

The Triticeae Toolbox: Small Grains Breeding Database



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Outline



1. Intro

- What is T3 and Breedbase?
- How can T3 serve as a Digital Ecosystem

2. Phenotype Upload

- How is data submitted to T3?
- Overview of Excel Upload Templates

3. Advanced Features

- Search Wizard
- Seedlots
- Barcodes

Part 1:

Intro

What is T3?

What is Breedbase?

What is T3?



- The Triticeae Toolbox is a centralized database for small grains breeders (wheat, oat, barley)

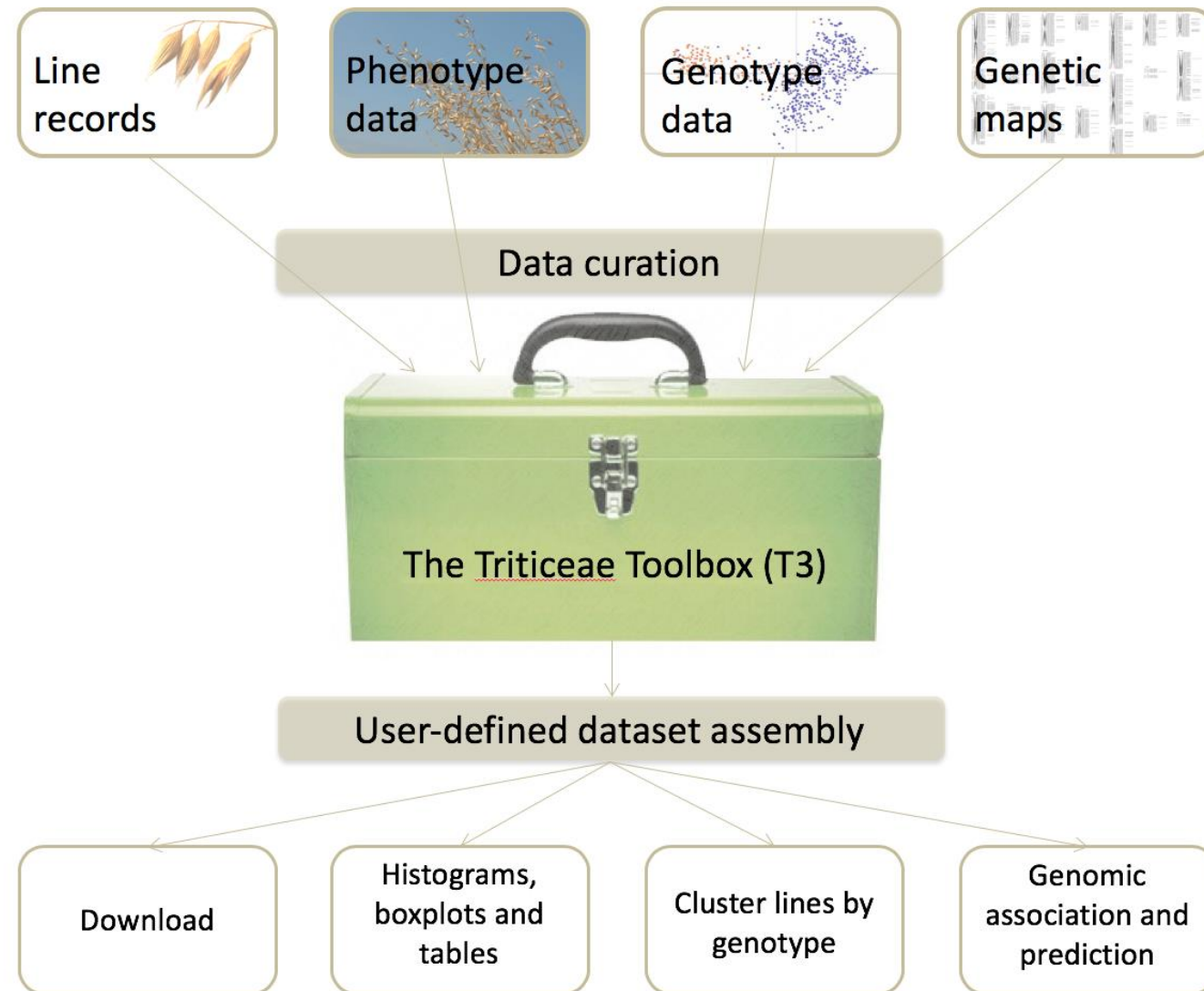
<https://wheat.triticeaetoolbox.org>

<https://barley.triticeaetoolbox.org>

<https://oat.triticeaetoolbox.org>

- Combines accession information, phenotype trial data, and genotype data from various sources
- Allow users to create custom datasets
- Provide summary and analytical tools

The T3 Method



What is Breedbase?

