



# Yambase Update

Lukas Mueller and Isaak Tecle  
Boyce Thompson Institute



# Acknowledgments

- Thanks to the entire Yam community
- And indeed the entire RTB community
- All the colleagues at BTI
- Thank you!!!



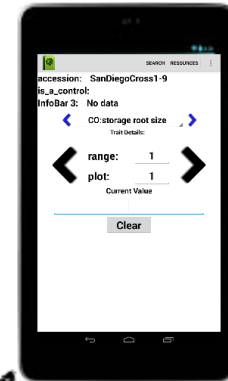


# Yambase “Digital Ecosystem”



ANALYZE

**Analysis**  
Make selections  
(genomic selection, etc.)



SELECT



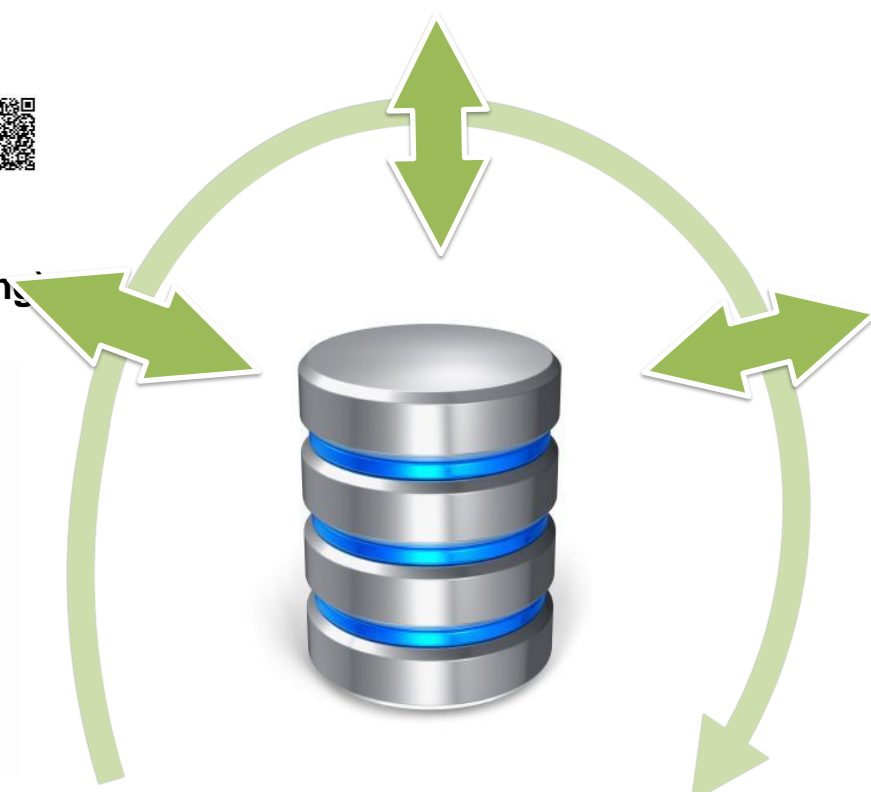
**Plan & perform crosses**  
**Manage pedigrees**



CREATE  
&  
EVALUATE



**Field layouts**  
**Evaluate**  
(phenotyping/genotyping)





# Yambase features

- Completely web-based
- Multi species, multi breeding program, multi user database
- Manage
  - accessions, fields, locations, traits, and measurements
  - genotypic information
  - Special high dimensionality phenotypes such as NIRS data
  - Product profiles
- Analyses
  - Mixed Models, Clustering, Stability, Heritability, SolGS



