New tools to improve efficiency of data analysis

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June, 2016

Nairobi, Kenya

SASHA Sweetpotato Action for Security and Health in Africa

BTI BOYCE THOMPSON INSTITUTE

CENTRO INTERNACIONAL DE LA PAPA CIP
A member of the CGIAR Consortium

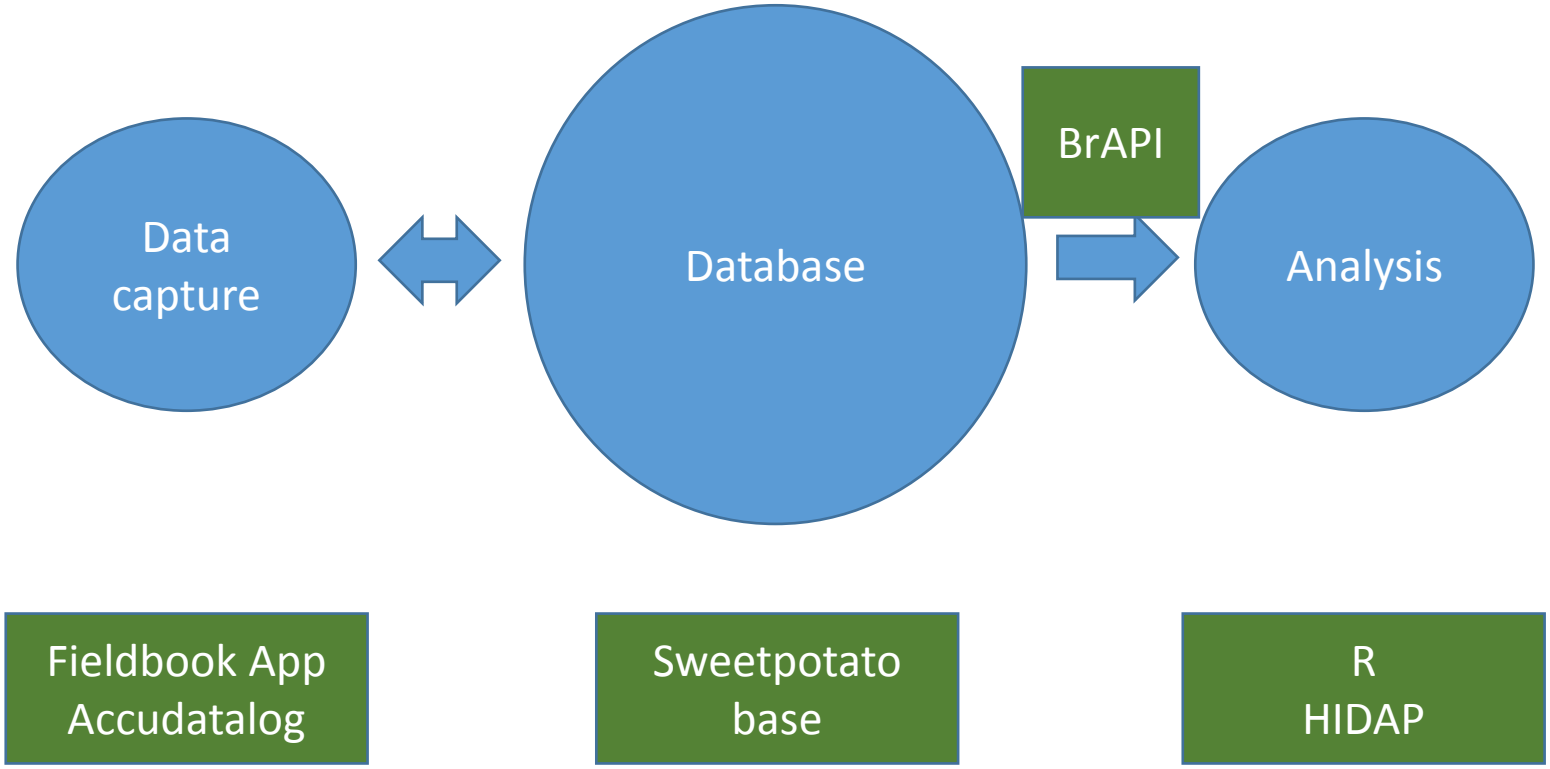
NC STATE UNIVERSITY

GT4SP

Motivation

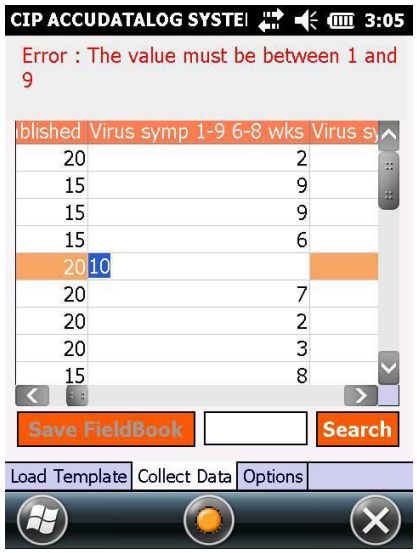
- Faster routine analysis of breeding trials
  - Building on current tools like CloneSelector
- Working with community tools:
  - Sweetpotatobase
  - KSU fieldbook app
  - Accu datalog
- Technical update to take better advantage of
  - Interactivity: Linked data & linked views
  - R reproducible reports for automating analyses
  - Ontologies to facilitate (statistical) handling of variables

The big picture …



AccuDataLog

- Mobile field data collection app.
- **Runs on Windows mobile for robust data collection in the field**
- **… and Android**
- **English, Swahili and Chinese**
- Developed by **CIP(SASHA)**
- Automatic Import of Fieldbooks into mobile device
- Field based data entry



Main Features

- Integrated barcode label technology (1D & 2D)
- Realtime data entry validation: numeric, date, string length, lower limits, upper limits, etc
- User defines lower and upper limits in excel
- Print on demand (POD) of barcode labels via mobile printing