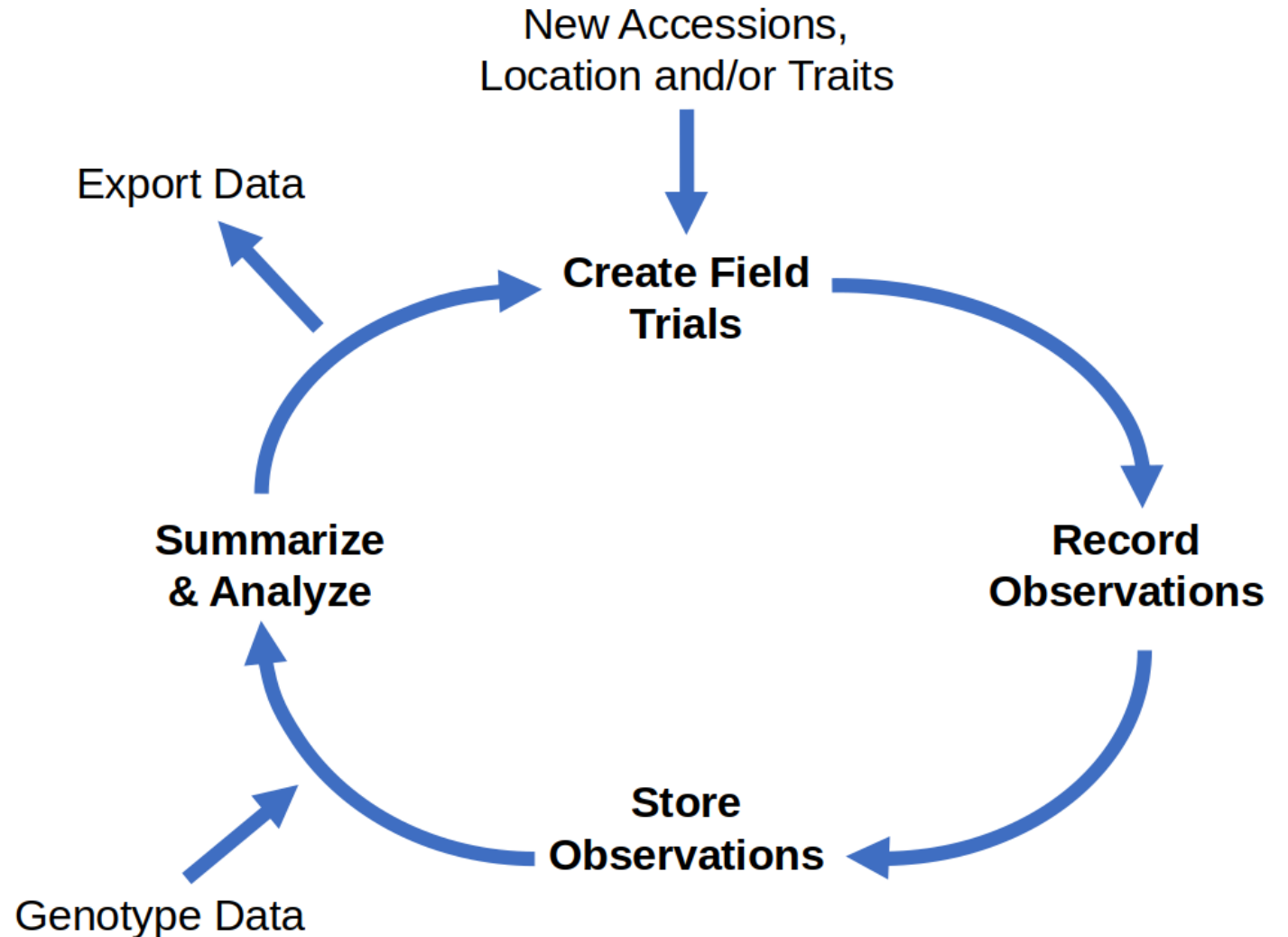


- A "comprehensive breeding management and analysis software"
- Database, analytical tools, and website
- Open-source (source on GitHub, run as a Docker image)
- Developed by Lukas Mueller's lab at Boyce Thompson Institute
- Currently used by multiple crops: cassava, sweet potato, banana, rice, Solanaceae crops
- Gaining adoption by more breeding programs and crops