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Software and Data Resources

Featured

## Breedbase: a digital ecosystem for modern plant breeding

Nicolas Morales <sup>1,2,†</sup> Alex C. Ogonna <sup>1,2,†</sup> Bryan J. Ellerbrock <sup>1,†</sup> Guillaume J. Bauchet <sup>1,16,†</sup> Titima Tantikanjana,<sup>1</sup> Isaaq Y. Teclé <sup>1</sup> Adrian F. Powell <sup>1</sup> David Lyon <sup>1,17</sup> Naama Menda <sup>1</sup> Christiano C. Simoes,<sup>1</sup> Surya Saha <sup>1</sup> Prashant Hosmani <sup>1,18</sup> Mirella Flores <sup>1</sup> Naftali Panitz <sup>1</sup> Ryan S. Preble,<sup>1</sup> Afolabi Agbona <sup>3</sup> Ismail Rabbi <sup>3</sup> Peter Kulakow <sup>3</sup> Prasad Peteti <sup>3</sup> Robert Kawuki <sup>4</sup> Williams Esuma <sup>4</sup> Micheal Kanaabi,<sup>4</sup> Doreen M. Chelangat <sup>4</sup> Ezenwanyi Uba,<sup>5</sup> Adeyemi Olojede <sup>5</sup> Joseph Onyeka,<sup>5</sup> Trushar Shah <sup>6</sup> Margaret Karanja <sup>6</sup> Chiedozi Egesi <sup>1,3,5</sup> Hale Tufan <sup>2</sup> Agre Paterne <sup>3</sup> Asrat Asfaw <sup>7</sup> Jean-Luc Jannink <sup>2,8</sup> Marnin Wolfe <sup>2</sup> Clay L. Birkett <sup>2,8</sup> David J. Waring <sup>2,8</sup> Jenna M. Hershberger <sup>2</sup> Michael A. Gore <sup>2</sup> Kelly R. Robbins <sup>2</sup> Trevor Rife <sup>9</sup> Chaney Courtney,<sup>9</sup> Jesse Poland <sup>9</sup> Elizabeth Amaud <sup>10</sup> Marie-Angélique Laporte <sup>10</sup> Heneriko Kulembeka,<sup>11</sup> Kasele Salum,<sup>11</sup> Emmanuel Mrema,<sup>11</sup> Allan Brown <sup>3</sup> Stanley Bayo,<sup>3</sup> Brigitte Uwimana <sup>3</sup> Violet Akech,<sup>3</sup> Craig Yencho <sup>12</sup> Bert de Boeck <sup>13</sup> Hugo Campos <sup>13</sup> Rony Swennen <sup>14</sup> Jeremy D. Edwards <sup>15</sup> Lukas A. Mueller <sup>1,\*</sup>

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<sup>14</sup>KU Leuven, 3000 Leuven, Belgium,

