenceCount is greater than one: [tag=VST.CLBJ.03311.2021, sampleClass=yearPlant].	Duplicates: Multiple records with this sampleID are being uploaded in this load attempt.
REGULAR_EXPRESSION	Validation failed for field 'plotID' in function MATCH_REGULAR_EXPRESSION. value 'PUUM_015.basePlot.bet' failed with pattern '^[A-Z]{4}'.	The parser is checking this value against a regular expression. Typically, HQ Science staff must address this error.
REQUIRE	Validation failed for field 'dryMass' in function REQUIRE. Input Value is required.	A required Fulcrum field is blank in a record. Required fields represent critical information for a data product. A data product is often less usable, or not useful, without all of the required data being present. A value in this field must be provided. This error may result when a hidden field in Fulcrum lacks a required value; reach out to HQ staff for additional help if needed.
REQUIRE_NULL	Validation failed for field 'sampleFate' in function REQUIRE_NULL. Input Value is not empty.	The value in this field needs to be NULL (empty). May be context dependent – i.e., the field is only conditionally required to be NULL.

Generic Error Message	Example message	Issue
Sample already exists	Sample already exists in the database: [tag=PRIN.SS.20220621.FIL, sampleClass=swc.asi.sdg.amc].	Indicates that the database has already loaded a particular identifier and a duplicate record exists in Fulcrum with the same sample identifier.
Sample does not exist	Sample does not exist: [tag=NEON.LTR.BART046852.20220607, sampleClass=ltr_fielddata_in.fieldSampleID]. Fulcrum ID=602fab18-7ae8-4116-828e-15f8965a7ea3.	Orphan sample: the sampleID is supposed to already be in the database from an earlier record, but it is not.
_THAN		The parser is expecting the value in this field to be greater than/less than/equal to another field (and the other field is not listed).

General workflow for troubleshooting and resolving parser errors:

1. Consult the Canary Shiny app or the weekly email notification from Canary to view applicable parser errors from your domain and for the data product(s)/load group(s) you are responsible for.

   REMINDER: The Canary Shiny app will automatically refresh daily at 10 AM (MST) so this is the most current resource to use versus the Monday morning email.

2. Review the entire row of information in the Shiny app/emailed report and make sure you understand what the message is telling you, see section **H.3** for a brief outline of each field in the app and remember one single error may appear multiple times, worded slightly differently.
   a. First you will want to review the **Error Message** – this provides most all of the details needed to resolve the error. For example, sample does not exist, duplicate sample exists, etc., the tag ID and sampleClass, as well as the Fulcrum Record ID in error.
   b. Next you will need to note the **Error Value** in the Canary Shiny app, this most often will be a sampleID or sample barcode that is causing the error but could also be a field within the data that is throwing the error.
3. Once you've established what the error message is telling you and which field or identifier you need to check, go to the Fulcrum application in which the record was created.

   TIP: This is easiest to do in a web browser versus a tablet.

4. Enter the identifier (barcode, sampleID) directly into the search bar or search for the Fulcrum Record ID given in the Canary Shiny app.
   a. If there is a duplicate issue – e.g., the same barcode is associated with more than one sampleID – it will result in multiple Fulcrum records from your query.

NOTE: To query the Fulcrum Record ID in Fulcrum, you need to click on the dropdown arrow under the field titled 'Record ID' and paste the Fulcrum Record ID into the search bar. If you do not see Record ID among the visible column headers, it is because you do not have it selected to view. To select it, click the three vertical lines next to the filter button and be sure Record ID has a blue checkmark next to it.

5. Review the the information that makes up the sampleID in question. Often sampleIDs are not directly editable but are comprised of one or more pieces of information that are editable – i.e., plotID, yearBoutBegan, etc..
    a. Correct the field value (if applicable).
    b. Determine what identifier combination is correct and fix the Fulcrum record.
    c. If you determine an incorrect identifier is already loaded into the database and the failing Fulcrum record is actually correct, then you will need to submit a Magpie update request, as you cannot edit a loaded record.
6. Once you believe you have corrected the error, return the next day to confirm the record has loaded.
    a. On the morning after the day the edit was made, the OS Parser should try again to pull the record into the NEON database, so checking the Canary Shiny app after 10 AM (MST) will tell you whether or not your edit was successful (if it no longer appears in the app).
    b. You can also check the Fulcrum record directly – the load_status will update to LOADED.
7. If you are unable to resolve a parser error on your own and you have exhausted all other resources, than you can create a ServiceNow incident outlining the error(s), what steps you've taken, where you are stuck or what you don't understand, and a HQ Science staff member will assist you.

Parser error case studies

Below are some case studies of various error messages and how to solve them. These are some of the most common parser errors seen:

1. In the *MAM: Trap Collection [PROD]* application there is a 'Changing Tag' error associated with barcode D00000082539 (Error Value), where it is associated with two different sampleID's, the Error Message is:

   "Changing Tag from HARV.20220622.R6812.B to HARV.20220623.R6812.B not allowed for Sample[[tag=HARV.20220622.R6812.B,barcode=D00000082539, sampleClass=mam_pertrapnight_in.bloodSampleID]]".

    a. This is saying that in Fulcrum this barcode D00000082539 is associated with both sampleID: HARV.20220622.R6812.B AND HARV.20220623.R6812.B

   b. Figure out the correct barcode associations for the sampleID's and correct the applicable Fulcrum record.

2. In the *SLS: Nitrogen Transformations [PROD]* application there is a 'Sample already exists' error associated with barcode B00000111234 (Error Value), where it is associated with two different sampleID's, the Error Message is:

   "Sample already exists in the database: [tag=JORN_004-M-21-20220705-KCL, barcode=B00000111234, sampleClass=ntr_internalLab_in.kclSampleID]. Fulcrum ID=78e9179a-c003-4025-95cb-7db06135339c".

   a. This is saying that this barcode B00000111234 is associated with another sampleID in the NEON database (that has already loaded). It is associated with: JORN_004-M-41-20220705-BM.

   b. Figure out the correct barcode associations for the sampleID's and correct the applicable Fulcrum record and/or submit a Magpie update request if applicable.

3. In the *LTR: Field Sampling [PROD]* application there is a 'Sample already exists' error associated with sampleID NEON.LTR.SJER064707.20220811 (Error Value), where the sampleID has already loaded into the NEON database, and the Error Message is:

   "Sample already exists in the database: [tag=NEON.LTR.SJER064707.20220811, sampleClass=ltr_fielddata_in.fieldSampleID]. Fulcrum ID=117ee765-d6a4-4d0f-95fb-7f4331c3ddc6."

   a. This is saying the sampleID has already loaded either via a different Fulcrum record and this one is a duplicate, or something else may be happening.

   b. After reviewing this Fulcrum Record ID's full history (see Appendix B and C for how to view record history), it loaded previously and then was re-synched on a tablet that had not been opened and synched for a while, thus rolling the record's load_status back to NONE from LOADED.

      i. The OS Parser is trying to re-load this but since the record has already loaded it is giving this error.

   c. Resolving this problem requires assistance from HQ Science staff because Field Science cannot adjust a Fulcrum record's load_status.

   d. Submit a ServiceNow incident to resolve.

4. In the *LTR: Lab Mass Data [PROD]* application there is a 'Sample already exists' error associated with sampleID NEON.LTR.BART046852.20220607 (Error Value), where the sampleID has already loaded into the NEON database and the Error Message is:

“Sample does not exist: [tag=NEON.LTR.BART046852.20220607, sampleClass=ltr_fielddata_in.fieldSampleID]. Fulcrum ID=602fab18-7ae8-4116-828e-15f8965a7ea3.”

   a. This is saying the sampleID does not exist in the *NEON database* , because it likely has changed since it was originally created.
   b. Upon inspection, the collectionDate changed after the record was initially created and therefore changed the sampleID from NEON.LTR.BART046852.*20220607* to NEON.LTR.BART046852.*20220608* in the NEON database and likely in the LTR: Field Sampling application. However, this update was not propagated to the LTR: Lab Mass Data application.
   c. The Lab Mass Data record, along with the child records, needs to be re-associated with the new, updated parent Field Sampling application by re-selecting it.

5. In the *(AOS) Plants - Lab [PROD]* application there is a ‘LESS_THAN’ error within the field: wetMass (Error Field) stating that: (5407.33 <= 5000) (Error Value) associated with one specific Fulcrum record. The Error Message states:

   “Validation failed for field wetMass in function LESS_THAN_OR_EQUAL_TO. Comparison failed (5407.33 <= 5000).”

   a. This is saying that you cannot have a value greater than 5000 for the wetMass and since the value input was 5407.33, it failed the parser validation.
   b. This is likely a typo, correct the wetMass value.

6. In the *(AOS) Reaeration [PROD]* application there is an ‘expected to be a date’ error within the field: loggerInWaterDateTime (Error Field) with an Error Value of: 2022-07-05Tundefined associated with one specific Fulcrum record. The Error Message states:

   “Validation failed for field 'loggerInWaterDateTime' in function CONVERT_TO_UTC. The incoming value '2022-07-05Tundefined' expected to be a date but instead is a 'StringC' type. Fulcrum ID=9fa12b47-357c-43d9-839f-48a2f66dac64.”

   a. This is saying that the date string (format) is not recognized as valid for the field, hobo_in_water_ingest.
   b. This is something HQ Science staff will need to correct in the Fulcrum record by exporting the record as a spreadsheet, making the correction, and importing back into Fulcrum as a spreadsheet. A ServiceNow incident can be created to move the process forward.