Digital Ecosystem



- All breeding data can exist from start to finish within T3/Breedbase
- T3/Breedbase aims at providing tools required for data management for each stage in a breeding cycle:
 - Crossing Experiment
 - Trial Design Tool
 - Android Field Book
 - Built-in Summary & Analysis Tools



T3/Breedbase is FAIR



T3 aims to make all of its data follow the FAIR principles:

Findable

Metadata and data should be easy to find

Accessible

Once a user finds the data, it should be easily accessible

Interoperable

Data should be integrated with other data

Reusable

Users should be able to combine data for new uses

Part 2:

Uploading Phenotypes

Upload Templates
Additional Resources

Uploading Phenotypes



General Workflow:

1. Create Upload Templates
2. Optional: Upload Templates to Sandbox
 - Test the format of the files
 - See how data is presented
3. Submit the Templates
 - Email directly to djw64@cornell.edu
 - Phenotype Submission Form

wheat-sandbox.triticeaetoolbox.org
barley-sandbox.triticeaetoolbox.org
oat-sandbox.triticeaetoolbox.org

Uploading Phenotypes



Example Templates

Download Excel templates from homepage

Blank Templates

- Have correct column headers
- Contain no data

Example Templates

- Have correct column headers
- Contain sample data from workshop



The screenshot shows the T3/Wheat website interface. On the left, a sidebar titled 'Templates' contains two sections: 'Blank Upload Templates' and 'Example Templates'. Both sections list the same set of files: 'Locations (.xls)', 'Accessions (.xls)', 'Pedigrees (.txt)', 'Trials (.xls)', and 'Phenotype Observations (.xls)'. The 'Example Templates' section includes a note about templates generated for a 2020 workshop. On the right, the main content area features a 'Submit Phenotype Data' section with instructions on how to submit data, a 'Phenotype Submission Form' button, and a 'Using the Sandbox' section with a 'Visit the T3/Wheat Sandbox' button. At the bottom, there is a 'Submit Genotype Data' section and a 'User Guides' section with buttons for 'Read Documentation' and 'Watch Tutorials'.

Accession Template



Abbreviated Accession Template:

Column	Description	Examples
accession_name	The unique name of the Accession	Ajax IL16-143-3
species_name	The name of the species	Triticum aestivum Triticum durum
organization_name(s)	The names of the Breeding Program(s) that use the line (comma-separated)	Cornell University University of Illinois
synonym(s)	Additional names for the line (comma-separated). Can include released variety names, experimental identifiers, variations in spelling / punctuation	AJAX IL16_143-3
notes(s)	Additional comments about the line	
accession_number(s)	Registered Accession numbers (from GRIN, etc) (comma-separated)	PI 1234 Cltr 5678
purdy_pedigree	The Purdy pedigree string	Female Parent/Male Parent

Required fields

Plot-level metadata

100

Trial Template



Trial-level metadata (repeated for each plot in the trial)

Column	Description	Examples
trial_name	The unique name of the Trial	CUMaster_2021_Snyder
breeding_program	The name of the Breeding Program that performed the Trial	Cornell University
location	The name of the Trial's location (must exist in the DB)	Ithaca, NY
year	The harvest year of the Trial	2022
design_type	The abbreviation of the experimental design	RCBD, MAD, p-rep, etc
description	Additional text about the Trial	Advanced Yield Trial, very dry spring
plot_width	The width of a plot (in m)	1
plot_length	The length of a plot (in m)	1
planting_date	The date of planting	2022-05-01
harvest_date	The date of harvest	2022-07-19

Required fields

Trial Template



Plot-level metadata (different for each plot in the trial)

Column	Description	Examples
plot_name	The unique name of the Plot <i>Must be unique across ALL trials in the database</i>	CUMaster_2021_Snyder-PLOT101
accession_name	The name of the Accession in the Plot	Ajax
plot_number	The plot number of the Plot within the Trial	101
block_number	The block number of the Plot within the Trial	1
rep_number	The replicate number of the Plot within the Trial	1
row_number	The row position of the Plot	1
col_number	The column position of the Plot	1
seedlot_name	The name of the Seedlot where seed for the Plot came from	Ajax-2022-SL1
num_seed_per_plot	The count of seed taken from the Seedlot and planted in the Plot	250
weight_gram_seed_per_plot	The weight (in grams) of the seed taken from the Seedlot and planted in the Plot	50