<sup>15</sup>USDA-ARS, Stuttgart, AR 72160, USA

<sup>16</sup>Present address: Terre de Lin, Saint Pierre le Viger, France





# Data in Yambase

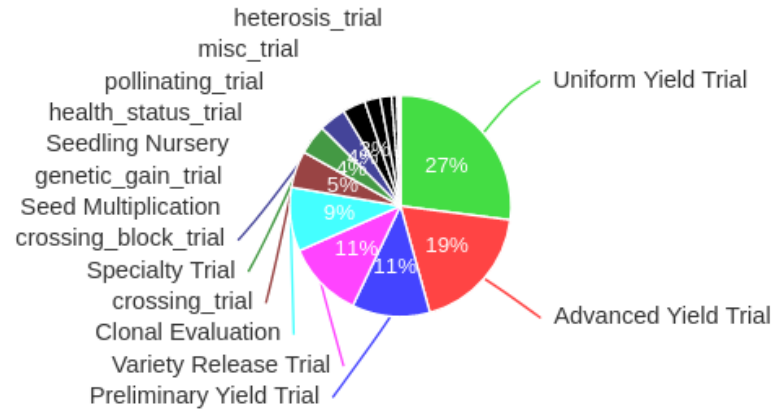
<https://yambase.org/breeders/dbstats>

## Database Stats

### Data categories

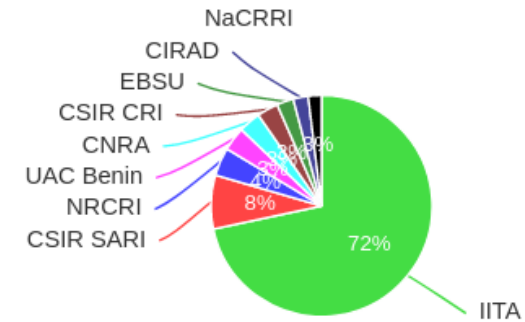
#### Trial Types

Showing 781 Total Trials



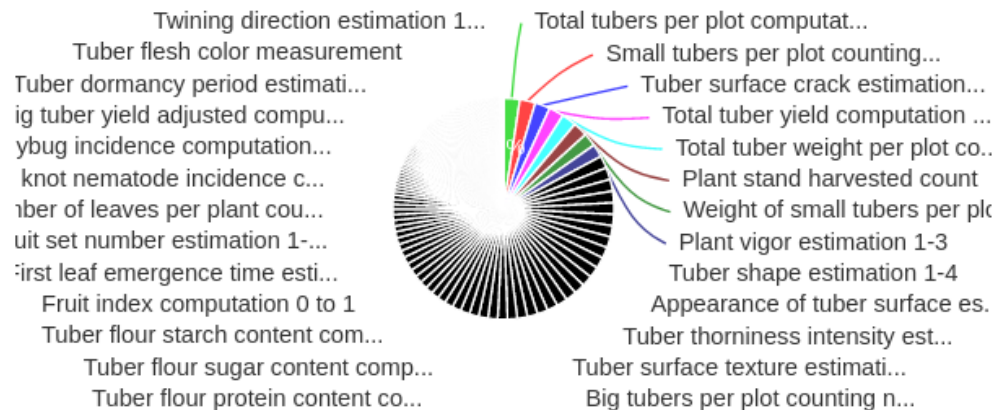
#### Trials by Breeding Program

Showing 776 Total Trials



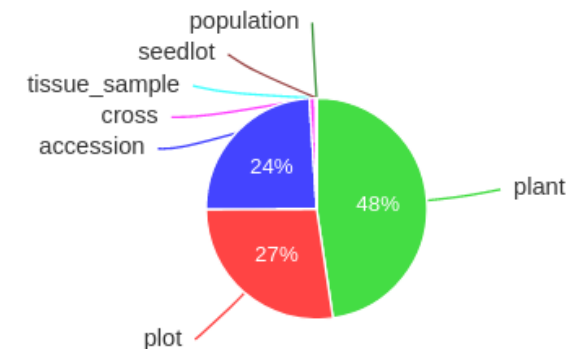
#### Traits

Total trait measurements: 1305371



#### Stock Types

Showing total of 299714 stocks



Analyze

Maps

Ab

## Analyses & Models

Breeder Tools

Selection Index

Genomic Selection

Population Structure

Clustering

Kinship & Inbreeding

Stability AMMI/GGE

Heritability

Accession Usage

Mixed Models

Compare Trials

Graphical Filtering

BoxPlotter Tool

GWAS

Image Analysis

Sequence Analysis

# Analysis Tools

- Many routine analyses available on Cassavabase
- “Analysis framework” – most analyses work in a similar way
- Review Cassavabase statistics capability



Alex Ogbonna



Titima Tantikanjana



Isaak Teclé



Bryan Ellerbrock



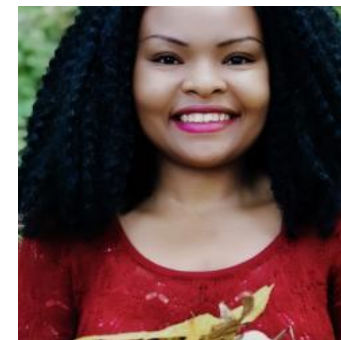
David Lyon



Adrian Powell



Chris Simoes

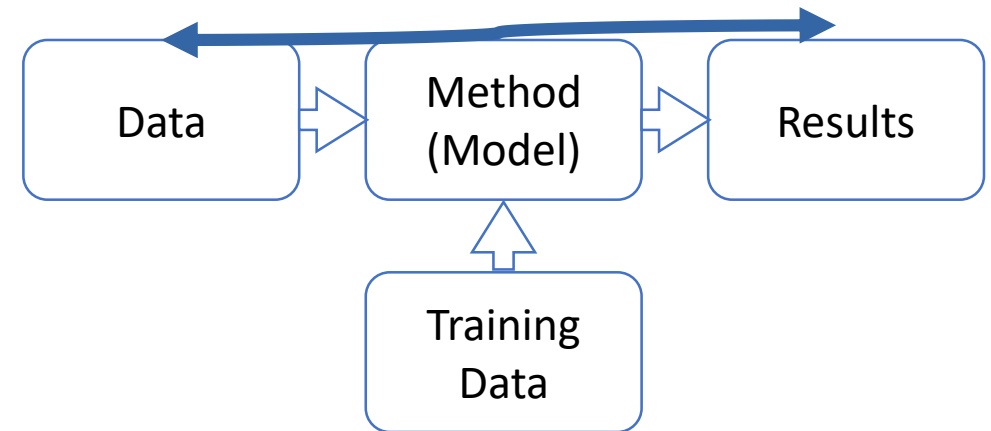


Christine Nyaga



# Working with Analyses

- Analyses consist of input data, methods, models, training data, and results
- All these metadata can be stored for an analysis
- Analysis results, for example, predictions from solGS, can be stored in the database to inform downstream breeding decisions (selection index etc)
- Stored analysis results can be used in other analyses