7. In the *(AOS) Dissolved Gas [PROD]* application there is a ‘Sample does not exist’ error with an Error Value of: MART.SS.20220906. The Error Message states:

"Sample does not exist: [tag=MART.SS.20220906, sampleClassSet=[swc.sdg, swc.asi.sdg, sdg, asi.sdg, asi.sdg.amc, swc.asi.sdg.amc, sdg.amc, swc.sdg.amc]]. Fulcrum ID=9a568b22-fa77-40c5-8611-b125ab77efaa."

a. This is saying that the sampleID: MART.SS.20220906 does not exist in the *upstream* (AOS) Water Chemistry [PROD] app, which creates the parent sampleID for this *downstream* application.

b. A likely scenario to cause this is a change in the sampling date.

c. Upon review of the records in the (AOS) Water Chemistry app affiliated with the date 20220906 or something near that date, it appears the correct parent sampleID is MART.SS.20220907

d. To correct, the record in the *(AOS) Dissolved Gas* app needs updating to reflect the correct date of 20220907.

   i. Edit the 'Date Processed' field which will propagate to the Reference Air Sample ID automatically.

   ii. To update the Water sampleID, click the child record and tap 'Select Parent Water Sample' to re-populate the field with the correct record with the correct date of 20220907.

H.5 Workflow for Resolving Shipping Parser Errors

Shipping samples to external labs is the last phase of a sample's chain of custody, and it is extremely important that data captured in the shipment receipt and manifest are accurate. Due to the sheer volume of samples shipped from NEON domains to external lab facilities, as well as the shipping application dependency upon all other applications to pull in accurate sample identifiers such as sampleID, barcode, sampleClass, etc., it is not uncommon to encounter errors with shipping data.

Shipping parser errors are most often related to sample identifiers (barcode/sampleID) not being found in the NEON database. This is usually caused by changes/edits made in the data collection upstream applications between when a shipment was created and sent, to when the OS Parser attempts to load the shipping data. The loadDelay for the shipping application is 45 days from record creation. Exacerbating the challenges to resolve shipping parser errors is the fact that the physical specimens are no longer in-house and thus cannot be physically checked.

However, Field Science staff members can and should be the first NEON staff to attempt to resolve shipping parser errors. If Field Science staff are unable to resolve the error on their own, then it is appropriate to reach out via ServiceNow for HQ Science staff assistance.

Follow the workflow below to troubleshoot and resolve shipping parser errors:

1. Consult the Canary Shiny app or the weekly email notification from Canary to view applicable current shipping parser errors.
2. Query the failed identifier in the Fulcrum *Shipping: Shipment Review [PROD]* Application – i.e., the **Error Value** in the Canary Shiny app, which will most often will be a sampleID or sample barcode.
    a. It is easiest to type this value directly into the search bar.
    b. This will bring up the entire shipment record that has the failed identifier as a child record.
    c. Open the child record view of the record and find the identifier, hint: use CTRL+F for a pop-up search window which will highlight the identifier for a large shipment.
    d. View the identifier combination – i.e., sampleID (if applicable) + barcode (if applicable) + sampleClass, etc.
3. Open another Fulcrum browser and open the applicable Fulcrum application where the record for the sample was originally created.
    a. Query the sample identifier (the same identifier from the Canary Shiny app).
    b. Compare the identifier combination between this record and the shipping record – *they will not match!*
4. Now you will need to troubleshoot and do some digging to resolve the mismatch.
    a. Was the sampleID or barcode or sampleClass for the failing sample changed in the original data application record?
        i. Was there a Magpie update request made and fulfilled? Check the Magpie Fulcrum application.
        ii. View the Fulcrum record history to see any changes made over time with the record (see **Appendix B** and **Appendix C** for how to view full record history).
    b. Was the sampleID or barcode or sampleClass for the failing sample changed in the shipping application after shipment?
        i. Was there a Magpie update request made and fulfilled? Check the Magpie Fulcrum application.
        ii. View the Fulcrum record history to see any changes made over time with the record.
        iii. Checking the shipment email sent out by the Stork application can also be handy – query your email to view the original manifest and compare that to both Fulcrum records if necessary.
        iv. Is there a duplicate shipping record?

1) There is potential for two shipping records to exist where one has the correct identifier combination, and the other does not.
2) One record could be loaded successfully and the other not.

NOTE: If a duplicate shipping record is discovered, always make sure to request the errant record for Deletion either via a Magpie Deletion request (NOT LOADED) or a Magpie Update request for deletion (LOADED).

5. Once you have figured out where/why the change occurred between the sample and the shipment, there are two options for resolution:
    a. Directly edit the Shipment Review shipping record to correct it:
        i. First, delete the errant sample's child record.
        ii. Save and close the record.
        iii. Reopen the record and add the sample back in, making sure the identifiers are all correct.
        iv. Save and close the record.
    b. If you are unable to determine which sample identifier is correct and have exhausted all your in-house resources, create a ServiceNow Incident outlining the shipping error and the applicable sample identifiers in question for a HQ staff member to assist you.

Shipping error case studies

Below are some case studies of various error messages and how to solve them. These are some of the most common parser errors seen for Shipping:

1. In the *Shipping: Shipment Review [PROD]* application there is a 'Sample does not exist' error associated with barcode B00000129130 (Error Value), with an Error Message of:

    "Sample does not exist: [tag=BARC.20220711.EPIPHYTON.1.CHLPHEO.1, barcode=B00000129130, sampleClass=alg_domainLab_in.sampleIDchem]. Fulcrum ID=f96216fe-c8eb-4645-a158-687f1add85aa."

    a. This is saying the sampleID and barcode combination has not loaded into the NEON database yet.
    b. This type of error typically occurs when a sample is shipped before it has loaded or if the associated record within the application where the sampleID was created has a parser error as well.
        i. If the shipped sample(s) have not yet hit the load_delay (viewable on Magpie), then it is usually best to wait until they do. Otherwise, HQ Science staff can assess and if deemed necessary manually load the records.

   ii. If the record is failing to ingest within the application where it was created, then it must be corrected and loaded before the shipping record will load.

   iii. In either of these scenarios, the actual shipping record does not need modification, it is the associated records in the *upstream* applications causing the issue.

2. In the *Shipping: Shipment Review [PROD]* application there are two 'has different tags' errors associated with barcodes A00000131300 and A00000131303 (Error Value), with Error Messages of:

   "Uploaded sample with barcode 'A00000131300' has different tags. (OSBS_063.20210603.IB.01, OSBS_063.20210520.IB.01) AND Uploaded sample with barcode 'A00000131303' has different tags. (OSBS_063.20210520.IB.01, OSBS_063.20210603.IB.01)"

   a. These error messages are saying that the two barcodes selected within the shipping application record do not correspond with the sampleID and barcode combination that is loaded to the NEON database.

      i. This is likely due to a change made in the barcode and/or sampleID within the *upstream* application, in this case the *BET: Lab Processing [PROD]* app, after the shipment record itself was created. It is also possible that a Domain Support Inventory app record was not updated after a change.

      ii. To fix, the upstream change needs to be propagated into the shipping record – i.e., these two barcode/sampleID combinations need to be removed from the shipping record and then added back in to match what is reflected in the *BET: Lab Processing [PROD]* application.

   <u>NOTE</u>: If you are unsure which barcode definitively should go with which sampleID, it may be necessary to ask HQ Science staff for assistance. For instance, these samples were shipped to archive at ASU, and a physical sample check may be necessary to confirm the correct combination.

3. In the *Shipping: Shipment Review [PROD]* application there is a 'Changing Barcode' error associated with A00000308847 (Error Value), with an Error Message of:

   "Changing Barcode from A00000308847 to A00000308830 not allowed for Sample [[tag=CARI.SS.20220802.RAW, barcode=A00000308847, sampleClass=swc_fieldData_in.rawSampleID]]."

   a. This is saying that the barcode associated with CARI.SS.20220802.RAW in the shipping record is A00000308830 while the barcode loaded to the NEON database is A00000308847.

      i. The barcode needs updating in the shipping record to match what is in the NEON database.

   <u>NOTE</u>: This error appears in the Canary Shiny app in two different ways. It also appears as: 'has different barcodes' error associated with CARI.SS.20220802.RAW (Error Value), with an Error

Message of: “Uploaded sample with tag 'CARI.SS.20220802.RAW' has different barcodes. (A00000308830, A00000308847).”

4. In the *Shipping: Shipment Review [PROD]* application there is a ‘NAMED_LOCATION_TYPE’ error within the field destinationFacility (Error Field) associated with 'Laragen Inc.' (Error Value), with an Error Message of:

   “Validation failed for field 'destinationFacility' in function NAMED_LOCATION_TYPE. 'Laragen Inc.' is not a recognized NEON named location. List of type codes: (('External Lab'|'DOMAIN')). Fulcrum ID=6c2d7334-530d-442b-9985-e96daedf015d.”

   a. This is saying the external laboratory is not a value recognized in the named location list in the NEON database.

      i. This is an error for HQ Science staff to correct.

SOP I Shipping Manifest Error Correction Workflow

Due to the sheer volume of shipments and samples sent from NEON domains to external laboratories, there will inevitably be errors in shipping manifest and/or receipt form files and packages. Some examples include:

- Samples listed on a manifest form that are not present physically in the shipping box,
- Samples physically found in the shipping box that are not listed on the manifest form, or
- A shipment notification sent but the physical box was not shipped.