Observations Template



Each row is a plot

Each column is a trait

Multiple trials can share the same template

Column	Description	Examples
observationunit_name	The name of the Plot from the trial template	CUMaster_2021_Snyder-PLOT101
{TRAIT_NAME} {TRAIT_ID}	<p>The column header is the trait name and trait id separated by a vertical pipe character -- </p> <p>The values are the trait values for each plot</p> <p>Missing observations should be left blank</p>	7906.3422
...more traits...	<i>Add an additional column for each trait you want to upload...</i>	

Required fields

Observations Template



Each row is a plot
Each column is a trait
Multiple trials can share the same template

Column	Description	Examples
observationunit_name	The name of the Plot from the trial template	CUMaster_2021_Snyder-PLOT101
{TRAIT_NAME} {TRAIT_ID}	The column header is the trait name and trait id separated by a vertical pipe character -- The values are the trait values for each plot Missing observations should be left blank	7906.3422
...more traits...	Add an additional column for each trait you want to upload...	



Required fields

These can be found from the
Search > Traits page

Observations Template



Example Template:

	A	B	C
1	observationunit_name	Grain yield - kg/ha CO_321:0001218	Plant height - cm CO_321:0001301
2	CUMaster_2021_Snyder-PLOT101	7906.342221	80.98518516
3	CUMaster_2021_Snyder-PLOT102	6705.001181	173.6942365
4	CUMaster_2021_Snyder-PLOT103	6027.165311	365.2943156
5	CUMaster_2021_Snyder-PLOT104	3269.901347	192.4721788
6	CUMaster_2021_Snyder-PLOT105	4176.461344	136.5286419
7	CUMaster_2021_Snyder-PLOT106	5868.602177	77.04386138
8	CUMaster_2021_Snyder-PLOT107	2988.553619	67.19944176
9	CUMaster_2021_Snyder-PLOT108	1210.94745	23.81049032
10	CUMaster_2021_Snyder-PLOT109	2967.699851	107.3495368
11	CUMaster_2021_Snyder-PLOT110	9410.667473	90.72844769

Template Upload (Optional)



Test load templates to Sandbox

Go to Sandbox database:

<https://wheat-sandbox.triticeaetoolbox.org>
<https://barley-sandbox.triticeaetoolbox.org>
<https://oat-sandbox.triticeaetoolbox.org>

Guided Workflow:

- Step-by-step instructions on how to upload each data type

Detailed Upload Instructions:

- Single page of upload instructions for each data type
- More information about the template requirements

The screenshot shows the T3/Wheat Sandbox website interface. At the top, a red banner reads "SANDBOX SITE - Data added to this site will be periodically cleared". The navigation bar includes "T3/Wheat SANDBOX", "Search", "Manage", "Analyze", "Maps", "About", "Contact Us", "Register", and "Login". A dropdown menu under "Manage" lists "Mixed Model analysis", "Seed Lots", and "Crosses". The main content area is titled "You must first log in to view the lists of experiments...". Below this, there are sections for "Submit Phenotype Data", "Submit Genotype Data", and "User Guides". A large orange arrow points from the "Detailed Upload Instructions" button in the bottom right to the "Sample Templates" section on the left. The "Sample Templates" section includes a list of data types (Locations, Accessions, Pedigrees, Trials, Phenotype Observations) and a list of steps for generating and uploading sample templates.

Manage (contact us to use these features)

- Mixed Model analysis
- Seed Lots
- Crosses

Templates

Blank Upload Templates

Below are blank upload templates for each data type.

- Locations (.xls)
- Accessions (.xls)
- Pedigrees (.txt)
- Trials (.xls)
- Phenotype Observations (.xls)

Sample Templates

Generate a set of sample templates for new accessions, locations, trials, and phenotype observations. These templates are formatted templates that can be used to practice uploading each data type to the sandbox.