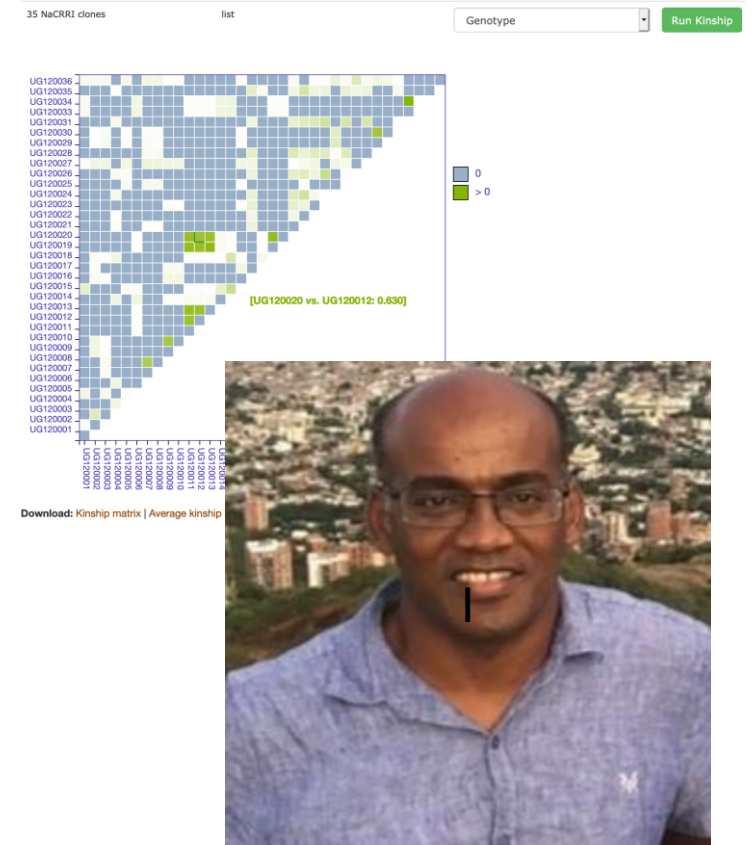






# Genomic Selection (solGS tool)

- Integrates genotypic and phenotypic data
- Training and prediction
- New features:
  - Input based on Wizard datasets
  - Explore data, estimate and visualize kinship and inbreeding coefficients
  - K-means clustering tool
  - Improved visualization of results
  - Store GEBVs in the database for further decision support
  - Performance improvements



Isaak Tecle



# Mate selection prediction

- Started with Africa Yam Project
- Predict best parent pairs
- Based on genomic predictions
- Implemented by Christine Nyaga, based on code by Marlee Labroo, Marnin Wolfe, and Isaak Tecle
- Re-implementation of Mixed Model tool using R-package “sommer” as backend to allow inclusion of more co-variates



Christine  
Nyaga



Marlee Labroo



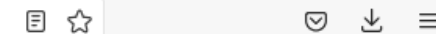
Isaak Tecle

With Agre Paterne and Asrat Amele



# GCPC Workflow

- Create Dataset with phenotypic and genotypic data using the Wizard
- Create Selection Index using Selection Index Tool
- Open GCPC tool, choose the Dataset and Selection Index
- Choose the
- Hit submit!



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## Search Wizard

Don't see your data?