It is important that NEON staff correct issues to ensure the receiving laboratory has the most accurate information to process the samples received. An accurate manifest is important for efficient laboratory work, and it is expected that NEON staff proactively communicate any errors discovered in the manifest with the external laboratory.

The standard chain of custody email created by the Stork Shiny application provides a receipt form to the receiving lab which they are required to complete and return to the NEON data portal within two weeks of receipt. Even though the receipt form offers the ability to record discrepancies in the manifest versus what was received, it is preferred that NEON staff provide the laboratories with accurate manifest and receipt form files when an error is discovered. This is important to reduce labor and possible confusion for the receiving laboratories. In addition, there are certain sampleTypes where the laboratory needs supplemental information to process the sample and data errors can be introduced when laboratories are forced to manually add unknown samples to their files.

External laboratories are instructed to notify NEON staff (CLA, HQ Science, and the sender) when they receive unknown samples in a package, or if samples appear to be missing from the box. Upon receiving this notification, NEON staff must correct the shipping files as soon as possible and provide the lab with updated digital materials via the normal workflow – i.e., via the Fulcrum Shipping application and the Stork Shiny app. This allows the lab staff to proceed with their data return and processing of samples in a timely manner.

This SOP describes how to correct Fulcrum shipping records and provide external laboratories updated manifests and receipt forms. Step by step instructions are provided along with **Figure 3**, which depicts the decision tree for correcting Fulcrum shipping records.

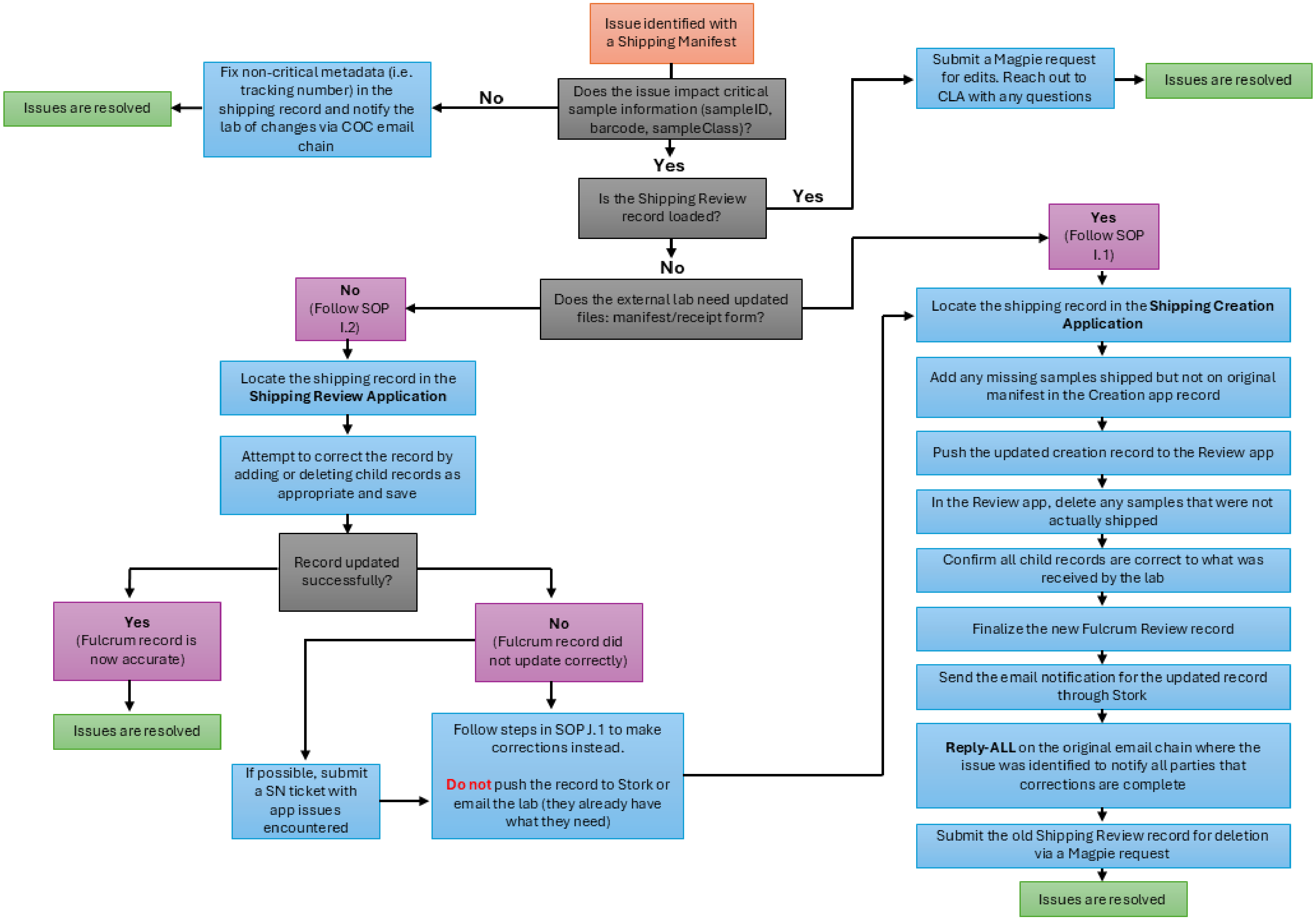


Figure 3. Decision tree for correcting Fulcrum shipping record where an issue was identified in the manifest. The colored rectangles represent the following: grey: decision point; blue: action item; purple: reference for further direction; green: resolution.

I.1 Workflow for Manifest with Errors – Laboratory requires updated materials

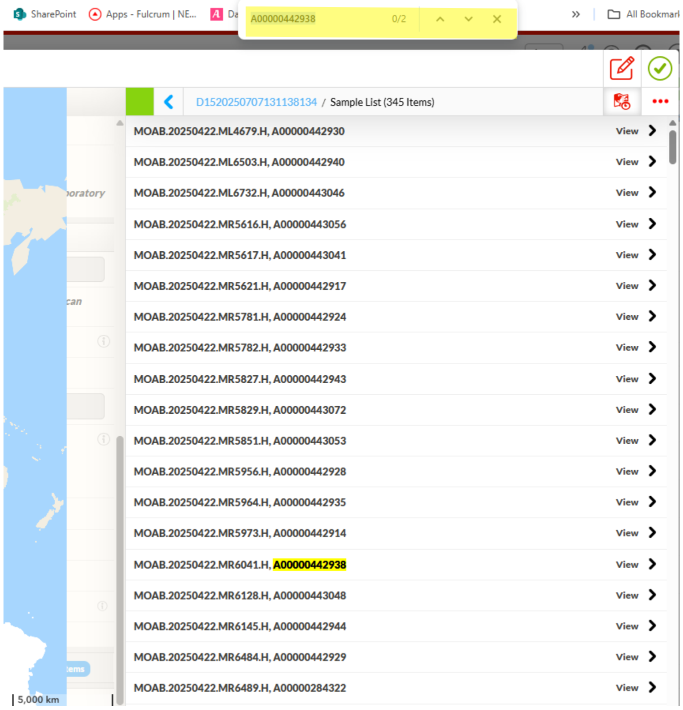
This section describes how to correct Fulcrum shipping records and provide external laboratories updated manifests and receipt forms via a new Stork notification email. There are multiple scenarios where this may occur:

- Sender realizes they made a mistake soon after shipment.
- Laboratory notifies NEON staff of discrepancies upon receipt of package and requests new documentation. For example:
  - More samples received than listed on manifest.
  - Different samples received than listed on manifest.
  - Fewer samples received than listed on manifest.

Since the laboratory will be waiting for updated materials to process samples and return required forms to NEON, it is imperative this work is completed as soon as possible. An entirely new Shipping Review record needs to be created in Fulcrum due to constraints in the Stork app, which will not let you submit a duplicate record for email notification. The Shipping Review record you create following the process below will have the exact same parent level metadata as the original – i.e., COC#, shipDate, etc.

1. In the Fulcrum *Shipping: Shipment Creation* application, find the applicable record.
2. Open the record to perform necessary edits:
   a. The 'Shipment Information' should likely remain the same.
   b. If new sample identifiers need to be added (left off on original manifest), use your preferred method to add the samples into the shipment record individually.
   c. If sample identifiers need to be removed (never actually sent but on manifest), it is best to do this in the Review application once the new record is pushed (see 3.b below).
3. Once editing is complete, select "Yes" for 'Shipment Complete' and proceed to the newly created record in the Shipment Review application.
   a. Open the new record in the Fulcrum Shipping: Shipment Review application and perform any remaining edits.
   b. Delete any sample identifiers that were not shipped by hitting the 'X' button in the child record page.

   TIP: If editing a large shipment, child records can be searched easily by hitting CTRL+F on your keyboard, this will pop up a search bar in the top right corner of the screen where you can query by sampleID/barcode and the child record will be highlighted in yellow.