1. Generate your set of sample templates
2. Follow the [Guided Phenotype Upload Workflow](#) to upload the template for each data type

Example Templates

Below are example templates

Submit Phenotype Data

To submit phenotype data to T3/Wheat follow these three general steps:

Step 1: Create Upload Templates

Data submitted to T3/Wheat should be in the format of the upload template for the data type you are submitting. [View the detailed upload instructions](#) for specific information on each data type.

Step 2: Add Data to Sandbox

Once you have your upload templates, you can test-load them on this Sandbox site to check for any errors.

Step 3: Submit Trial Data

If your trial data has been successfully added to the Sandbox you can submit your trials directly to the production site by clicking the **Submit Trial** button on the trial detail page.

If your data has not been added to the Sandbox or if you would prefer to submit your files directly to the production site, you can submit your individual upload templates or data files to us using the [Phenotype Submission Form](#).

Submit Genotype Data

Please [Contact Us](#) if you have genotype data you would like to submit to T3/Wheat.

User Guides

[New to T3/Wheat?](#)

[Guided Workflow](#) [Detailed Upload Instructions](#)

Template Upload (Optional)



Test load templates to Sandbox

Go to Sandbox database:

<https://wheat-sandbox.triticeaetoolbox.org>

<https://barley-sandbox.triticeaetoolbox.org>

<https://oat-sandbox.triticeaetoolbox.org>

About > Field Trial Tutorial

- 2020 Workshop on Uploading Trials
- Includes sample data
- Video recordings going through each step

The screenshot shows the T3/Wheat Sandbox website interface. The browser address bar displays <https://wheat-sandbox.triticeaetoolbox.org>. A red banner at the top states "SANDBOX SITE - Data added to this site will be periodically cleared". The navigation bar includes links for Search, Manage, Analyze, Maps, and About, along with buttons for Contact Us, Register, and Login. A dropdown menu is open under the "About" link, showing options such as "About", "How to Cite T3/Wheat", "Content Status", "Genotype Protocol description", "Breedbase Manual", "Video Tutorials", "Field Book App", "Field Trial Tutorial", "Generate Sample Templates", and "Contact Us". An orange arrow points from the "Field Trial Tutorial" link in the dropdown menu to the "Sample Templates" section on the main page. The "Sample Templates" section describes how to generate sample templates for new accessions, locations, trials, and trait observations. It includes a list of data types: Locations (.xls), Accessions (.xls), Pedigrees (.txt), Trials (.xls), and Phenotype Observations (.xls). Below this, it provides a numbered list of steps: 1. Generate your set of sample templates, and 2. Follow the Guided Phenotype Upload Workflow to upload the template for each data type. The "Example Templates" section is partially visible at the bottom.

Template Submission



Send us templates without uploading them first

Go to Production database:

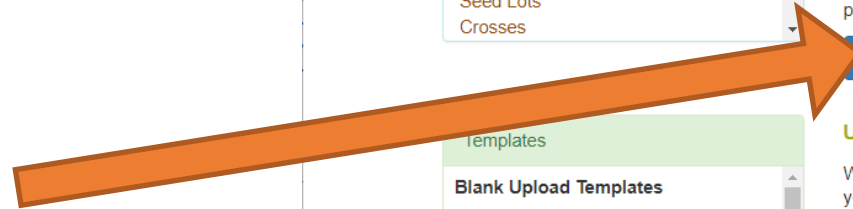
<https://wheat.triticeaetoolbox.org>

<https://barley.triticeaetoolbox.org>

<https://oat.triticeaetoolbox.org>

Phenotype Submission Form

- Upload templates via website
- We'll check for errors / issues / duplicates
- We'll upload to the database



The screenshot shows the T3/Wheat website interface. The browser address bar displays <https://wheat.triticeaetoolbox.org>. The website has a navigation bar with links: T3/Wheat, Search, Manage, Analyze, Maps, About, Contact Us, and a user profile for 'dwaring87'. Below the navigation bar, there are sections for 'v Watkins language collection' (Exome capture Watkins, WheatCAP Regulatory, GBS KSU 2020), 'Site update' (November 1, 2020 SGN-285.0), and 'Analysis' (Population Structure (PCA), Clustering (k-means), Manage (contact us to use these features), Mixed Model analysis, Seed Lots, Crosses). A large orange arrow points from the 'Phenotype Submission Form' text to a blue button labeled 'Phenotype Submission Form' in the right-hand section. Other sections include 'Submit Phenotype Data' (explaining two ways to submit data), 'Submitting files directly to us' (explaining the submission process), 'Using the Sandbox' (explaining the sandbox workflow), 'Submit Genotype Data' (requesting contact for genotype data), and 'User Guides' (providing documentation links).