Refresh Lists

Update Wizard

Breeding Programs	Genotyping Protocols	Accessions	Traits
<div style="border: 1px solid #ccc; padding: 5px;"> <div style="display: flex; justify-content: space-between; align-items: center;"> <span>Breeding Programs</span> <span>▼</span> </div> <div style="border: 1px solid #ccc; padding: 2px; margin: 5px 0;">Search</div> <div style="display: flex; justify-content: space-between; align-items: center; margin: 5px 0;"> <span>Select All</span> <span style="background-color: #007bff; color: white; padding: 2px 5px;">1/10</span> <span>Clear</span> </div> <div style="border: 1px solid #ccc; padding: 5px;"> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: green;">+</span> <span>EBSU</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: green;">+</span> <span>NaCRRI</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: green;">+</span> <span>NRCRI</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: green;">+</span> <span>RTBFoods</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: green;">+</span> <span>UAC Benin</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: red;">×</span> <span>IITA</span> </div> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin: 5px 0;"> <span>Match</span> <span style="background-color: #007bff; color: white; padding: 2px 5px;">ANY</span> <span>ALL</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin: 5px 0;"> <span>Add to List...</span> <span style="background-color: #007bff; color: white; padding: 2px 5px;">Add</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin: 5px 0;"> <span>Create New List...</span> <span style="background-color: #007bff; color: white; padding: 2px 5px;">Create</span> </div> </div>	<div style="border: 1px solid #ccc; padding: 5px;"> <div style="display: flex; justify-content: space-between; align-items: center;"> <span>Genotyping Protocols</span> <span>▼</span> </div> <div style="border: 1px solid #ccc; padding: 2px; margin: 5px 0;">Search</div> <div style="display: flex; justify-content: space-between; align-items: center; margin: 5px 0;"> <span>Select All</span> <span style="background-color: #007bff; color: white; padding: 2px 5px;">1/5</span> <span>Clear</span> </div> <div style="border: 1px solid #ccc; padding: 5px;"> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: green;">+</span> <span>GBS ApeK1 DR_PseudoChromosome_21_v</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: green;">+</span> <span>GBS_D.alata reference genome</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: green;">+</span> <span>GBS for yam testset</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: green;">+</span> <span>new protocol for test data</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: red;">×</span> <span>DArT sequencing</span> </div> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin: 5px 0;"> <span>Match</span> <span style="background-color: #007bff; color: white; padding: 2px 5px;">ANY</span> <span>ALL</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin: 5px 0;"> <span>Add to List...</span> <span style="background-color: #007bff; color: white; padding: 2px 5px;">Add</span> </div> <div style="display: flex; justify-content: space-between; 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margin-bottom: 5px;"> <span style="color: red;">×</span> <span>TDa0000194</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: red;">×</span> <span>TDa0100004</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: red;">×</span> <span>TDa0100029</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: red;">×</span> <span>TDa0100039</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin: 5px 0;"> <span>Match</span> <span style="background-color: #007bff; color: white; padding: 2px 5px;">ANY</span> <span>ALL</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin: 5px 0;"> <span>Add to List...</span> <span style="background-color: #007bff; color: white; padding: 2px 5px;">Add</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin: 5px 0;"> <span>Create New List...</span> <span style="background-color: #007bff; color: white; padding: 2px 5px;">Create</span> </div> </div>	<div style="border: 1px solid #ccc; padding: 5px;"> <div style="display: flex; justify-content: space-between; align-items: center;"> <span>Traits</span> <span>▼</span> </div> <div style="border: 1px solid #ccc; padding: 2px; margin: 5px 0;">Search</div> <div style="display: flex; justify-content: space-between; align-items: center; margin: 5px 0;"> <span>Select All</span> <span style="background-color: #007bff; color: white; padding: 2px 5px;">2/137</span> <span>Clear</span> </div> <div style="border: 1px solid #ccc; padding: 5px;"> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: green;">+</span> <span>50% sprout emergence time computation in d</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: green;">+</span> <span>50% sprout emergence time estimation in yy/</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: green;">+</span> <span>Appearance of tuber surface estimation 1-4 C</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: green;">+</span> <span>Average tuber weight computation in kg CO_3</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: green;">+</span> <span>Big tuber average weight computation in kg C</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: red;">×</span> <span>Average tuber length measurement in cm CO</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin-bottom: 5px;"> <span style="color: red;">×</span> <span>Average tuber width computation in cm CO_3</span> </div> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin: 5px 0;"> <span>Add to List...</span> <span style="background-color: #007bff; color: white; padding: 2px 5px;">Add</span> </div> <div style="display: flex; justify-content: space-between; align-items: center; margin: 5px 0;"> <span>Create New List...</span> <span style="background-color: #007bff; color: white; padding: 2px 5px;">Create</span> </div> </div>

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## Build a Selection Index ℹ️