D15202507071311138134 / Sample List (345 Items)

MOAB.20250422.ML4679.H, A00000442930 View
MOAB.20250422.ML6503.H, A00000442940 View
MOAB.20250422.ML6732.H, A00000443046 View
MOAB.20250422.MR5616.H, A00000443056 View
MOAB.20250422.MR5617.H, A00000443041 View
MOAB.20250422.MR5621.H, A00000442917 View
MOAB.20250422.MR5781.H, A00000442924 View
MOAB.20250422.MR5782.H, A00000442933 View
MOAB.20250422.MR5827.H, A00000442943 View
MOAB.20250422.MR5829.H, A00000443072 View
MOAB.20250422.MR5851.H, A00000443053 View
MOAB.20250422.MR5956.H, A00000442928 View
MOAB.20250422.MR5964.H, A00000442935 View
MOAB.20250422.MR5973.H, A00000442914 View
MOAB.20250422.MR6041.H, A00000442938 View
MOAB.20250422.MR6128.H, A00000443048 View
MOAB.20250422.MR6145.H, A00000442944 View
MOAB.20250422.MR6484.H, A00000442929 View
MOAB.20250422.MR6489.H, A00000284322 View

Figure 4. Screenshot of how to search using keyboard shortcut CTRL+F.

4. Confirm the shipment record is accurate and complete.
5. Finalize the shipment record.
6. Proceed to the Stork shiny app and push the email notification (as normal).
7. Reply-ALL on the email chain to notify all parties (lab, CLA, HQ Sci) that the issue has been resolved and updated materials have been sent.
8. Request the old, shipping review record for deletion via a Magpie deletion request.
    a. Do not wait on this step! The duplicate shipping records can/will load to the database if this step is not completed before the load delay is expires.

I.2 Workflow for Manifest with Errors – Laboratory does not require updated materials

This section describes how to correct Fulcrum shipping records when the external laboratory does not require an updated manifest or receipt. There are multiple scenarios where this may occur:

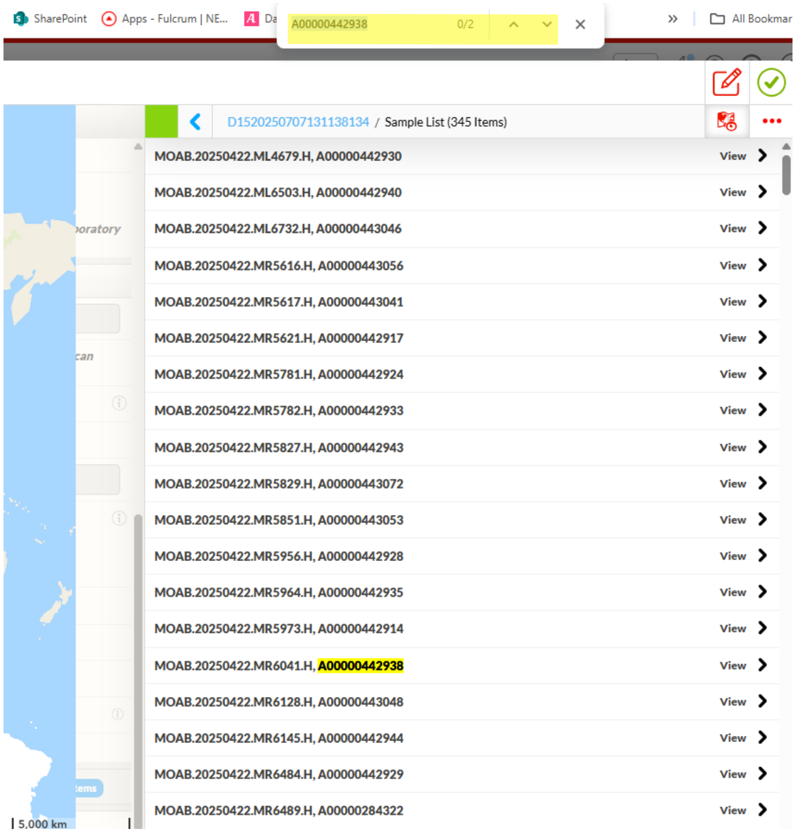
- Sender realizes they made a mistake a while after shipment.
- Laboratory notifies NEON staff of discrepancies upon receipt of package but advises they were able to return receipt data without issue:
    - More samples received than listed on manifest.

  - Different samples received than listed on manifest.
  - Less samples received than listed on manifest.

NOTE: The only time constraint for this workflow is to prioritize completion before the shipping record loads to the NEON database (load delay = 45 days). If this is not possible or the issue is caught much later, Field Science will not be able to edit the record and a Magpie update request should be submitted.

1. In the Fulcrum *Shipping: Shipment Review* application, find the applicable record.
2. Open the child record view of the record by clicking on the 'Sample List' field.
3. After clicking on the 'edit' icon.
   a. Child records may be deleted by hitting the 'X' button (if they were not actually shipped).
   b. OR new child records can be added using the '+' sign (if they were shipped but not listed).

   TIP: If editing a large shipment, child records can be searched easily by hitting CTRL+F on your keyboard. This will pop up a search bar in the top right corner of the screen where you can query by sampleID/barcode and the child record will be highlighted in yellow.



A00000442938

D1520250707131138134 / Sample List (345 Items)

MOAB.20250422.ML4679.H, A00000442930 View
MOAB.20250422.ML6503.H, A00000442940 View
MOAB.20250422.ML6732.H, A00000443046 View
MOAB.20250422.MR5616.H, A00000443056 View
MOAB.20250422.MR5617.H, A00000443041 View
MOAB.20250422.MR5621.H, A00000442917 View
MOAB.20250422.MR5781.H, A00000442924 View
MOAB.20250422.MR5782.H, A00000442933 View
MOAB.20250422.MR5827.H, A00000442943 View
MOAB.20250422.MR5829.H, A00000443072 View
MOAB.20250422.MR5851.H, A00000443053 View
MOAB.20250422.MR5956.H, A00000442928 View
MOAB.20250422.MR5964.H, A00000442935 View
MOAB.20250422.MR5973.H, A00000442914 View
MOAB.20250422.MR6041.H, A00000442938 View
MOAB.20250422.MR6128.H, A00000443048 View
MOAB.20250422.MR6145.H, A00000442944 View
MOAB.20250422.MR6484.H, A00000442929 View
MOAB.20250422.MR6489.H, A00000284322 View

Figure 5. Screenshot of how to search using keyboard shortcut CTRL+F.

c. When adding new child records, the following needs to be correctly populated:

   i. The **sampleType** is constrained by the selection originally made in the creation application.

   ii. The new identifier can be added either by the **sampleID*** (required) or the barcode field (optional).

   iii. The **sampleFate** should automatically populate to 'active'.

   iv. The **sampleClass*** (required) will automatically populate.

   v. The location* (required) will automatically populate.

   vi. The **collectDate** will automatically populate.

d. Once editing is complete, save the record.

<u>NOTE:</u> If this procedure is not working – i.e., some of the required fields are not populating correctly, or at all, or you cannot add in the new sample identifier – proceed to **SOP I.1** and follow that workflow instead, but omit sending any of the email communications.

8 REFERENCES

Chapman, A.D. 2005. Principles of Data Quality – Report for the Global Biodiversity Information Facility 2004. Copenhagen: GBIF.

Fisher, C., Eitel, L., Chengalur-Smith, S., and R. Wang. Introduction to information quality. Cambridge, MA: MIT Information Quality Program.

Michener, W.K. and J.W. Brunt. 2000. Data Management Principles, Implementation and Administration. Ecological Data – Design, Management, and Processing (ed. W.K. Michener and J.W. Brunt), Blackwell Science Ltd, Oxford.

N.J. Van Lanen, C.M. White, J.A. Fogg, and M. F. McLaren. 2012. Integrated Monitoring In Bird Conservation Regions (IMBCR): Data Entry Protocol. Unpublished report. Rocky Mountain Bird Observatory, Brighton, CO, USA. URL: rmbo.org/v3/Portals/0/Documents/Science/Protocols/

Sebastian-Coleman, L. Measuring Data Quality for Ongoing Improvement: A Data Quality Assessment Framework. 2013. Elsevier Inc: Waltham, MA.

APPENDIX A DATA ENTRY TRAINING CHECKLIST

So, you are ready to begin entering _____________________ data.

(protocol)

Make sure you complete the following checklist before beginning. A permanent staff member or designated lead technician will need to sign off on your checklist before actual data entry can begin. Confirm with your lead technician if any sections of the Data Management Protocol can be skipped if you are not involved in those activities – e.g., using the Magpie tool or resolving parser errors, etc.

- ☐ Read through the Data Management protocol (if time limited, then emphasize sections pertinent to your job duties).
- ☐ Review Data Management Training Materials (Presentations, quizzes, worksheets).
- ☐ Read relevant protocol-specific Fulcrum User Manual(s).
- ☐ Enter at least one datasheet, plot or subplot of data into the training data entry application (CERT) for the relevant protocol.
- ☐ Talk through the process of:
    - ☐ Annotating datasheets
    - ☐ NEON data entry webpage login, ability to navigate to protocol-specific apps
    - ☐ Appropriate remarks, use of commas and special characters
    - ☐ Manual data transcription QAQC process
    - ☐ Proper datasheet procedures after completion
    - ☐ Importance of catching and reporting duplicates
    - ☐ Use of the Magpie tool (may only be applicable to year-round staff)
    - ☐ Evaluating and resolving parser errors (may only be applicable to year-round staff)

______________________________	__________	______________________________	__________
Trainee Signature	Date	Trainer Signature	Date