Part 3:

Advanced Features

Search Wizard

Seedlots

Barcodes

Search Wizard



Menu: Search > Wizard

- Filter data on 1-4 dimensions
- Combine data from different sources
- Subset data (by location, trait, accession, etc)
- Download selected phenotype data
- Download related genotype data (for selected accessions)



DEMO: Search Wizard

Search Wizard

Don't see your data? [Refresh Lists](#) [Update Wizard](#)

Traits

fhb

Select All 1/228 Clear

+ FHB incidence - 0-9 percent

+ FHB ISK index - %|CO_321:00

+ FHB plant response - 1-9 res

+ FHB severity - %|CO_321:00

+ FHB severity - Greenhouse -

×

FHB incidence - %|CO_321:00

Match ANY ALL

Add to List... Add

Create New List Create

Locations

IL

Select All 3/42 Clear

+ Clarksville, MD

+ Evansville, IN

+ Fayetteville, AR

+ Merrill, MI

×

Champaign, IL

×

Highland, IL

×

Urbana, IL

Match ANY ALL

Add to List... Add

Create New List Create

Trials

Search

Select All 63/63 Clear

×

5STADV_2001_Urbana

×

5STADV_2002_Urbana

×

5STADV_2003_Urbana

×

5STADV_2004_Urbana

×

5STADV_2005_Urbana

Match ANY ALL

Add to List... Add

Create New List Create

Accessions

Search

Select All 0/1529 Clear

+ 011007A1-14

+ 011007A1-14-2

+ 011007A1-14-44

+ 011010A1-15

+ 011034A1-3

Match ANY ALL

Add to List... Add

Create New List Create

Search Wizard



Saving & Sharing Selections

Lists:

Saved items of a single data type

Datasets:

Saved items from multiple data types

Accessions ▼

IL19

Select All 300/41778 Clear

×

 IL19-1020
× IL19-10243
× IL19-10849
× IL19-10856
× IL19-10904

Match ANY ALL

Add to List... ▼ Add

IL 2019 Lines Create

Select Column Type ▼

Search

Select All 0/0 Clear

Select Column Type ▼

Search

Select All 0/0 Clear

Select Column Type ▼

Search

Select All 0/0 Clear

Create a list of Illinois Accessions from 2019

Search Wizard



Saving & Sharing Selections

Lists:

Saved items of a single data type

Datasets:

Saved items from multiple data types

Create a dataset with the selected traits, locations, and trials

Traits

Search

Select All 2/4632 Clear

+ Aboveground biomass at matu

+ Aboveground biomass at matu

+ Aboveground biomass - glCO₂

+ Agronomic Merit - 1-9 Agronon

+ Agronomic Merit - 1-9 Agronon

×

 Grain yield - kg/ha|CO₂321:00012

×

 Plant height - cm|CO₂321:000130

Match ANY ALL

Add to List... Add

IL 2019 Lines Create

Locations

Search

Select All 4/210 Clear

+ Aberdeen, ID

+ Aberdeen, SD

+ Agar, SD

+ Akron, CO

+ Alliance, NE

×

 Belleville, IL

×

 Brownstown, IL

×

 Carmi, IL

×

 Champaign, IL

Match ANY ALL

Add to List... Add

Create New List... Create

Trials

Search

Select All 73/73 Clear

×

 5STADV_2001_Brownstown

×

 5STADV_2002_Brownstown

×

 5STADV_2004_Brownstown

×

 5STADV_2005_Brownstown

×

 5STADV_2006_Brownstown

Match ANY ALL

Add to List... Add

Create New List... Create

Select Column Type

Search

Select All 0/0 Clear

Load/Create Datasets using Match Columns

Load Dataset

Load

Make Public

Delete

IL yield & height trials Create

Related Genotype Data

Related Trial Metadata

Related Trial Phenotypes

Seedlots



Seedlot AJAX-2002-SL1

Details

[\[Edit Seedlot Details\]](#)

Breeding Program	Cornell University
Seedlot Name	AJAX-2002-SL1
Seedlot Description	Collected on June 1, 2022
Organization	Cornell University
Location Code	Room 105
Box Name	Box A
Quality issues	
Contents	AJAX (accession)
Current count	500
Current weight (g)	NA
Submitters	dwaring87