### Parameters ⬆️

#### Trial:

01aytTDrAB(breedersline) ⌵

#### Traits and coefficients for 01aytTDrAB(breedersline):

Trait name	Trait synonym	Index coefficient	Normalize with a control?	Remove?
<a href="#">Plant stand harvested count</a>	None	<input type="text" value="1"/>	No controls found <span>⌵</span>	<span>✖</span>
<a href="#">Total tubers per plot computation</a>	None	<input type="text" value="3"/>	No controls found <span>⌵</span>	<span>✖</span>
<a href="#">virus severity estimation in 1-5</a>	VRSS	<input type="text" value="2"/>	No controls found <span>⌵</span>	<span>✖</span>

[virus severity estimation in 1-5](#) ⌵





## Genomic Prediction of Cross Performance (GCPC)

## Select a Genotyped Dataset

Available Datasets

[Help ?](#)

Show 2 entries

Search:

Select	Dataset Name	Contents						
<input type="checkbox"/>	example dataset	<table border="1"><thead><tr><th>Breeding_programs</th><th>Locations</th><th>Years</th></tr></thead><tbody><tr><td>IITA</td><td>Abuja Ibadan</td><td>2018 2019</td></tr></tbody></table>	Breeding_programs	Locations	Years	IITA	Abuja Ibadan	2018 2019
Breeding_programs	Locations	Years						
IITA	Abuja Ibadan	2018 2019						
<input type="checkbox"/>	new dataset	<table border="1"><thead><tr><th>Locations</th><th>Years</th><th>Accessions</th></tr></thead><tbody><tr><td>Abakaliki Abomey</td><td>2018 2020</td><td>TDa0200061 TDa0700015 TDa0700154 TDa0900128</td></tr></tbody></table>	Locations	Years	Accessions	Abakaliki Abomey	2018 2020	TDa0200061 TDa0700015 TDa0700154 TDa0900128
Locations	Years	Accessions						
Abakaliki Abomey	2018 2020	TDa0200061 TDa0700015 TDa0700154 TDa0900128						



## Genomic Prediction of Cross Performance (GCPC)

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Breeding_programs	Locations	Years						
IITA	Abuja Ibadan	2018 2019						
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Locations	Years	Accessions						
Abakaliki Abomey	2018 2020	TDa0200061 TDa0700015 TDa0700154 TDa0900128						

Proceed to Factor Selection

### Select fixed and random factors to be included in the model

locationName

fixed  random  None

replicate

fixed  random  None

germplasmName

random

ultimate selection index



*This is a drop-down menu showing your pre-constructed selection indices. Select one and proceed to run the model.*

Run GCPC

This is a drop-down menu showing your pre-constructed selection indices. Select one and proceed to run the model.

Run GCPC

Download Results

Output

Plant Sex info: 1= Male, 2=Female, 3= Monoecious male (m>f) and 4= Monoecious female(f>m)

Show 10 entries

Search:

Cross #	Parent 1	Parent 2	Cross Predicted Merit	Parent1 Sex	Parent2 Sex
10325	TDr1615003	TDr1619204	1.81256644943338	2	1
10854	TDr1615003	TDr1774001	1.78515821688158	2	1
806	TDr1621012	TDr1615003	1.78142414874577	1	2
10727	TDr1615003	TDr1685017AB	1.74883184716264	2	1
10294	TDr1615003	TDr1612901	1.71457601416463	2	1
68691	TDr1618715	TDr1774001	1.70089942571952	2	1
62328	TDr1619306	TDr1774001	1.69940200793324	2	1
68563	TDr1618715	TDr1689033AB	1.68707850758771	2	4
10288	TDr1615003	TDr1619803	1.68598559238079	2	1
68162	TDr1618715	TDr1619204	1.67799070197507	2	1

Showing 1 to 10 of 100 entries

Previous 1 2 3 4 5 ... 10 Next



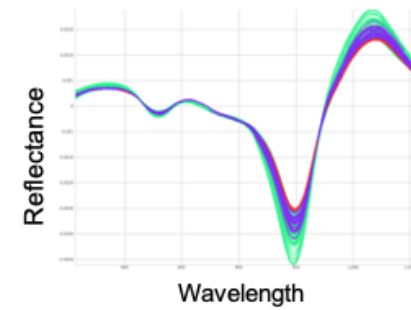
# Multi-dimensional Phenotypes

- Datatypes that don't consist of one value per measurement, but a series of values or more complex structures
  - Expression data
  - Proteomics data
  - Metabolomics data
  - Ground Penetrating Radar (GPR) Data
- Collaboration with Jean-Luc Jannink's group
- Data exchange standard development with Peter Selby (BrAPI)





# NIRS Analyses



- NIRS spectra can be uploaded to Breedbase databases
- NIRS calibration can be performed in Cassavabase (based on standardized lab measurements)
- Collaboration with Jenna Hershberger (Michael Gore Lab, Cornell University).