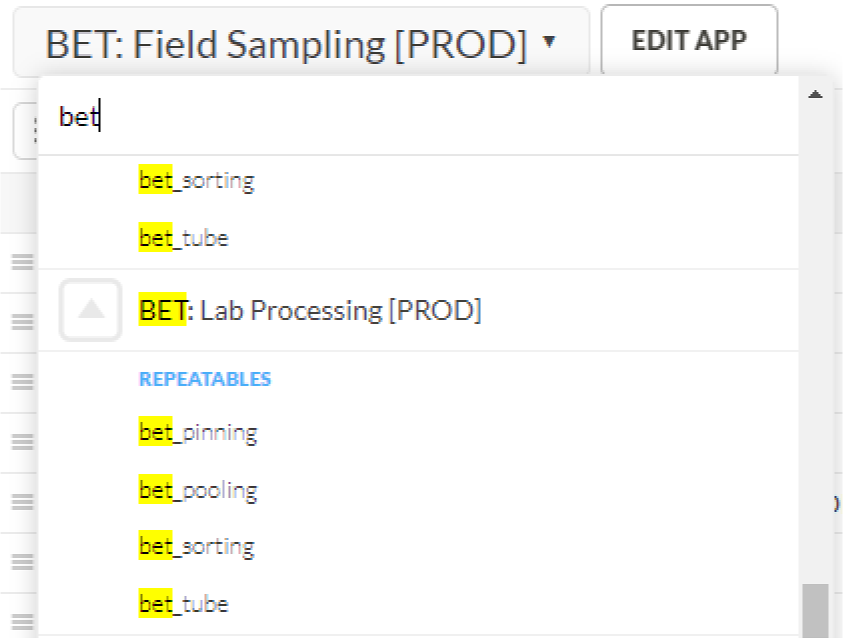
APPENDIX B HOW TO FILTER AND VIEW FULCRUM DATA IN THE WEBUI

This appendix describes how to set up filters, select specific columns, and how to efficiently view Fulcrum data via the webUI. A quick data review is much more efficient if you are only viewing those data of interest. Proper filtering will also set up your data for potential export into Excel for further investigation if needed (see **Appendix C**).

1. From the application dashboard (url: https://web.fulcrumapp.com/) query and click on the desired application. This brings you to the App Dashboard which will default to viewing the 'Record Activity'.
   a. Click the 'View Records' button, upper right-hand corner, far left icon.
   b. Make sure you are in 'Table View' (upper right-hand corner icon), not 'Map View'.

   c. To toggle between applications, tap on the application name bar at the top left-hand side of the screen and begin typing in the first few characters of the application name.

TIP: You can view a table of child records in the web browser as well. When using the search bar, child records, if applicable, will be displayed under 'REPEATABLES' for a given parent application.



2. Once an app is selected, the view defaults to showing all the records for a given application from your domain.
   a. Quick Filters are available on the left-hand side bar, which include dates and record status which may be useful filters.

   b. Click the ‘Toggle Quick Filters’ button to remove the Quick Filters bar (three horizontal lines with a dot to the left of the main search bar).

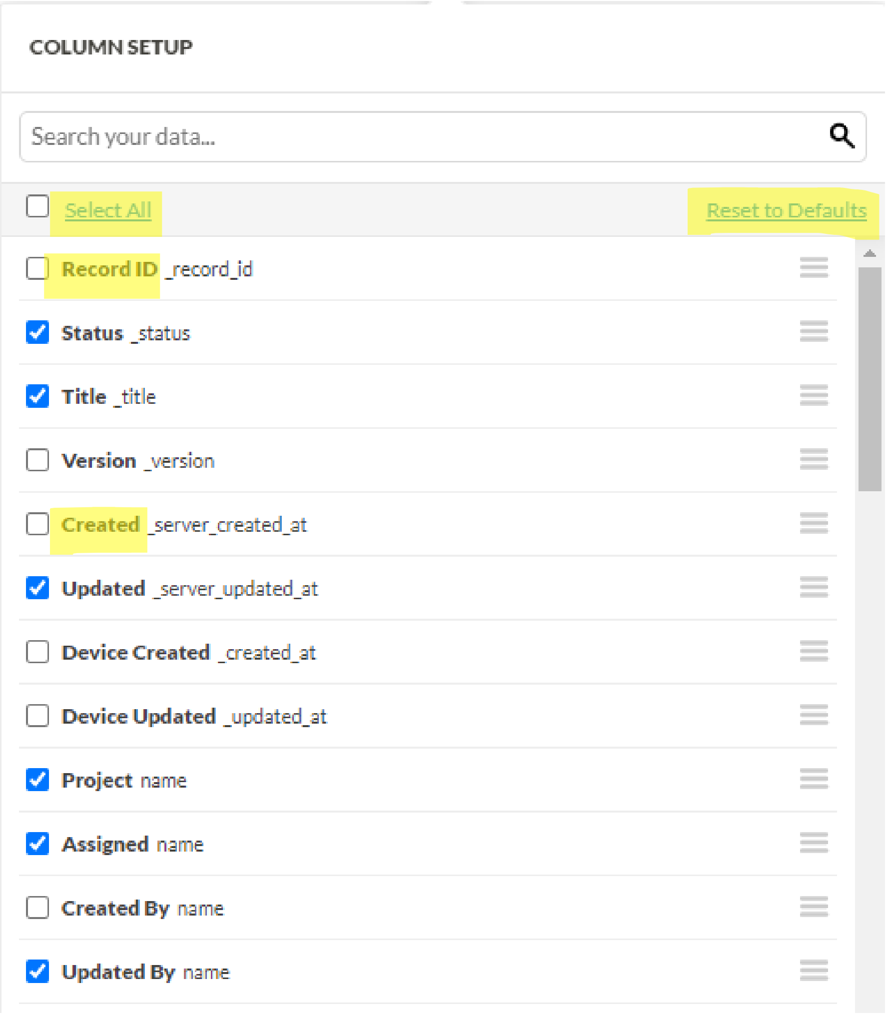
3. When first viewing records, Fulcrum has a default view comprising a subset of columns for a particular application. It is often necessary to add more columns for effective data viewing and QC checking. Additionally, when exporting data (see **Appendix C**), only those columns selected will be in the downloaded file.

   a. Hit the ‘Column setup’ button (three vertical lines) to manually add or remove columns that will display by checking the box to the left of the column name.

      TIP: When displaying the column setup list, click on the horizontal lines and drag to rearrange the columns.

   b. There are options to ‘Select All’ or to ‘Reset to Defaults’ which can come in handy.

   c. **Record ID** is often very useful to have displayed, this is the FulcrumID.



COLUMN SETUP

Search your data...

☐ Select All   Reset to Defaults

☐ **Record ID** _record_id
☑ **Status** _status
☑ **Title** _title
☐ **Version** _version
☐ **Created** _server_created_at
☑ **Updated** _server_updated_at
☐ **Device Created** _created_at
☐ **Device Updated** _updated_at
☑ **Project** name
☑ **Assigned** name
☐ **Created By** name
☑ **Updated By** name

   d. **Created** is when the record was synched and when it was created on a tablet, respectively, and those dates are important to know for QC.

   e. **LOAD_STATUS** is a default column. Make sure to keep this column visible, as it will tell you the current status of the record – i.e., NONE, SKIP, LOADED, PARSE_FAIL.

4. There are several options for filtering data, and Fulcrum has published a how-to article here: Fulcrum instructions to filter data

   a. The main search bar is useful for a particular identifier – e.g., sampleID, barcode, siteID, etc.

      i. The search functionality will also query child records that may not be displayed within the parent record but will locate an identifier within that child record.

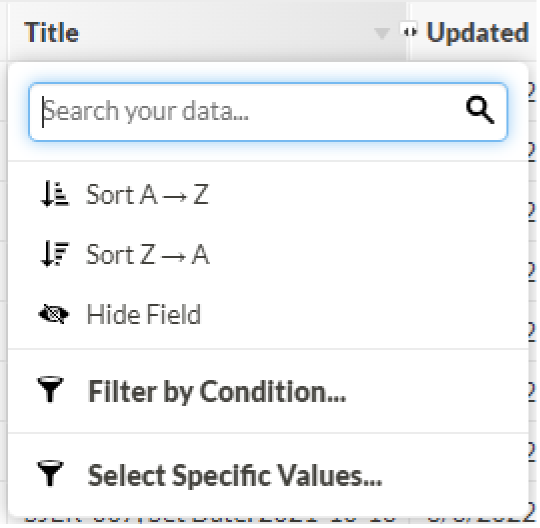
   b. Clicking on any column header will allow further filtering or sorting functionality:

      i. **Sort** alphabetically – A-Z or Z-A.

      ii. **Filter by Condition** – use logical operator.

      iii. **Select Range** – toggle range of values or type in directly.

      iv. **Select Specific Values** – type directly in search bar and/or manually check boxes.



   c. The ‘Custom Filters’ button (to the left of the Column Setup button) allows multiple levels of filters using logical operators.

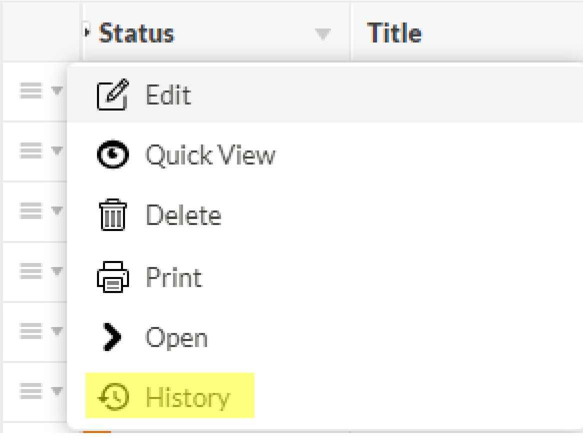
   d. The ‘Clear all filters’ button is used to clear filters. CLEAR ALL FILTERS

5. The ‘Save View’ button can be used to save a particular filter set for quick viewing next time. Give your custom view a meaningful title and click ‘Confirm’. SAVE VIEW

   a. Your saved view will be displayed in the application bar at the top of the screen underneath the application name titled ‘Views’.