Transactions

Transactions Table

[\[Add New Transaction\]](#)

Show 10 entries

Search:

Transaction Id	Transaction Date	From	To	Transaction Num Seeds	Transaction Weight (g)	Operator	Transaction Description	Options
1466620	Thu Dec 1 14:47:14 2022	AJAX (accession)	AJAX-2002-SL1 (seedlot)	+500	NA	dwaring87		[Edit]

Showing 1 to 1 of 1 entries

Previous 1 Next

A Seedlot represents a single packet of collected seed

Properties:

- Unique Name
- Location
- Box Name
- Accession
- Contents
 - Count
 - Weight

Transactions:

- Created each time seed is added or removed from the Seedlot
- Linked to Plots that use seed from the Seedlot
- Linked to other Seedlots when splitting / combining

Seedlots



Creating Seedlots

Upload Template:

- Create an Excel template that has the metadata and initial amount of each Seedlot
- Upload file to website

Create Seedlots from Trial:

- Guided workflow to generate Seedlots from a field trial
- Option to create **one Seedlot per plot** or **one Seedlot per Accession**
- Template for Seedlot names
- Initial contents:
 - Constant value for all Seedlots
 - Trait value observed in the Trial
 - Computed from a trait value

The screenshot shows a web-based workflow titled "Create Seedlots from a Trial". At the top, a progress bar consists of eight numbered steps: 1. Intro, 2. Select Trial, 3. Select Seedlots (currently active), 4. Name Seedlots, 5. Set Contents, 6. Set Metadata, 7. Confirm, and 8. Create. Below the progress bar, the main content area is titled "Select Seedlots". It contains the text: "Seedlots can be generated from either each **plot** or **accession** in this trial." followed by two bullet points: "• If you select **plots**: 30 seedlots will be created" and "• If you select **accessions**: 10 seedlots will be created". Below this text is a dropdown menu currently showing "Plots". At the bottom right of the content area is a blue button labeled "Go to Next Step".



DEMO: Create Seedlots from a Trial

Barcodes



Barcodes can be generated for:

- Accessions
- Trials
- Plots
- Genotyping Plates

Features:

- 1D or 2D (QR Codes) supported
- Pre-defined templates
- Custom label designer
- Custom templates can be saved & shared

Use Cases:

- Barcoded Plots:
 - Generate a unique barcode for each Plot in a Trial
 - Use Android Field Book app to scan the barcode before recording observations
 - Ensures the user is recording traits for the correct plot
- Seedlots:
 - Generate a unique barcode for each Seedlot
 - Use the Android Coordinate app to scan the barcode when collecting samples for Genotyping
 - Ensures the correct Seedlot is recorded for each sample

Barcodes



Custom Label Designer:

1. Choose Data Source
 - Field Trial
 - Genotyping Plate
 - List
2. Select Page Size & Label Dimensions
3. Add Components to Label
 - Barcode
 - Additional Text
4. Download PDF