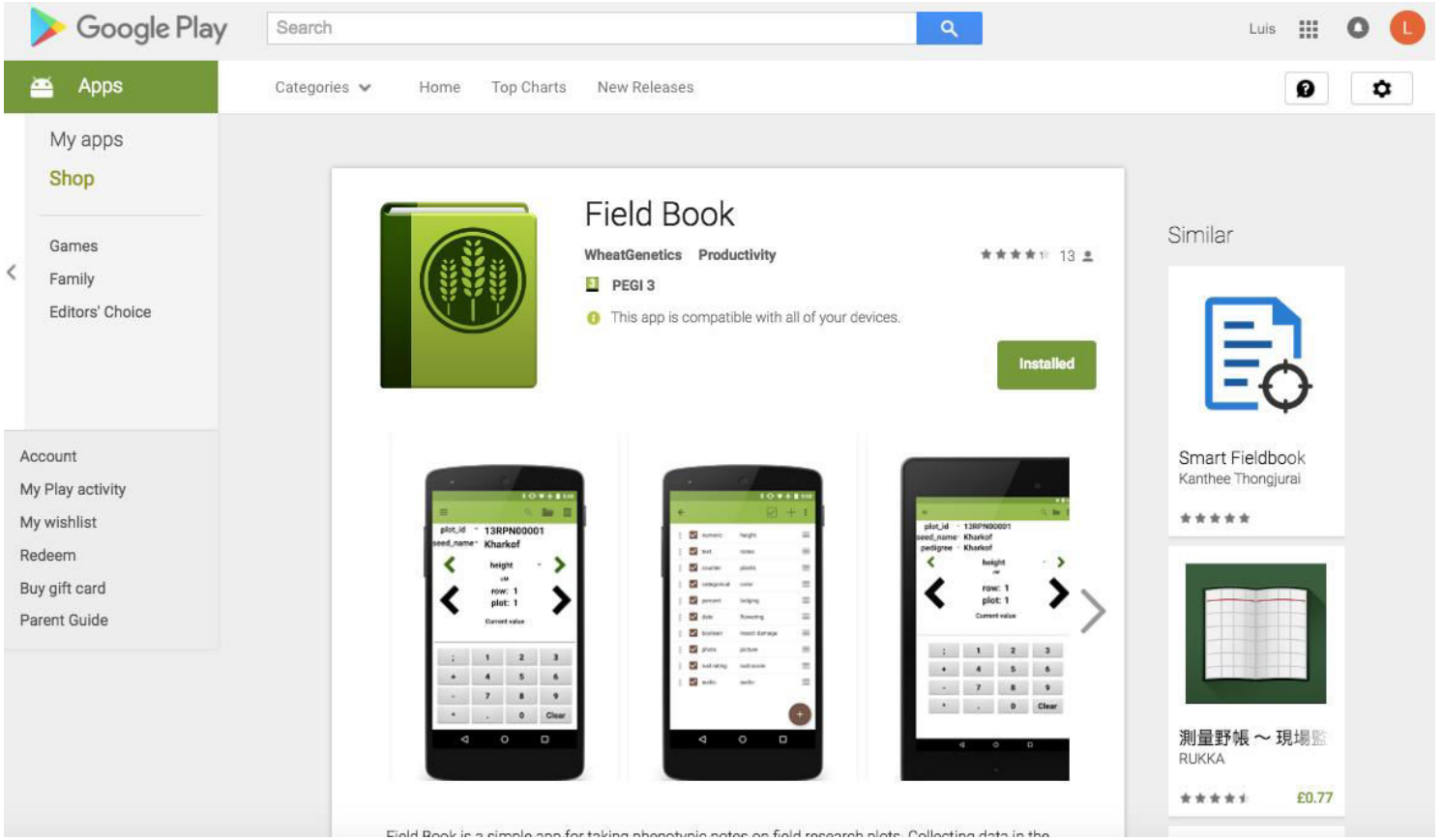
AccuDataLog Adoption

Ghana

Mozambique

Uganda

https://play.google.com/store/apps/details?id=com.fieldbook.tracker&hl=en




SAMSUNG
12:45 PM
Mon, 16 September
Swipe screen to unlock


SAMSUNG

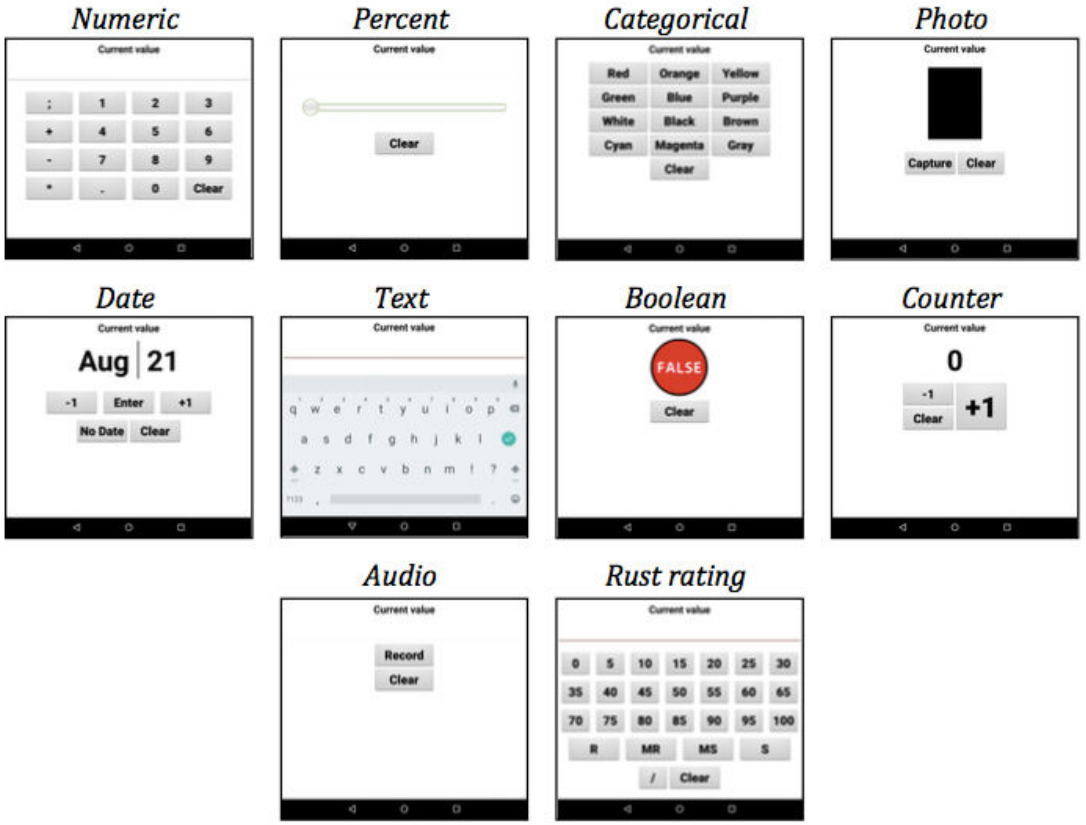

Otter
Otter


SanDisk
32GB
microSD
HC

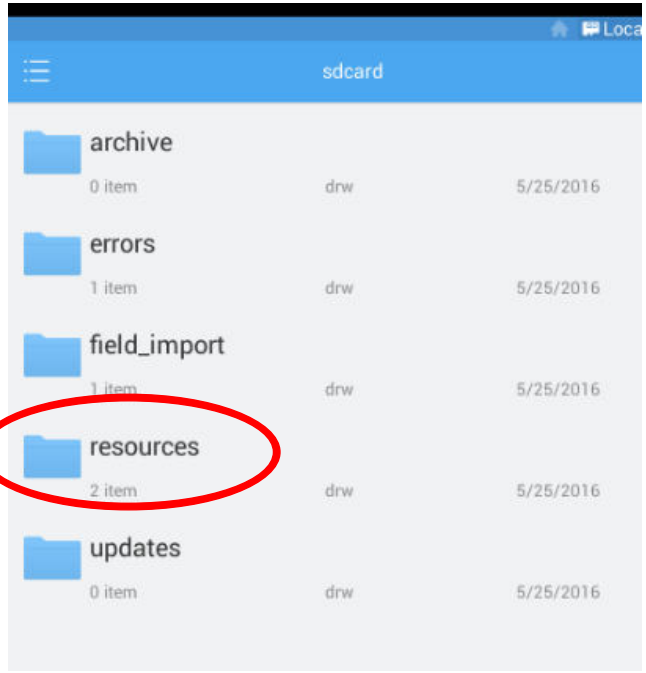

SAMSUNG
12:45 PM

Trait formats

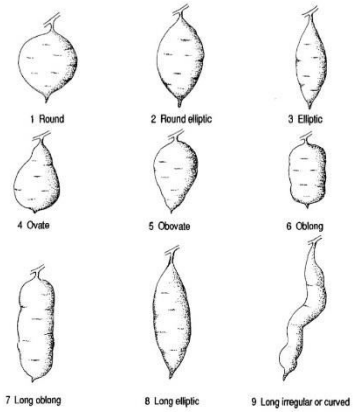
- Numeric
- Percent
- Categorical
- Date
- Text
- Boolean
- Counter
- Photo
- Audio