6. An individual record can be edited, viewed, or popped out into another browser window by selecting the filter button (down arrow and three horizontal lines) ≡ ▾
   a. **Edit** – will fully open record to modify.
   b. **Quick View** – will open record in a pop-up view.
   c. **Print** – will open a printable pdf.
   d. **Open** – will pop out the individual record for easy viewing in another browser window.
   e. **History** – this will display all the changes made to a record over time and will pop out in another web browser.

<u>NOTE</u>: The history of a record can be very useful for resolving parser errors as changes made to sampleID, taxon, or barcodes etc. after a record was initially created will often lead to downstream errors in lab or shipping applications.



APPENDIX C HOW TO EXPORT FULCRUM DATA IN THE WEBUI

This appendix describes how to export data from Fulcrum. You may need to export data for QC review or other reporting purposes. It is typically easier to export data from Fulcrum and then manipulate and filter those data in Excel than it is to filter and summarize data in Fulcrum via the webUI. In addition, it can be very helpful to download and view the full version history of a record. This can be especially true when the full version history of a record is needed to resolve an ingest failure.

C.1 Exporting Data from the Record Editor

1. From the application dashboard (***url***: https://web.fulcrumapp.com/), navigate and click on the "records" button of an application for which you wish to export data.

   This brings you to what is called the "Record Editor" – i.e., the location for entering records through a web browser.

2. Make sure you have your desired filters selected to narrow down the subset of records you would like to export, see **Appendix B** for further details.

3. You may also customize which columns are exported using the "Column Setup" button (three vertical lines).

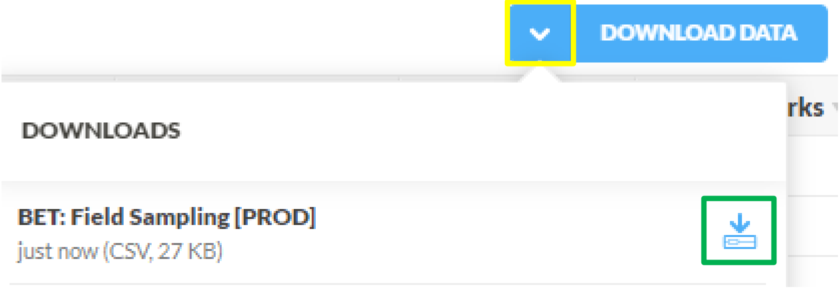
   NOTE: Only those columns selected within the "Column Setup" will be included in your data download!

4. After any custom filters are in place, click on the blue "DOWNLOAD DATA" button in the top right-hand corner of the Record Editor.

5. A new window will pop up prompting you to select the desired file format.
   a. Both .CSV and .XLSX file formats can be opened in Microsoft Excel.
      i. Select .CSV if you intend to pull your data into a software program such as R.
      ii. Select .XLSX if you would like both parent and child records downloaded as one spreadsheet with multiple tabs
   b. 'Record Links' pulls in the FulcrumID via the record title or the record ID.
      i. Select *Title* for logistical referencing and *ID* for relational joining.
   c. *If applicable*, select the type of 'Media Fields' to download.

7. Click "Start" after selecting a file format, the window will then say "Processing".
   a. This process will take more time with increasing numbers of records and child records.

8. Click the blue down arrow button next to the "DOWNLOAD DATA" button, then highlight and select the data you just prepared for download.

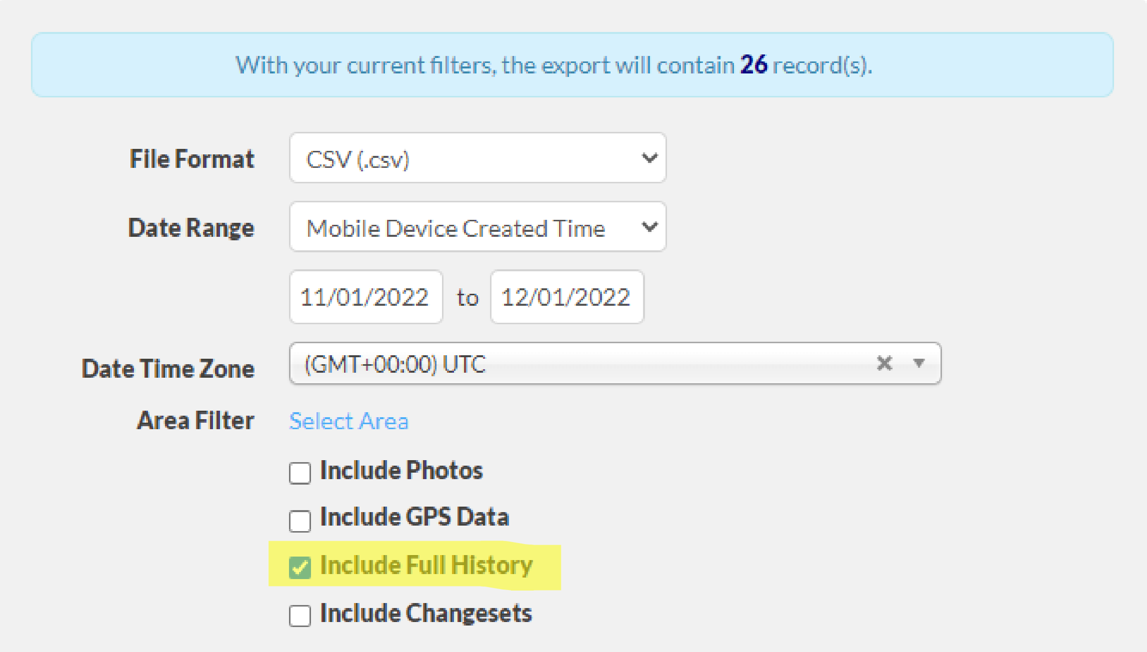


BET: Field Sampling [PROD]
just now (CSV, 27 KB)

9. The data will automatically save to the “Downloads” folder of your local computer.
   a. For applications with child and/or grandchild records, *the exported data will be divided into separate files* (“child” and “grandchild” are not keywords in the file names) UNLESS you have selected .XLSX in which case there will be one file with multiple tabs:
      - One **parent** file.
      - One or more **child** files (if applicable).
      - One or more **grandchild** files (if applicable).
   b. Rows in these separate files are related by several columns:
      - **Parent** files will have a single unique identifier column named “_record_id.”
      - **Child** and **grandchild** files will have three record identifier columns: “_child_record_id”, “_record_id”, and “_parent_id.”
        - In **Child** files, the “_record_id” and “_parent_id” columns will be equal to each other. Both of these fields correspond to the “_record_id” value in a parent file.
        - In **Grandchild** files, the “_record_id” value equals the “_record_id” in the parent file. However, in this case the “_parent_id” equals the “_child_record_id” in the child file (because the child records are the direct “parent” of the grandchild record).
      - Instructions for merging dozens of data columns across hundreds or thousands of child/grandchild records in Excel or other software are complex, error prone, and beyond the scope of this document. If you require merged records, data exported from the Magpie applications are delivered as a single, fully merged file.
        - A tutorial on how to use and manipulate data in Excel is provided in the Field Science Training Center (link).

C.2 Exploring full version history for a record

1. From the application dashboard (***url***: https://web.fulcrumapp.com/), click on the '+' sign in the upper righthand corner of the screen, a menu will pop up with several options, select 'Export'.
2. **File Format** should be either CSV or Excel XLSX.
3. Select a **Date Range** – be sure to include the date the record was created.
4. For **Area Filter**, be sure to **check the box 'Include Full History'.**
5. For **Apps**, select the application of interest, it is best practice to only select one at a time for download.
6. For **Projects**, select your domains Project ID.
7. Download the data from Fulcrum to your local machine.



With your current filters, the export will contain **26** record(s).

File Format CSV (.csv)

Date Range Mobile Device Created Time

11/01/2022 to 12/01/2022

Date Time Zone (GMT+00:00) UTC

Area Filter Select Area

☐ Include Photos

☐ Include GPS Data

☑ Include Full History

☐ Include Changesets

a. Scroll back up to the top of the page where there will be a light blue box displaying the number of records that will be contained in your export.

b. Select NEXT.

c. The Export Summary will be displayed, select CONFIRM.

d. The Exports page will display downloads you've made over time, highlight the one of interest and select the Download icon to download your results locally.

8. The downloaded file will have the same conventions as other Fulcrum downloads, with a parent file, and if applicable, “child” and “grandchild” files.
    - The parent file will give details such as version history, load status, error remarks, dates changes to the record were made, etc. Fields such as these may come in handy to pinpoint when a particular error arose and what the error message means.
    - The child or grandchild file will generally give details such as the sample identifier – i.e., the sampleID or the barcode. It is then easy to see if sampleIDs or barcodes have changed over the lifetime of the record and could lead to a parser error.

APPENDIX D SUPPLEMENTAL PARSER ERROR RESOLUTION WORKFLOWS

This appendix describes specific parser error resolution workflows, including a few protocol-specific errors that may be encountered and ways to resolve them.

D.1 Parser Error: Sample Does Not Exist

Problem

A record's sampleID should have a matching value in another "upstream" application but does not. Usually, this means a Lab record does not directly link to a Field record.