Chris Simoes



Nick Morales



Jenna Hershberger



# Ground penetrating radar (GPR)

- Non destructive method of root visualization
- Current on-going work at IITA Ibadan by IDL (Delgado et al.)
- Providing support the GPR group with database infrastructure
- Storage of raw (currently) and analyzed data (in the future)
- Thanks for the dinner! :-)



Ground penetrating radar



# Quality data and vocabularies



- Add food quality and processing terms, ontologies and data
- Creation of post-composed ontologies
- RTBfoods major driver for NIRS integration
- Dominique Dufour and Eglantine Fauvelle (Cirad), Thierry Tran, Karima Meghar (CIAT), ...
- Elizabeth Arnaud, Marie Angélique Laporte (Bioversity)



# Product Profiles & Stage Gates

- Product Profiles management integrated in Cassavabase
- Product Profiles are described in terms of traits and trait values
- Future: Product profiles can be used to search matching/exceeding accessions
- Stage gate and roles integration

## We mapped the Cassava Pipeline process to the Stage Gate Decision process

Stages & Gates	Stage 0	A	Stage 1	B	Stage 2	C	Stage 3	D	Stage 4	E	Stage 5
Stage Title	Product Design		Discovery / Create Variation		Early Development Screen		Late Development Test & Stabilize		Pre-release Place & Scale		Release and Deployment
Stage Descriptions	Market research, Product Design, PPC		Parent selection and production of new genetic variation		Clone development, small plot testing		Advanced clones in replicated multi-site		National Performance Trials and On-Farm trials		Official release and product launch
Duration			2 years		1-2 years		3 years		2 years		
# combinations # clones			500 25-30k		1700-2000		130-150		7-14		
Pipeline Process			PxP	F1	Clonal eval.	Prelim. YT	Adv YT	Uniform YT	National Performance trials		Range Management
Stage Gate Decisions		Define combinations		Select St 2 Clones		Select St 3 Clones		St 4 PAM		St 5 PAM	
Team that decides		Breeders (technical) Market (trait parameters)		Breeders		Limited CF Team		Almost full CF Team		Full CF Team	



# Genotype Search

- Allows searching specific allele states in the database
- Based on MarkerSets
  - A markerset is a group of markers and specifies which allele is being searched
- List of accessions
  - The accessions that will be searched
- For example, a MarkerSet could correspond to a Intertek marker set



Titima Tantikanjana





# Ordering System

- Request by Banana Breeding Project
- Users can order stocks from other users in Breedbase
- Users with the Vendor role can elevate stocks to be listed in the Catalog
- Vendor can set status of the order etc.
- Coming to all RTBbases soon



Titima Tantikanjana



# BrAPI support



- Important technology underpinning Breedbase functions
- Breeding Application Programming Interface – different systems can exchange data programmatically, such as Cassavabase and Fieldbook
- Evolving standard, need to adapt from time to time
- Hackathon 2022 in October



Mirella Flores



# Yambase FTP site

- FTP protocol is inherently insecure has been phased out
- FTP site contents is now available through the website, at:
  - <https://yambase.org/ftp>