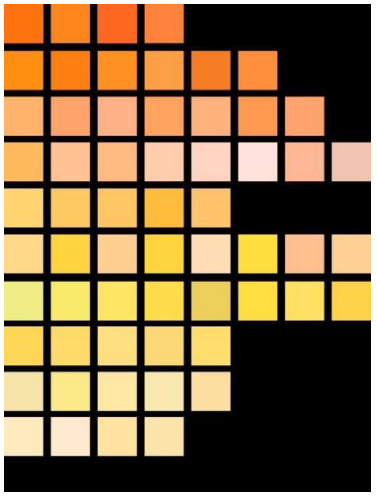


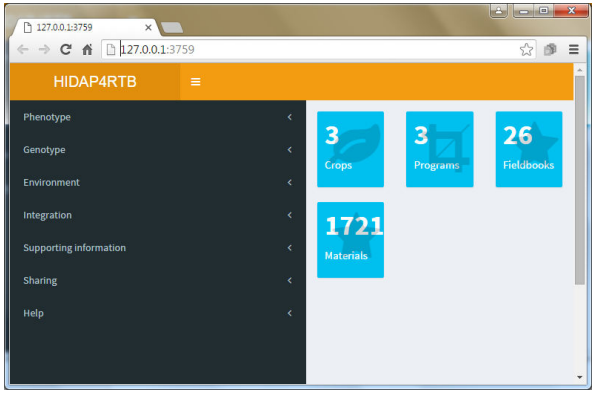
Resources Folder

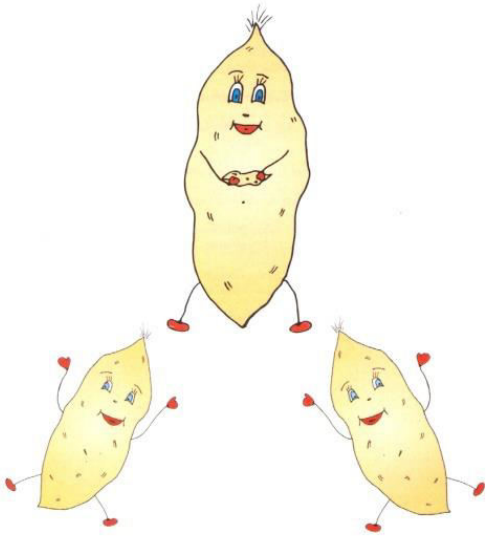


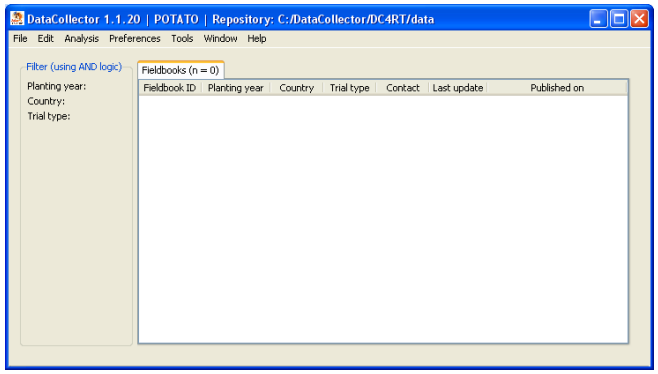
- Resources folder: user can upload cheat sheets, pictures, images, etc. to aid phenotyping

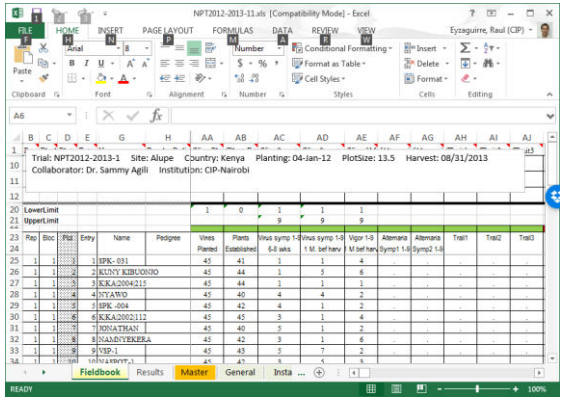












Data collector

Clone selector

HIDAP

Phenotype

Analysis

Fieldbook

SPYLAT2013_MZ-Gurue

Environment

Fieldbook

Show 10 entries

Search:

	PLOT	plotDbId	BLOCK	REP	germplasmDbId	germplasmName	Beta carotene content measuring mg per 100g	Fibers in cooked samples 1 estimating 1-9	Harvest index computing percent	Number of commercial storage roots counting number per plot	non-s num
73	1	38843	1	1	38837	MGSG 1065-4	11.03	1	40.1	19	
34	2	38845	1	1	38844	MGSG 1007-13	7.23	1	29	5	
55	3	38847	1	1	38846	MGSG 1012-9	7.23	1	62.7	14	
76	4	38849	1	1	38848	MGSG 1068-1	7.23	1	14.9	4	
10	5	38851	1	1	38850	MGSG 1001-7	3.03	3	58.7	10	
67	6	38852	1	1	38835	MGSG 1051-1	7.76	1	15	7	
19	7	38854	1	1	38853	MGSG 1004-27	7.23	1	66.9	12	
70	8	38856	1	1	38855	MGSG 1061-3	7.23	1	62.3	25	
37	9	38858	1	1	38857	MGSG 1007-9	6.12	1	8	4	
46	10	38860	1	1	38859	MGSG 1010-10	7.23	1	51.5	17	