Causes

- Changes to metadata values used to construct the sampleID in upstream records, AFTER downstream records were created.
- Upstream records deleted but downstream records still exist.
- Upstream records have not yet loaded.

Check For…

- (**Solution A**) SampleIDs that do not match ***exactly*** between upstream and downstream records.
- (**Solution B & C**) Missing records in the upstream app.
- (**Solution D**) All sampleIDs match between upstream and downstream records.

Solutions

Solution A

FULCRUM DOES NOT AUTOMATICALLY UPDATE DATA ACROSS LINKED RECORDS

If upstream record data are correct but downstream record data are not updated:

1. Open the downstream record.
2. De-select the currently selected upstream record.
3. Re-select the upstream record. This action forces Fulcrum to bring the updated upstream metadata into the downstream record.
4. Save the record (and re-sync if editing on a tablet).

Solution B

If the upstream record/sampleID no longer exists and should NOT exist:

1. Request downstream records for deletion. If the downstream record is a Fulcrum child record that has not yet loaded, then Field Science staff may delete the record and a Magpie request is not needed.

Solution C

If the upstream record/sampleID no longer exists and SHOULD exist:

1. Create a new upstream record, if possible. This record’s sampleID must match the downstream record’s sampleID.
2. Recall that a new record will have a “fresh” load delay time, thus the parser error message will persist until this new record is ingested.
    a. Contact Science for assistance if the wait period is excessive – e.g., samples need to be shipped, and records need to be manually loaded ahead of the load delay.

Solution D

The upstream record already exists, SHOULD exist, and SHOULD allow the downstream record to load (because the upstream record sampleID is correct). This is usually caused by one of the following scenarios:

1. **Load Delay Time**:
    a. Remember that every record has a load delay that starts counting down from the **"created_date".**
    b. If you just created a new record to match a downstream sampleID, you will see the parser error until the new record's load delay is reached.

    SOLUTION: Wait until the load delay time is met.
2. **Other Record Parser Failures**:
    a. Recall that data are ingested in "sets" or "groups" of records per domain and per load group, from potentially multiple applications.
    b. A single error in a loading data set will cause all records to not ingest.
        i. ***Example***: 10 records have met the load delay time. There is one record with a parser error, therefore ALL 10 records will NOT load.

    SOLUTION: Fix parser errors in other records.

D.2 Parser Error: _THAN (Fails Comparison)

Problem

A numeric value or date is compared to another value for validation or plausibility purposes. This error generally occurs when a reported value is outside an expected range or reported dates are out of an expected order (e.g., a sample collection date is reported as occurring *before* the trap is set). Comparison may be made to an absolute value (e.g., basalStemDiameter < 30) or as a comparison to another measurement field (e.g., vdBaseHeight < vdApexHeight).

Causes

- Typographical error, value includes an extra digit or numbers have been transposed.
- Incorrect units used for measurement.
- Protocol confusion.
- SampleID errors in already loaded records.

Check For…

- (**Solution A**) Typographical error in values.
- (**Solution B**) Transposition of values across data fields.
- (**Solution C**) SampleID errors. ***Note****: Errors may be caused by other records.*
- (**Solution D**) Incomplete records.

Table 6. Table of common _THAN requirements by TOS protocol.

Data Product	Field	operator	comparisonValue
BET	identifiedDate	>	collectDate
VST	measurementHeight	≤	200
CDW, HBP, LTR, SLS	ovenEndDate	>	ovenStartDate
CDW, HBP, LTR	weighDate	≥	ovenEndDate
CDW, VST	ninety…Diameter	≤	max... Diameter
HBP, LTR, MOS, TCK	collectDate	>	setDate
HBP, LTR, SLS	ovenStartDate	≥	collectDate
VST	measurementHeight	≤	200
VST	vdBaseBreakHeight	<	vdApexBreakHeight
VST	vdApexHeight	>	vdBaseHeight
VST	basalStemDiameterMsrmntHeight	<	100
SLS	freshMassBoatMass	>	dryMassBoatMass
SLS	dryMassBoatMass	<	freshMassBoatMass

Solutions

Solution A

Typographical errors in values

1. If it is clear that the error is caused by a data entry error and the intended value is clear (e.g., measurementHeight = 1300 when standard measurementHeight = 130, or stemAzimuth = 725 which is a likely transposition of 275, based on pointID and subplotID):
    a. Open the record with the incorrect value.
    b. Edit the value.
    c. Save/Sync.
2. If it is not clear what caused the error:
    a. If the sample is still available, re-measure and edit the record accordingly, OR
    b. If the sample is not available and the field is not required, nullify after consulting with the protocol author, OR
    c. If the error cannot be resolved, and the field is required, delete the record (child), or request deletion through Magpie (parent).

Solution B

Transposition of values across data fields

1. Look at both fields being compared (note that only the field causing the error will appear in the Parser error output). If it is clear that the intended values are switched:
    a. Open the record.
    b. Switch values to correct fields.
    c. Save/Sync.

Solution C

SampleID error in an already loaded record. Since the sampleID already exists in the database, the parser ignores internal, within record comparisons, and defaults to the value/date associated with the already loaded record. This could occur if an update to a parent sampleID isn't propagated to the child record.

1. Look up the Fulcrum record that is causing the error.
2. Copy the sampleID.
3. Open the child sample view for the app (selecting underneath the 'REPEATABLES' blue text.
4. Filter on sampleID.

5. If > 1 record comes up and one or more have load_status = 'LOADED', review the loaded records, for parent / child sampleID mismatches.
6. Submit a Magpie L0 update request.

Solution D

Incomplete records: e.g., errorField = nullFieldValidation; errorValue = (0 > 0). This error occurs when a set of the expected data fields are all null.

7. Look up the Fulcrum record that is causing the error.
8. If the record is a child record, use the child record view (selecting underneath the 'REPEATABLES' blue text.
9. Filter data columns by Parent ID = fulcrumRecordID.
10. Left click the data column that is in error, under 'Filter by Condition…', select 'Is blank'.
11. Identify null records, containing no data.
12. Edit record if appropriate.
13. Delete if unresolvable, and the record is a child record.
14. Request deletion if the error is unresolvable and the record is a parent record.
15. Repeat process if more than one data column is in error.

<u>Protocol Specific Solutions</u>

***Vegetation Structure*: VST – nullFieldValidation (0 > 0)**

This field does not exist in Fulcrum; it is generated on ingest to check that each record actually has data in it. The requirement is 1 or more fields in the list below:

- stemDiameter
- basalStemDiameter
- vdApexHeight
- maxCrownDiameter
- ninetyCrownDiameter

At least one of the above fields must be NON NULL if **plantStatus** is *not* one of the following values:

- Removed
- No longer qualifies
- Lost, burned
- Lost, herbivory
- Lost, presumed dead
- Lost, tag damaged
- Lost, fate unknown

- Downed

In other words, if **plantStatus** = “live”, “standing dead”, “broken bole”, or any of the live but damaged options, there must be data in one of the stem diameter, height, or crown diameter fields listed above.

D.3 Parser Error: ReferenceCount

Problem

There is a duplicate sample identifier within the dataset being uploaded. Sample identifier fields must be unique; if not, then the data associated with an identifier cannot be traced back to one individual sample, thereby breaking the sample chain. This error typically occurs across records (i.e., rows of data) rather than within a single record.

Note that the same rules apply for sample barcodes in that they must be unique, although this parser error currently only captures duplication of non-barcode sample identifier fields.

Causes

While some data entry applications can stop you from generating duplicate sampleIDs in child records, this functionality is not possible for parent records.

Some common causes of this error are:

- An identical record for a sample was inadvertently created more than once.
- A sample was inadvertently created more than once at different times and/or by different people.
- In many Fulcrum applications, the sampleIDs are generated behind-the-scenes by concatenating different pieces of metadata that, when joined together, create a unique ID. A duplicated value in one of these metadata values can create a duplicate identifier.
- A sample identifier created in an upstream app was accidentally selected more than once in the downstream app in which the duplication error occurred.

Check For…

- (**Solution A**) Identical *records* in the same app, and all associated metadata values are correct.
  Example: Data for a batch of samples is entered one sample at a time, and the data for one sample is accidentally entered more than once. In this instance, every value in the affected records is an exact match.
- (**Solution B**) Identical *sample identifiers* in more than one record in the same app, but the metadata associated with the records is different and values are correct.
  Example: A soil sample was inadvertently processed and measured for soil pH twice and the data were entered twice.
- (**Solution C**) Identical *sample identifiers* in the same app due to incorrect metadata values being selected.

Example: For two different plots sampled on the same day, the same plotID was accidentally selected for two different records.

- (**Solution D**) Identical *sample identifiers* in the same app due to the incorrect sample identifier being selected from a drop-down list of available sample identifiers.

Solutions

This error is generally straightforward to address because you know that the duplicate entry occurred within the specific dataset that the parser is attempting to load.

Solution A

If an identical record was accidentally created:

1. For parent records: Submit a deletion request for the record containing the duplicated identifier.
2. For child records: While these are typically caught by the app before you can save a parent record, it is still possible for a child record to be duplicated. To correct:
   a. Open the duplicated record.
   b. Delete the record from the app.
   c. Save the record (and re-sync if editing on a tablet).

Solution B

If a record containing the same sample identifier was accidentally created:

1. Only one of the records can be kept, so it is important to review all metadata values in the affected records and determine which record to keep.
2. For parent records: Submit a deletion request for the record to be deleted.
3. For child records: While these are typically caught by the app before you can save a parent record, it is still possible for a child record to be duplicated. To correct:
   a. Open the duplicated record.
   b. Delete the record from the app.
   c. Save the record (and re-sync if editing on a tablet).