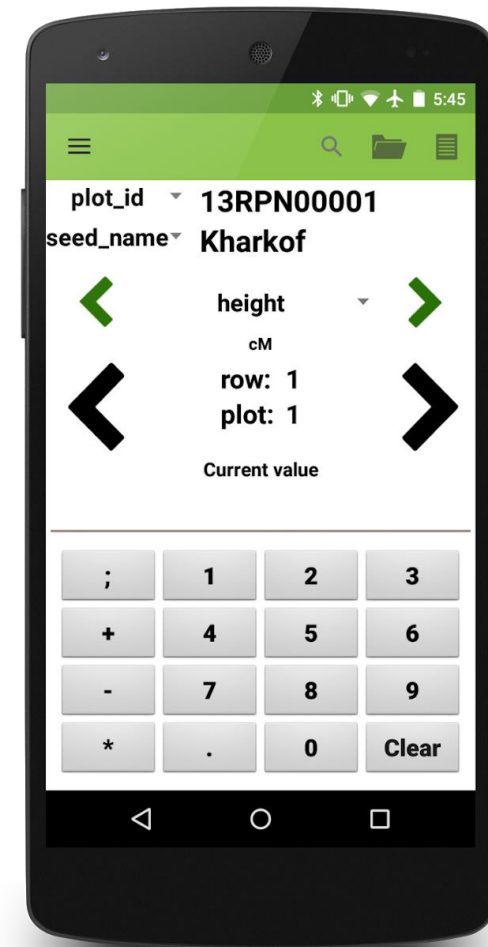
DEMO: Design Trial Barcodes

The screenshot shows the 'T3/Wheat' web application interface for the 'Label Designer' tool. The browser address bar shows the URL: https://wheat-sandbox.triticeaetoolbox.org/tools/label_designer. A red banner at the top states: 'SANDBOX SITE - Data added to this site will be periodically cleared'. The navigation bar includes links for Search, Manage, Analyze, Maps, About, Contact Us, and a user profile for 'dwaring87'. The main content area features a progress bar with four steps: 1. Intro and Data Source (highlighted), 2. Set Page and Label Size, 3. Design Your Label, and 4. More Options, Save, And Download. Below the progress bar, a welcome message reads: 'Welcome to the Label Designer. This workflow will guide you through each step of the design process. For detailed explanations of each step please refer to the [label designer section of the manual](#). To start, select a data source and a data level. The data source can be a list, crossing experiment, trial, or genotyping plate. When you are finished, click 'Next''. The 'Data Source' dropdown menu is set to 'Select a list, crossing exp, trial, or GT'. The 'Label For Every' dropdown menu is empty. A 'Next' button is located at the bottom right of the main content area. The footer contains three sections: 'Powered By' with the BREEDBASE logo, 'Partners' with logos for USDA NIFA (National Institute of Food and Agriculture) and USDA ARS (Agricultural Research Service), and 'Funded By' with text stating 'T3 is part of the Wheat CAP project, supported by Agriculture and Food Research Initiative Competitive Grant no. 2011-68002-30029 from the USDA National Institute of Food and Agriculture.' The footer also includes version information: 'Version cd49b84eb sgn-334.0 Mon Nov 28 15:04:33 2022 -0500' and the 'US Wheat and Barley Scab Initiative' logo.



Android App for Data Collection

- Load Fields & Traits from DB (via BrAPI or files)
- Record data for each plot in the app
 - Numeric
 - Counter
 - Categorical
 - Boolean
 - Text
 - Photos
- Integrated barcode scanner
- Export data to store in DB (via BrAPI or files)



Field Book



About > Field Book App

Instruction Manual

- Download links
- Links to tutorials
- Setup Instructions
 - Connect app to DB via BrAPI
 - Authorization
- Importing Fields
- Importing Traits
- Exporting Observations

The screenshot shows the T3/Wheat website at <https://wheat.triticeaetoolbox.org>. The navigation bar includes links for T3/Wheat, Search, Manage, Analyze, Maps, and About. The 'About' dropdown menu is open, showing options: About, How to Cite T3/Wheat, Content Status, Genotype Protocol description, Breedbase Manual, Video Tutorials, FTP data, Field Book App (highlighted by an orange arrow), Field Trial Tutorial, Generate Sample Templates, and Contact Us. The main content area features a 'Welcome to T3/Wheat' section, a 'Data Usage Policy', and a 'Citation' section. A 'News' sidebar on the left lists updates like 'IWGSC RefSeq v2.1 Assembly' and 'Genotype projects added'. The 'Explore T3/Wheat' section on the right includes registration and login buttons, a quick search bar, and a search wizard.

https://wheat.triticeaetoolbox.org/static_content/files/FieldBookAppT3.pdf

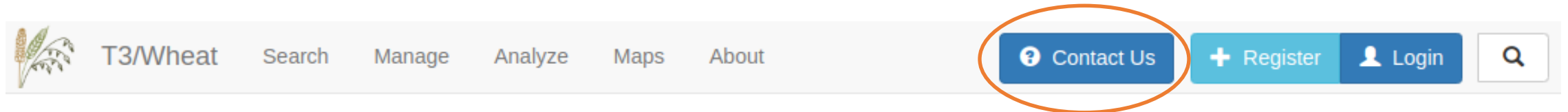
Questions?



Get In Touch:

Email: djw64@cornell.edu

Website: "Contact Us" form



Survey

Interested in a more in-depth hands-on workshop?

Fill out this survey:



tinyurl.com/t3workshops

Acknowledgements

The Triticeae Toolbox

Jean-Luc Jannink

Clay Birkett

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Breedbase

Lukas Mueller's Lab

Boyce Thompson Institute