Showing 1 to 10 of 81 entries

Previous 1 2 3 4 5 … 9 Next

HIDAP

≡

Phenotype

Analysis

Fieldbook

SPYLAT2013_MZ-Gurue

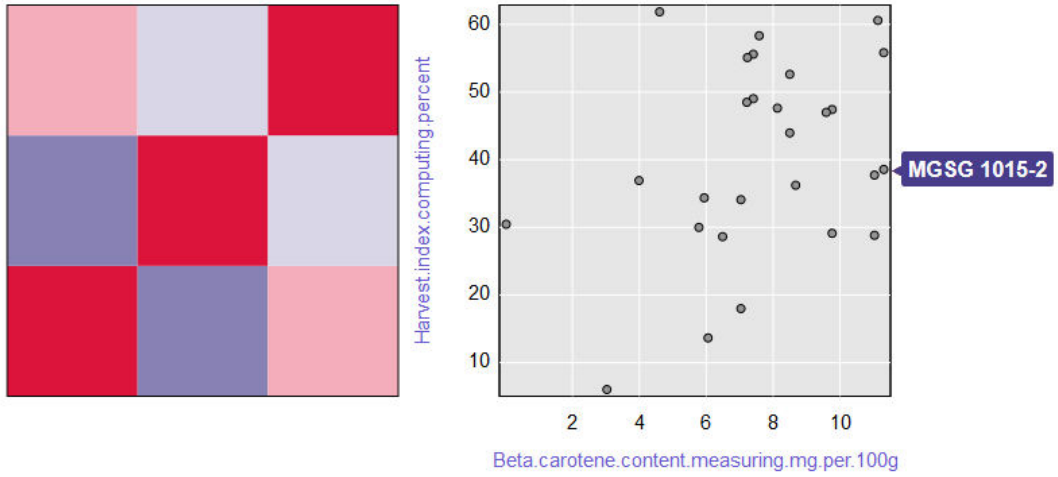
Environment

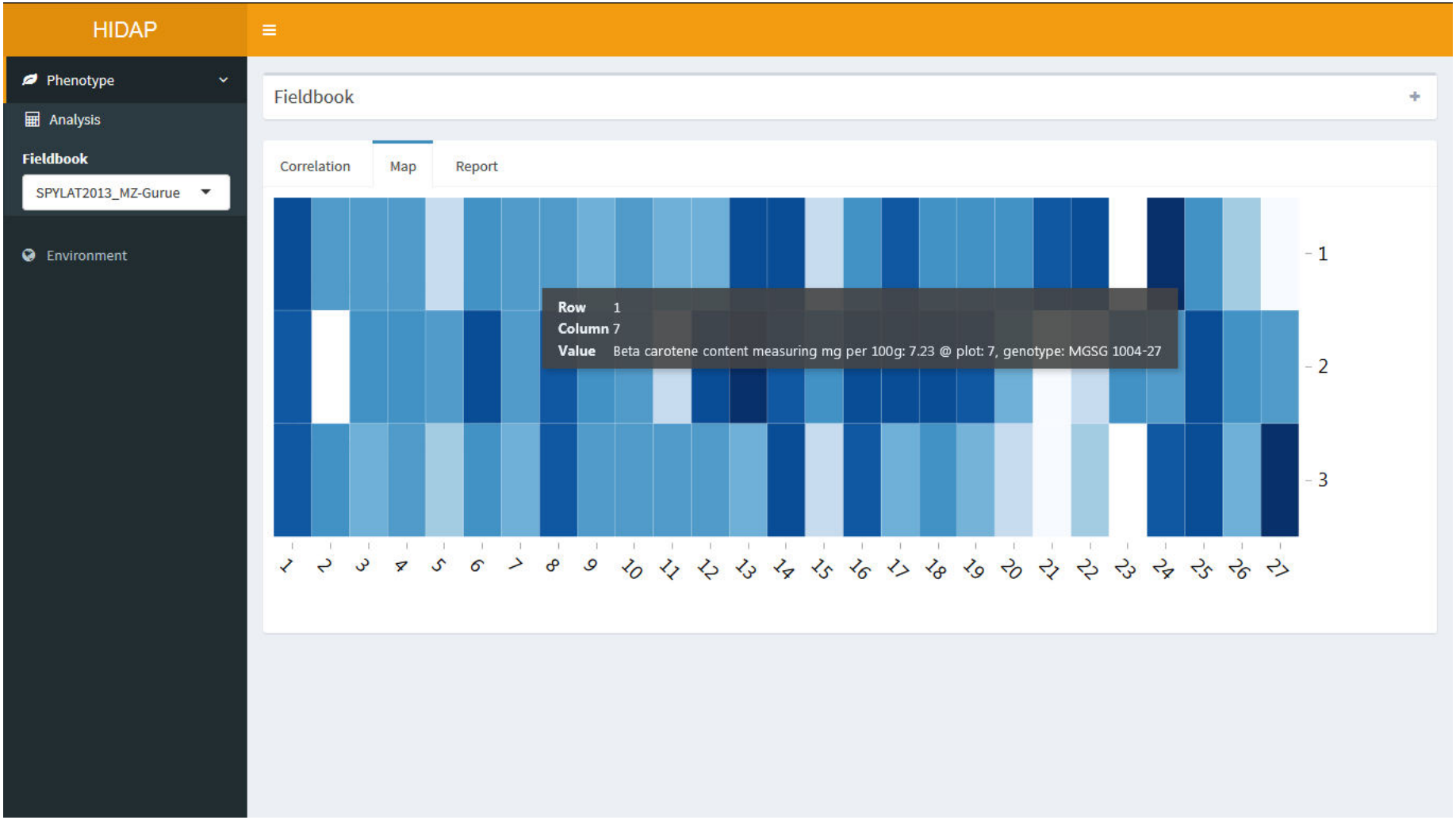
Fieldbook +

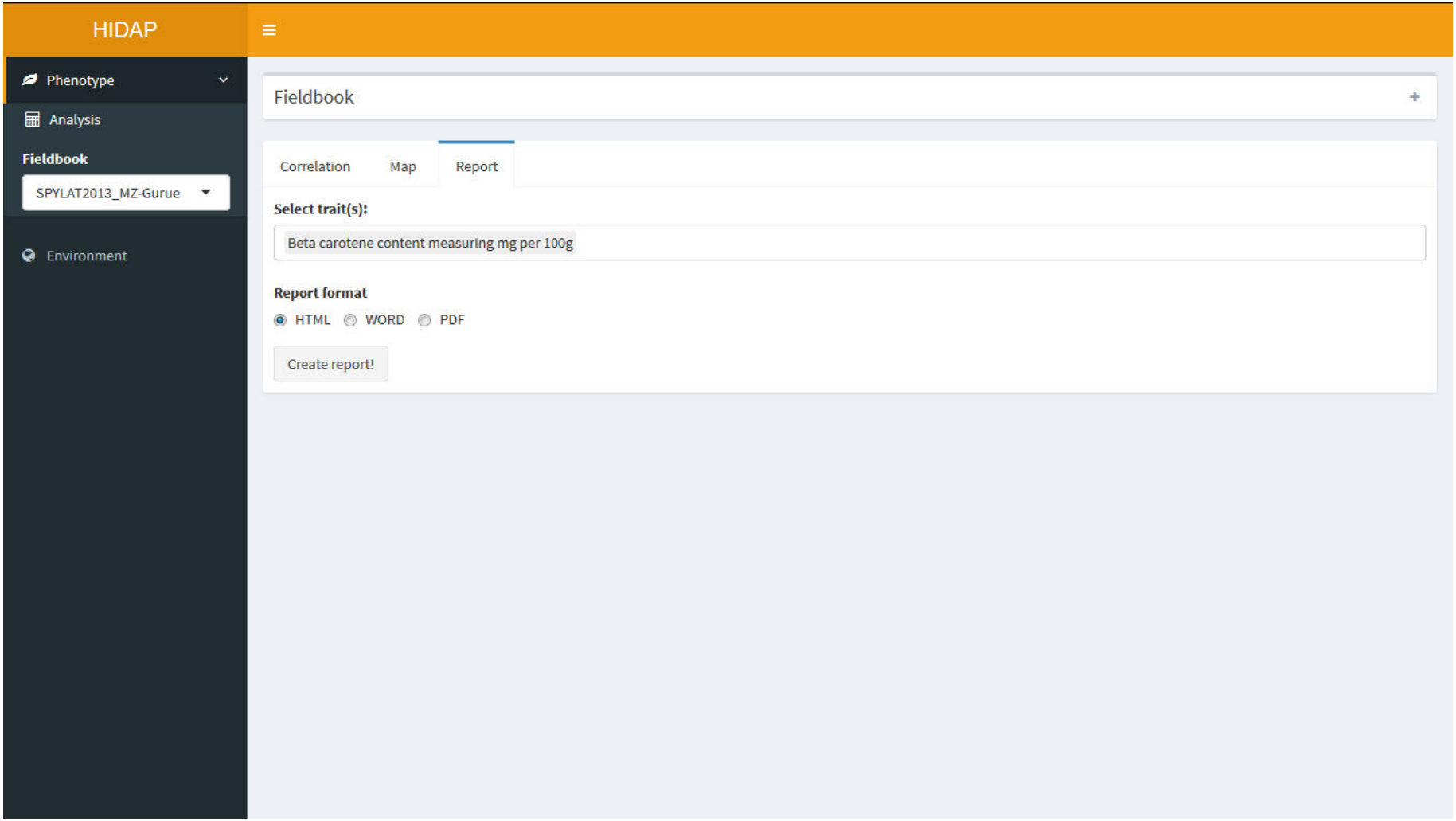
Correlation | Map | Report

Select two or more traits:

Beta carotene content measuring mg per 100g | Fibers in cooked samples 1 estimating 1-9 | Harvest index computing percent




HIDAP
Phenotype
Analysis
Fieldbook
SPYLAT2013_MZ-Gurue
Environment
Fieldbook
Correlation
Map
Report
Row 1
Column 7
Value Beta carotene content measuring mg per 100g: 7.23 @ plot: 7, genotype: MGSG 1004-27
1
2
3
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27


HIDAP
Phenotype
Analysis
Fieldbook
SPYLAT2013_MZ-Gurue
Environment
Fieldbook
Correlation
Map
Report
Select trait(s):
Beta carotene content measuring mg per 100g
Report format
HTML
WORD
PDF
Create report!