Solution C

If a sample identifier was accidentally created in the app due to incorrect metadata values in the affected record:

1. If you can identify which record contains the incorrect sample identifier and you have the correct metadata values:
   a. Open the record.
   b. Modify the incorrect metadata value(s).

   c. Save the record (and re-sync if editing on a tablet).

2. If you can identify which record contains the incorrect sample identifier but cannot determine how to correct the metadata, then:
   a. Submit a deletion request (for parent records).
   b. Or delete the record (for child records only; be sure to save the changes!).
3. If you cannot identify which record contains the incorrect sample identifier, then all affected records may need to be deleted.
   a. Contact Science for further guidance.

Solution D

If a sample identifier created in an upstream app was accidentally selected more than once in the downstream app where the duplication occurred:

1. If you can identify which record contains the incorrect sample identifier and you know how to fix it:
   a. Open the record.
   b. Modify the record by selecting the correct identifier, if the correct identifier exists.
   c. Save the record (and re-sync if editing on a tablet).
2. If the correct identifier does not appear as an option in the downstream app, it may be that the sample identifier was not created in the upstream app.
   a. Open the upstream app.
   b. If the correct sample identifier exists in the upstream record but still isn't appearing in the downstream app for selection, this could be because Fulcrum does not automatically update data across linked records. To fix:
      i. First check that the upstream data are synched.
      ii. Then, open the downstream record, de-select the current sampleID, then re-select the correct sampleID.
      iii. In some cases, you may also need to delete the information in the plot field first, and then re-select the plot before the correct sampleIDs will appear.
      iv. Save the record (and re-sync if editing on a tablet).
   c. If the correct sample identifier does not exist in the upstream app because of a data entry error in an upstream record:
      i. Open the upstream record that contains the error.
      ii. Fix the data entry error(s).

iii. Save the record (and re-sync if editing on a tablet).

d. If the correct sample identifier does not exist in the upstream app because the upstream record was never created, then create a record for the missing sample and save the record (and re-sync if editing on a tablet).

3. If you can identify which record contains the incorrect sample identifier but do not know how to fix it, then:
   a. Submit a deletion request (for parent records), OR
   b. Delete the record (for child records only; be sure to save the changes!).
4. If you cannot identify which record contains the incorrect sample identifier, then all affected records may need to be deleted.
   a. Contact Science for further guidance.

Protocol Specific Solutions

Here's a quick snapshot of common types of soil protocol-specific errors and possible solutions.

Application	Common cause of error	Possible solutions
sls_soilpH, sls_soilMoisture	Duplicated measurement; accidentally selected upstream record from drop-down list more than once	B, C, D
sls_soilCoreCollection	Accidentally entered same sample more than once	A, B, C

D.4 Parser Error: Changing Tag

Problem

The Parser has detected duplicate barcode values in a data set. Barcodes are treated like sample identifiers on ingest and must therefore be unique across all records. One way duplicate barcodes arise is when the same barcode is associated with two or more different sampleIDs.

Example: ONE barcode (A00000007572) is associated with TWO different records where the sampleIDs = SITE_001-M-**5.5-38.5**-20180509 and SITE_001-M-**38.5-5.5**-20180509 (note the reversed values in bold). The Parser cannot determine which sampleID should be associated with the barcode.

Causes

Duplicate barcodes may be:

- In the same record,
- In different records within the ***same app***, or
- In different records within ***different apps.***
- Duplicate barcodes may be located within only ingested (LOAD_STATUS = "LOADED") and/or non-ingested (LOAD_STATUS = "NONE") records.

Solutions

Follow the suggestions outlined below to resolve these types of errors:

1. **Pay attention to the errorMessage text:** The errorMessage presents three useful pieces of information in the following format:
    a. "***barcode = x, tag = y, sampleClass = z***": The barcode noted here is used multiple times, use this to search for Fulcrum records.
    b. "***Changing tag from sampleID1 to sampleID2***": This tells you whether the barcode is associated with multiple different sampleIDs.
        i. ***Example***: "SITE_006-M-0.5-26.5-20180510 to SITE_006-M-26.5-0.5-20180510" are NOT the same sampleID, so one barcode is pointing to two different samples, potentially.
    c. "***sampleClass from ingestTable.A to ingestTable.B***": This information denotes whether the barcode is being used in different TYPES of samples – e.g., a soil sample and a beetle sample might have the same barcode value.
2. **Determine what the errors are with a desktop or laptop computer.**
    a. Copy the barcode from step 1.a.
    b. Analyze the text in step 1.b "Changing tag from..."
        i. ***If sampleID1 does NOT EQUAL sampleID2***, the same barcode has been used with two different sampleIDs.
            1) ***Example***: "SITE_048-**O**-36.5-25.5-20180621 to SITE_048-**M**-36.5-25.5-20180621" are NOT matching sampleIDs.
    c. Analyze the text in step 1.c "sampleClass from..."
        i. **If "*ingestTable.A does NOT EQUAL ingestTable.B*"**, the same barcode has been used with two different sampleIDs of different sampleTypes.
3. **Find all records with the same barcode.**
    a. Navigate to the application noted in the "ingestTable" column.
    b. Determine if the application has a linked "upstream" application.
        i. *Example*: ingestTable = sls_soilMoisture_in; this is the Soil Moisture app and is linked to the upstream Soil Core Collection app.
    c. Paste the barcode into the search bar of the downstream app.
        i. Fulcrum will find the associated record even if the barcode is in a child record.
    d. Open another browser tab if there is an upstream app, and paste the barcode into the search bar of the upstream app.

4. **Determine the error.**
   a. *Within the same application:*
      i. If a search for a single barcode returns more than one record, then the barcode is duplicated across multiple records. This situation is equivalent to having a duplicate sampleID.
         1) To fix, use a different barcode where the duplicate value appears.
      ii. If a search for a single barcode returns one record, then check all barcode fields within the record.
         1) CTRL+F and paste the barcode value.
         2) If the same barcode is used across multiple barcode fields within the same record, update one or more barcode values.
   b. *Across separate unrelated applications:*
      i. The same barcode may have accidentally been used in two unrelated applications.

         Example: Barcode = A000000001 is used in both Mosquitoes (Application 1) and Ticks (Application 2)
         1) Determine the correct barcode associations for both sampleIDs and update the barcode values accordingly.

D.5 Parser Error: VERIFY_URL

Problem

The parser is using a **URL** created either by Fulcrum upon ingest to find an externally hosted file that it is not able to locate. URLs are constructed from file path information, and the Fulcrum file path must exactly match the file path of the external file.

Causes

- The external file does not exist, and the Fulcrum file path is correct.
- The external file exists and:
  - There is an error in the external file path; the Fulcrum file path is correct.
  - The external file path is correct; there is an error in the Fulcrum file path.
  - There are errors in both the external file path and the Fulcrum file path.

Check For…

- (**Solution A**) Required files have been copied to the external location.
- (**Solution B**) Errors in external file paths. Look to ensure that:
  - The correct files are copied into the correct folders and subfolders.
  - Folder structure, folder names, file names, and file types conform to protocol specifications, including case-sensitivity.

- (**Solution C**) Errors in the Fulcrum file path.
    - Look for errors in input fields that Fulcrum uses to auto-create the file path (and URL).

<u>Protocol Specific Solutions</u>

Digital Hemispherical Photos for Leaf Area Index

Solution A

Problem: Required files have not been copied to the external host location, and the parser cannot find file paths (URLs) that do not exist. To resolve:

1. Verify required files are organized properly. For the Leaf Area Index protocol, use the 'Warbler' Shiny QAQC tool to organize and copy images based on Fulcrum file path data. Look to ensure that:
    a. The required files have been uploaded to the GCS ingest bucket.
    b. Folder structure, folder names, and file names all conform to protocol specifications, including case-sensitivity.
    c. The file type is correctly specified in Fulcrum. Fulcrum defaults to ".NEF" but if ".JPG" files were accidentally generated in the field, the "JPG" file type must be specified in Fulcrum for the Image File Path to match the files that were uploaded to the ingest bucket.
2. Use Warbler to upload properly organized files to the GCS ingest bucket. An automated job transfers files from the ingest bucket to the publication bucket on a weekly basis.

Solution B

Problem: Required files have been uploaded to the GCS ingest bucket, and an error is discovered in one or more file paths in Fulcrum (child records). To resolve:

1. Update any incorrect input data that Fulcrum uses to construct the **Image File Path**.
2. Once **Image File Path** data in all child records have been verified to be correct, use the 'Warbler' Shiny QAQC tool to re-organize images based on the corrected Fulcrum file path data.
3. Verify that the expected number of files exist in each terminal subfolder.
4. Repeat steps (1)–(3) if any folder or file names are discovered that do not conform to naming conventions specified in the protocol.
5. Use Warbler to upload a new copy of the corrected files to the GCS ingest bucket.
6. Submit a ServiceNow Incident to request deletion of images that were uploaded with incorrect file path metadata.

Solution C

Problem: There is an error in one or more Fulcrum file paths. To resolve:

1. View file paths in Fulcrum table format.
    a. View Child Records in Fulcrum since file path data are contained in child records.
2. Identify the record(s) with one or more errors in the file path.
3. Edit the record(s) to fix input data that are the source of the error(s).
4. Save record(s).