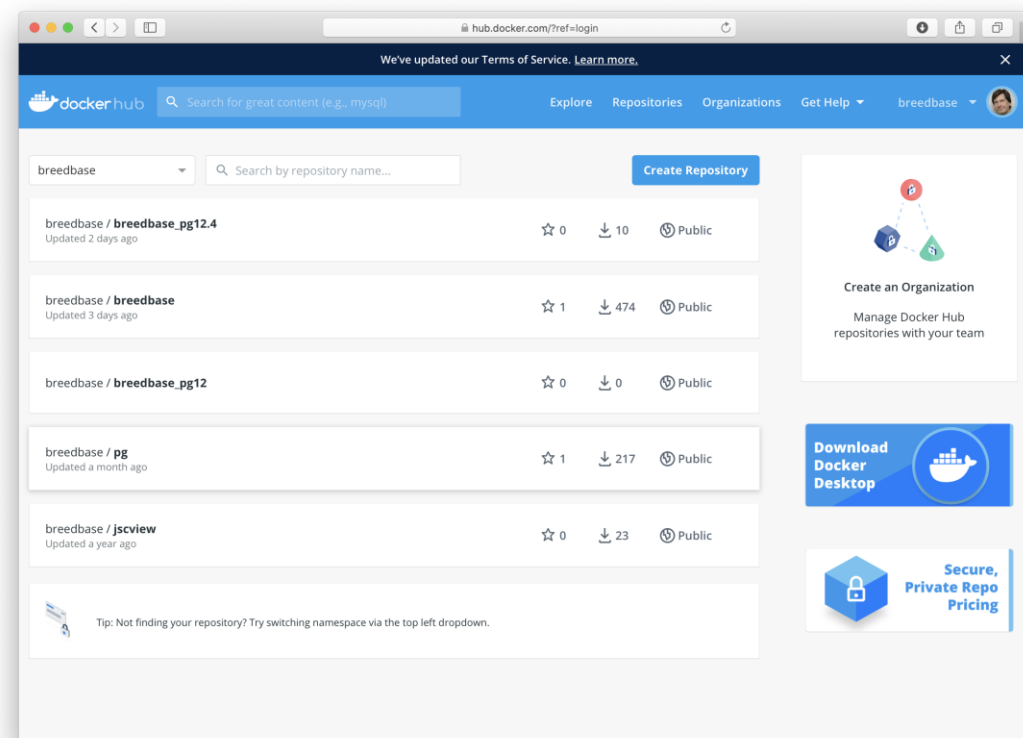
A screenshot of a web browser window showing the index of the FTP site. The browser's address bar displays "cassavabase.org/ftp/". The page title is "Index of /ftp/". The index lists various directories and files with their last modification dates and times. The entries are as follows:

../		
<a href="#">3primeRNAseqRawData/</a>	09-Jun-2021 22:09	-
<a href="#">CASS/</a>	18-Feb-2020 22:15	-
<a href="#">CIAT/</a>	18-Jul-2016 13:56	-
<a href="#">Cassava3primeRNAseqRawReads/</a>	08-Jun-2021 21:09	-
<a href="#">GenotypeStoragePaper/</a>	11-May-2020 13:26	-
<a href="#">HapMapII/</a>	15-Jan-2018 20:29	-
<a href="#">Manihot_v6.1/</a>	14-Dec-2015 16:40	-
<a href="#">Qchamps/</a>	01-Mar-2019 12:44	-
<a href="#">documents/</a>	09-Jun-2021 00:29	-
<a href="#">filtered_gbs_data/</a>	20-Mar-2015 02:54	-
<a href="#">ftp/</a>	05-Sep-2021 19:01	-
<a href="#">genotypes/</a>	04-Apr-2014 15:04	-
<a href="#">images/</a>	17-Jul-2018 20:43	-
<a href="#">intertek/</a>	15-Mar-2019 19:59	-
<a href="#">jbrowse/</a>	05-Nov-2015 21:11	-
<a href="#">manuscripts/</a>	03-Jul-2021 20:18	-
<a href="#">maps/</a>	13-Jan-2014 08:03	-
<a href="#">marnin_datasets/</a>	11-Aug-2021 13:33	-
<a href="#">static_content/</a>	03-Nov-2020 18:04	-
<a href="#">static_content_test/</a>	04-Oct-2019 13:47	-
<a href="#">ugo/</a>	21-Apr-2015 17:27	-
<a href="#">user_requests/</a>	12-Nov-2020 21:24	-
<a href="#">workshops/</a>	26-Apr-2018 15:06	-
<a href="#">df_STAR_HTSseq_counts_cassava_DESeq2_vstNormaliz...&gt;</a>	10-Jul-2018 17:15	397070315
<a href="#">news.txt</a>	04-Sep-2015 18:31	763



# Docker technology for development and deployment

- Simplifies development and deployment of software
- Generated 49 releases in 2 years
- about 1 release every two weeks
- Docker images were downloaded about 4000 times





Thank you!