ANOVA for a RCBD trial: SPYLAT2013_MZ-Gurue

HIDAP

June 07, 2016, 10:12h


```
# This is an automatedly created report.

# See more details in section on materials.
```

Abstract

This trial has the identifier SPYLAT2013_MZ-Gurue. It was conducted under the supervision of x y as a Advanced Trial as part of a Yield Breeding Program in Gurue, Mozambique, Z in 2016. A total of 27 clones (including reference clones) were evaluated for 1 traits.

Materials and Methods

Model specification and data description

There is data from 27 treatments, evaluated using a randomize complete block design with 1, 2, 3 blocks. The statistical model is

$$y_{ij} = \mu + \tau_i + \beta_j + \epsilon_{ij}$$

where

- y_{ij} is the observed response with treatment i and block j.
- μ is the mean response over all treatments and blocks.
- τ_i is the effect for treatment i.

Trait analyses

The following traits were not analyzed since they had too many missing values (>= 10%): . For the remaining traits missing values were imputed using all available information.

Valid traits: **Beta carotene content measuring mg per 100g**.

Analysis of **Beta carotene content measuring mg per 100g**

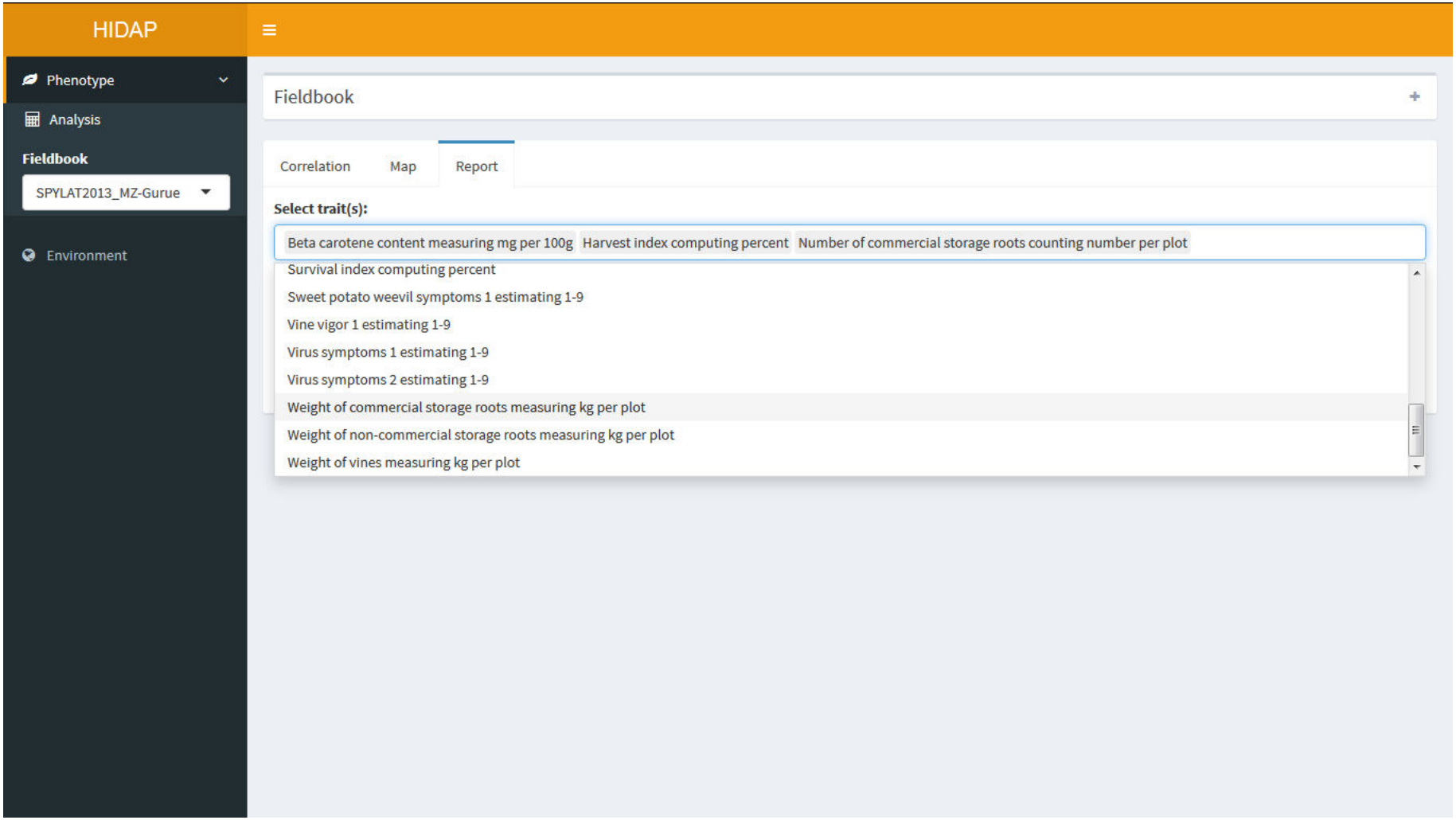
You have fitted a linear model for a RCBD. The ANOVA table for your model is:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	26	562.042	21.617	16.5482	5.16033e-17
REP	2	16.3471	8.17357	6.25703	0.00367343
Residuals	52	67.9276	1.3063	NA	NA

The p-value for treatments is 0.00000000000000000516033 which is significant at the 5% level.

The means of your treatments are:

germplasmName	Beta carotene content measuring mg per 100g
Chingova	0.02
Jonathan	3.99
MGSG 1001-36	11.1
MGSG 1001-7	4.61
MGSG 1002-49	8.5
MGSG 1003-27	7.73
MGSG 1004-2	9.76
MGSG 1004-27	7.41
MGSG 1005-17	5.94


HIDAP
Phenotype
Analysis
Fieldbook
SPYLAT2013_MZ-Gurue
Environment
Fieldbook
Correlation
Map
Report
Select trait(s):
Beta carotene content measuring mg per 100g
Harvest index computing percent
Number of commercial storage roots counting number per plot
Survival index computing percent
Sweet potato weevil symptoms 1 estimating 1-9
Vine vigor 1 estimating 1-9
Virus symptoms 1 estimating 1-9
Virus symptoms 2 estimating 1-9
Weight of commercial storage roots measuring kg per plot
Weight of non-commercial storage roots measuring kg per plot
Weight of vines measuring kg per plot

ANOVA for a RCBD trial: SPYLAT2013_MZ-Gurue

HIDAP

June 07, 2016, 10:13h

Contents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# This is an automatedly created report.

# See more details in section on materials
```

Analysis of Harvest index computing percent

You have fitted a linear model for a RCBD. The ANOVA table for your model is:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	26	16327	627.961	5.16952	2.46623e-07
REP	2	101.453	50.7264	0.417592	0.66082
Residuals	52	6316.63	121.474	NA	NA

The p-value for treatments is 0.000000246623 which is significant at the 5% level.

The means of your treatments are:

germplasmName	Harvest index computing percent
Chingova	30.5
Jonathan	36.9
MGSG 1001-36	60.6
MGSG 1001-7	61.9
MGSG 1002-49	52.6
MGSG 1003-27	30
MGSG 1004-2	47.4
MGSG 1004-27	55.6
MGSG 1005-17	34.4
MGSG 1006-7	47
MGSG 1006-9	34.1
MGSG 1007-13	47.6
MGSG 1007-9	13.7
MGSG 1008-8	28.6
MGSG 1009-3	58.3
MGSG 1010-10	49
MGSG 1010-4	55.8
MGSG 1011-5	48.5
MGSG 1012-9	44
MGSG 1015-17	28.8
MGSG 1015-2	38.6

Model specification and data description

There is data from 27 treatments, evaluated using a randomize complete block design with 1, 2, 3 blocks. The statistical model is

$$y_{ij} = \mu + \tau_i + \beta_j + \epsilon_{ij}$$

where

- y_{ij} is the observed response with treatment i and block j.
- μ is the mean response over all treatments and blocks.
- τ_i is the effect for treatment i.
- β_j is the effect for block j.
- ϵ_{ij} is the error term.

In this model we assume that the errors are independent and have a normal distribution with common variance, that is, $\epsilon_{ij} \sim N(0, \sigma_\epsilon^2)$.

The following traits are analyzed: **Beta carotene content measuring mg per 100g, Harvest index computing percent, Weight of commercial storage roots measuring kg per plot.**

The following germplasm was analyzed: MGSG 1065-4, MGSG 1007-13, MGSG 1012-9, MGSG 1068-1, MGSG 1001-7, MGSG 1051-1, MGSG 1004-27, MGSG 1061-3, MGSG 1007-9,

Analysis of Beta carotene content measuring mg per 100g

You have fitted a linear model for a RCBD. The ANOVA table for your model is:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
germplasmName	26	562.082	21.6186	16.3243	6.95787e-17
REP	2	17.1183	8.55914	6.46305	0.00311304
Residuals	52	68.8645	1.32432	NA	NA

The p-value for treatments is 0.000000000000000695787 which is significant at the 5% level.

The means of your treatments are:

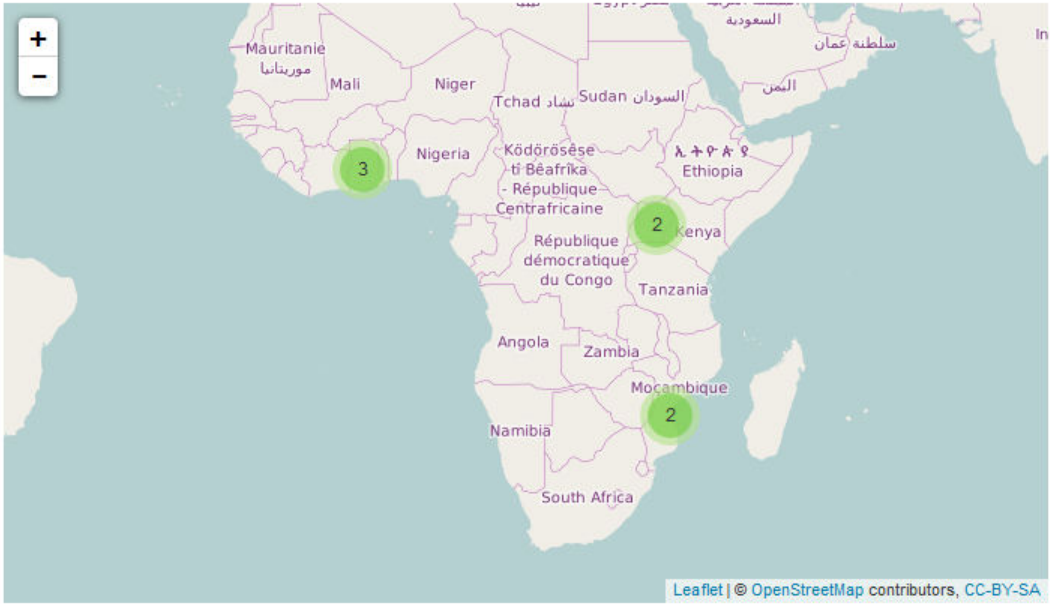
germplasmName	Beta carotene content measuring mg per 100g
Chingova	0.02
Jonathan	3.99
MGSG 1001-36	11.1
MGSG 1001-7	4.61
MGSG 1002-49	8.5
MGSG 1003-27	7.81
MGSG 1004-2	9.76
MGSG 1004-27	7.41
MGSG 1005-17	5.94
MGSG 1006-7	9.59
MGSG 1006-9	7.04
MGSG 1007-13	8.13
MGSG 1007-9	6.05
MGSG 1008-8	6.49
MGSG 1009-3	7.58

HIDAP

Phenotype

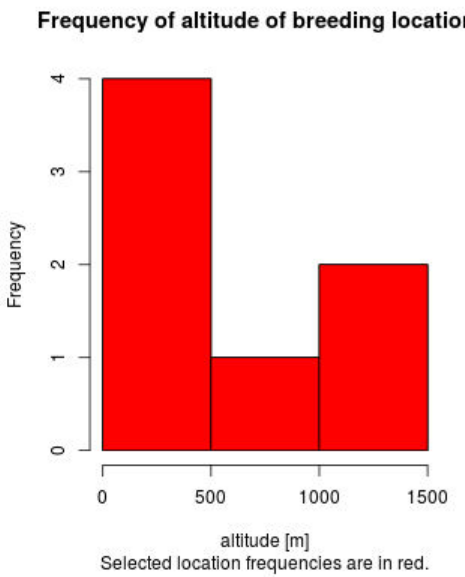
Environment

Map | Report



Histogram | Info | Fieldtrials

Genotypes | Site



Location table

Show 10 entries | Search:

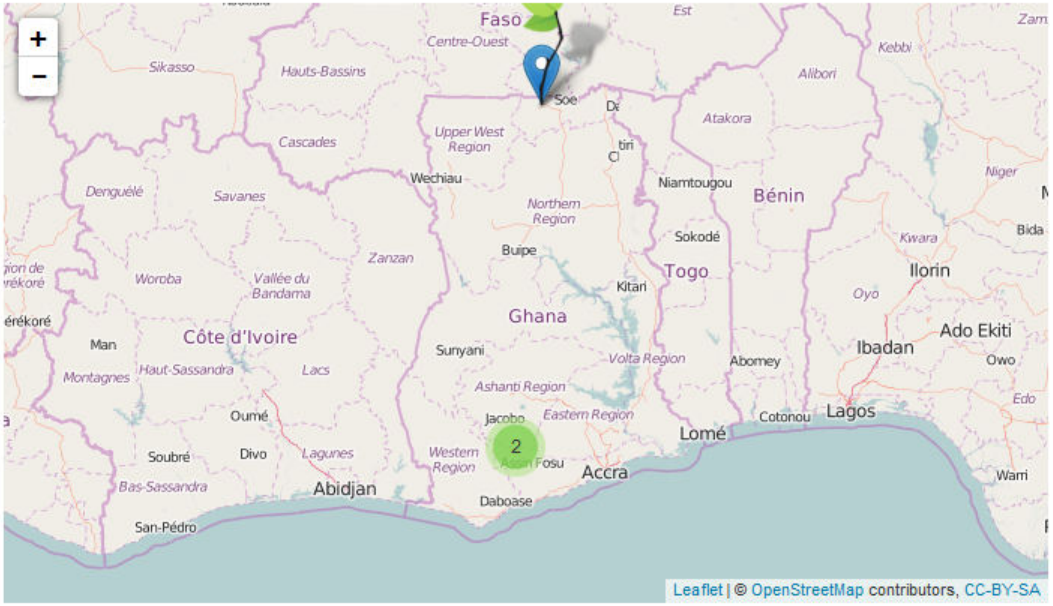
	locationDbId	altitude	countryCode	countryName	name	longitude
1	10				Cornell Biotech	

HIDAP

Phenotype

Environment

Map | Report



Location table

Show 10 entries Search:

	locationDbId	altitude	countryCode	countryName	name	longitude
1	10				Cornell Biotech	
2	12				Clinton, NC	

Histogram | Info | Fieldtrials

Genotypes Site

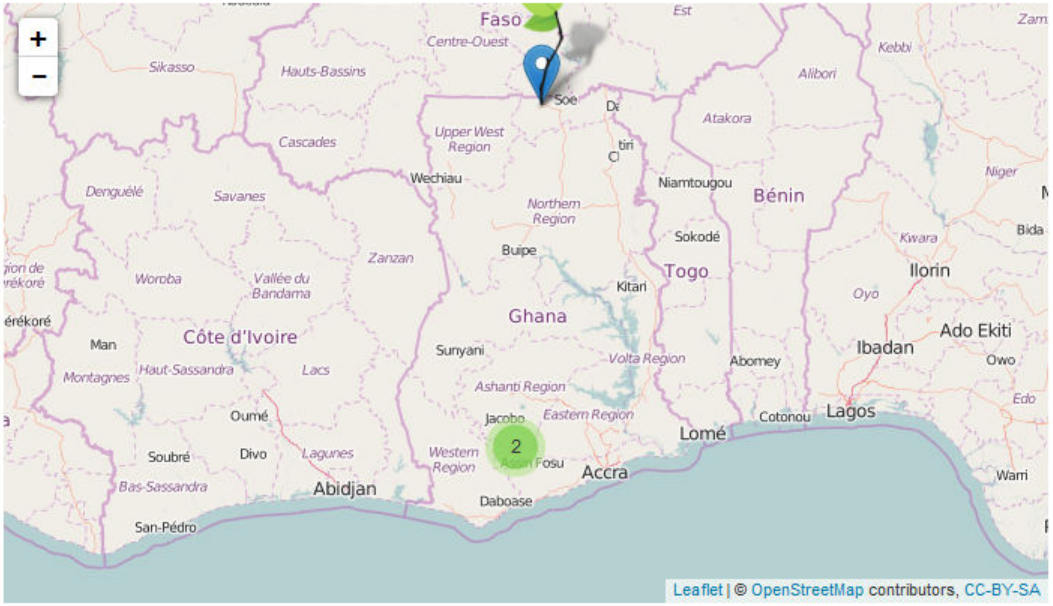
	Attribute	Value
1	locationDbId	18
5	name	Tono, Ghana
9	Uniquename	
4	countryName	
3	countryCode	
2	altitude	183
6	longitude	-1.1466
7	latitude	10.87
8	geodetic.datum	
10	Agricultural.Ecological.Zone	
12	adm1	
13	adm2	
14	adm3	
11	Continent	

HIDAP

Phenotype

Environment

Map | Report



Histogram | Info | Fieldtrials

Genotypes

Site

SPYLPT2013_GH-Tono

Location table

Show 10 entries

Search:

	locationDbId	altitude	countryCode	countryName	name	longitude
1	10				Cornell Biotech	
2	12				Clinton, NC	

Trial detail for SPYLPT2013_GH-Tono

Trial details

Breeding Program	Ghana (Ghana)	
Trial Name	SPYLPT2013_GH-Tono	[change]
Trial Type	PYT	[change]
Year	2013	[change]
Trial Location	Tono, Ghana	[change]
Planting Date	[No Planting Date]	[change]
Harvest Date	[No Harvest Date]	[change]
Description	163 sweetpotato clones were assayed in this Preliminary Trial of a yield breeding program for 25 traits at Tono	[edit]

Folder [New Folder] | [Change]

Ghana

HIDAP Trial Analysis

Phenotype Plot Map | Phenotype Correlation | Analysis Report

Physical Trial Layout

[Upload trial coordinates]

HIDAP

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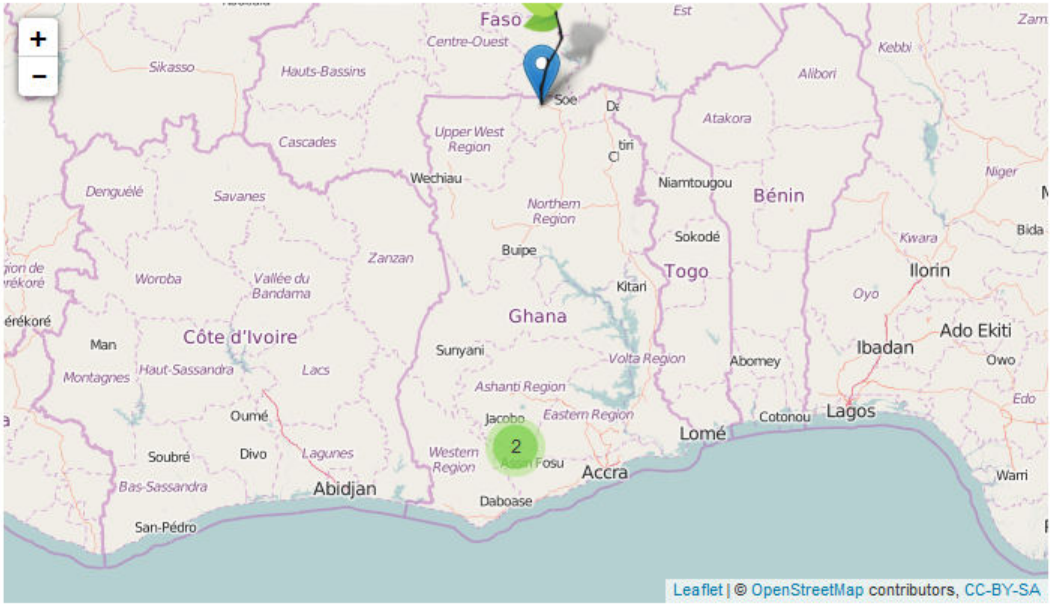
Phenotype

Environment

Map | Report



Location table

Show 10 entries Search:

	locationDbId	altitude	countryCode	countryName	name	longitude
1	10				Cornell Biotech	
2	12				Clinton, NC	

Histogram | Info | Fieldtrials

Genotypes

Site

Top genotypes for trait (Harvest index) from most recent (2013) fieldbook: SPYLPT2013_GH-Tono for location: :
PGB12162-4 (64.3), PG12170-4 (63.2), PG12151-26 (57.3), Apomuden (56.8)

Accession: Apomuden

Stock details New QTL population | Back to stock search

[New] [Edit] [Delete]

Organism	**Ipomoea batatas**
Stock type	**accession**
Stock name	**Apomuden**
Uniquename	**Apomuden**
Description	

SPB stock 40582 (Apomuden)

SPB40582

Stock editors: Reinhard Simon

Synonyms [Add]

Additional information [Add]

Associated loci (0)

Experimental data

Pedigree [Add parent] [Remove parent]

Descendants None

Pedigree string

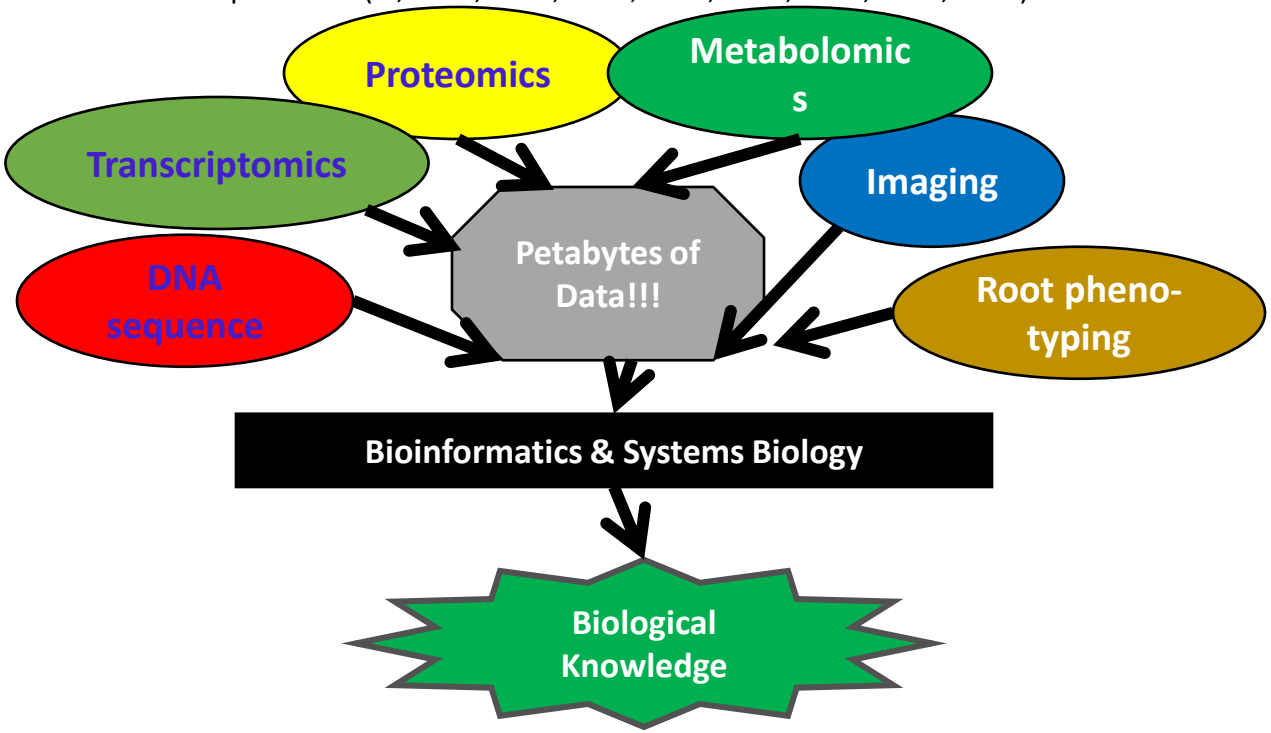
Parents

In the pipeline …

- Version 1.0 windows installer
- MET view
- Genotype data

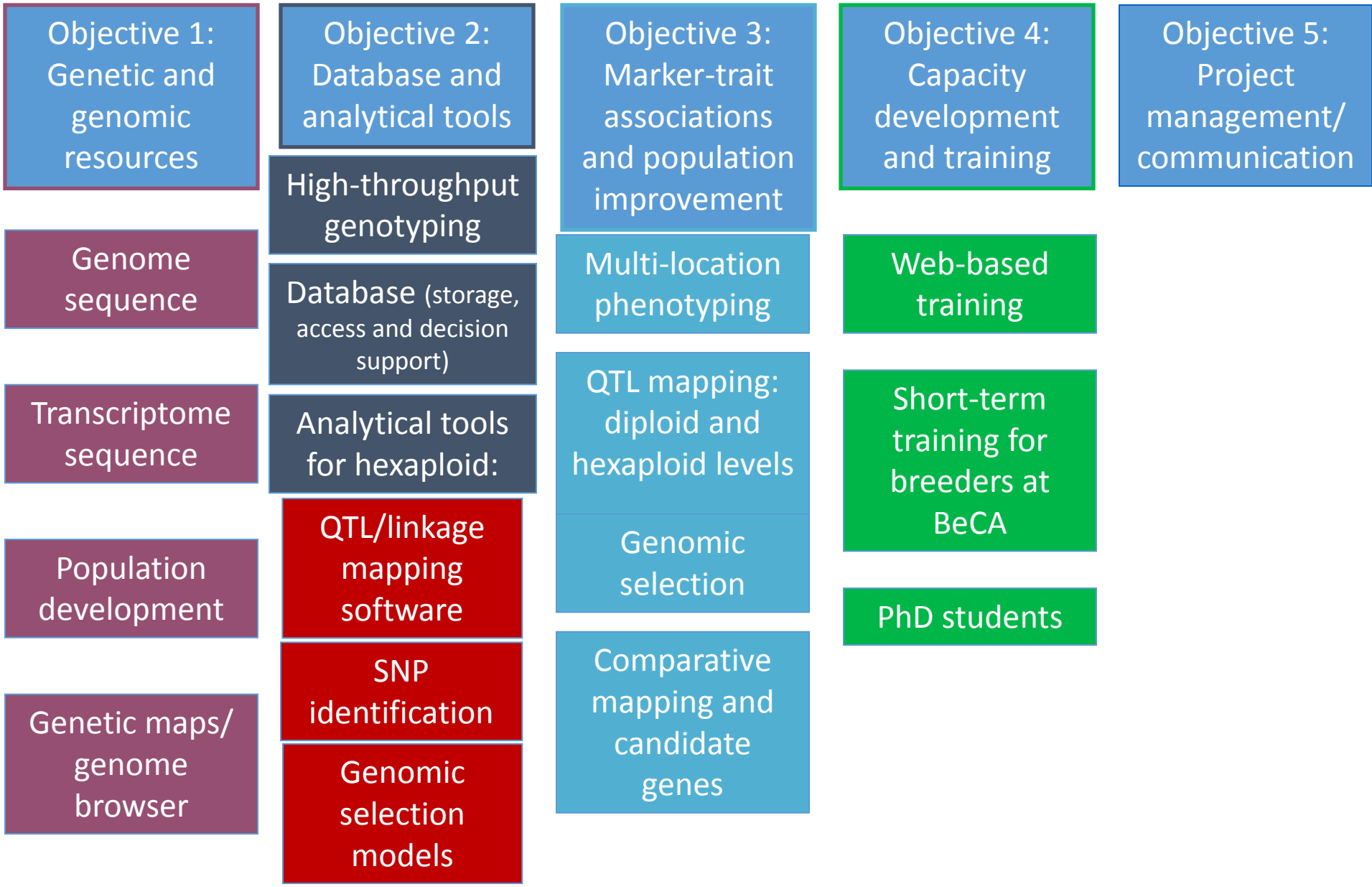
Integrated Analysis

The problem: improved genome sequencing and phenotyping have generated an enormous amount of data. In the near future, yottabytes of data can be expected (1,000,000,000,000,000,000,000,000)!!!



Outlook: new tools are needed for processing all this data, and integrating it for actual biological insights.

GT4SP Objectives



HIDAP: Next steps

- Stabilize the version with functionalities so far

- **Implement additional functionalities and tools developed by GT4SP colleagues at NCSU, UQ, MSU and BTI for integrated analysis of next generation multi-dimensional data sets** (QTL mapping, association mapping, selection schemes (MAS and GS))