




HIDAP training: Fieldbook creation, data quality of field data and statistical analysis.

JUN 05, 2018



Fieldbooks in HIDAP

You can create fieldbooks for several designs in HIDAP.



HIDAP
HIGHLY INTERACTIVE
DATA ANALYSIS PLATFORM

- Phenotype
- Material Management
- Fieldbook management**
 - New fieldbook**
 - Open fieldbook
 - Exploratory analysis
 - Check fieldbook
 - Data transformation
- Single Trial Analysis
- PVS Trial Analysis

Design of Field Experiments

Standard Modules

Special Modules

Fieldbook ID

PTAbiotic stress062018_CHIANGA

Crop & Location

Material List

Fieldbook Traits

Statistical Design

Environment

Plant Installation

Design

Randomized Complete Block Design (RCBD)

Replications

2

Choose exportation:

HIDAP format FieldBookApp format

Download

Fieldbooks in HIDAP – Exercise 1: Westcott

Create a fieldbook for 200 genotypes, one replication, following the Westcott method with checks Dagga and Cemsa, three plants per plot. Consider a field with room for 50 columns and 10 columns between checks.

The screenshot displays the HIDAP web interface for creating a fieldbook. The interface is divided into several sections:

- Sidebar (Left):** Contains navigation options such as "Phenotype", "Material Management", "Fieldbook management", "Open fieldbook", "Check fieldbook", "Data transformation", "Single Trial Analysis", "PVS Trial Analysis", "MET Analysis", "Index Selection", "Geographic Information", "Documentation", "Help", and "About". The "New fieldbook" option under "Fieldbook management" is highlighted with a red box.
- Top Navigation Bar:** Features icons for "Crop & Location", "Material List", "Fieldbook Traits", and "Statistical Design". The "Material List" and "Statistical Design" icons are highlighted with red boxes.
- Main Content Area:**
 - Define Genotypes:** Includes options for "Local List" and "Template". The "Download Template" button is highlighted with a red box.
 - Upload filled template:** Contains a "Browse..." button and a "No file selected" status.
 - Design:** Includes a dropdown menu for "Westcott Design (WD)".
 - Number of columns:** A text input field containing the value "50".
 - Number of columns between two check columns:** A text input field containing the value "10".
- Bottom Section:** A blue box with an upload icon and the text: "UPLOAD your material list file. Or, press the button below to download and fill the template."

Orange arrows indicate the workflow: from "New fieldbook" in the sidebar to "Material List" in the top bar, then to "Download Template" in the "Define Genotypes" section, and finally to "Statistical Design" in the top bar.

Fieldbooks in HIDAP – Exercise 2: RCBD

Create a fieldbook for 20 genotypes, three replications, following a RCBD, 3 rows per plot, 10 plants per row.

The screenshot displays the HIDAP web interface for creating a fieldbook. The left sidebar contains a navigation menu with the following items: Phenotype, Material Management, Fieldbook management, Single Trial Analysis, PVS Trial Analysis, MET Analysis, Index Selection, Geographic Information, Documentation, Help, and About. The 'Fieldbook management' section is expanded, and the 'New fieldbook' option is highlighted with a red box. An orange arrow points from this option to the 'Material List' tab in the main content area, which is also highlighted with a red box. Below the 'Material List' tab, the 'Define Genotypes' section is visible, with the 'Template' radio button selected. The 'Download Template' button is highlighted with a red box, and an orange arrow points from it to the 'Statistical Design' tab in the main content area, which is also highlighted with a red box. The 'Statistical Design' tab is active, showing the 'Design' section with 'Randomized Complete Block Design (RCBD)' selected and the 'Replications' section with the value '3' entered. An orange arrow points from the 'Download Template' button to the 'Design' section. At the bottom of the main content area, there is a blue box with an upload icon and the text: 'UPLOAD your material list file. Or, press the button below to download and fill the template.'

Fieldbooks in HIDAP – FieldBookApp file format

Choose exportation:

HIDAP format FieldBookApp format

Enter abbreviation user

Download FieldBookApp file



	A	B	C	D	E
1	plot_name	abbre_user	plot	rep	germplasm_name
2	17PPTS24SCTT_1016_1_NCP06-0020_G3				
3	17PPTS24SCTT_1015_1_NCP14-0099				
4	17PPTS24SCTT_1015_1_NCP14-0099				
5	17PPTS24SCTT_1015_1_NCP14-0099				
6	17PPTS24SCTT_1015_1_NCP14-0099				
7	17PPTS24SCTT_1015_1_NCP14-0099				

FieldBookApp file format



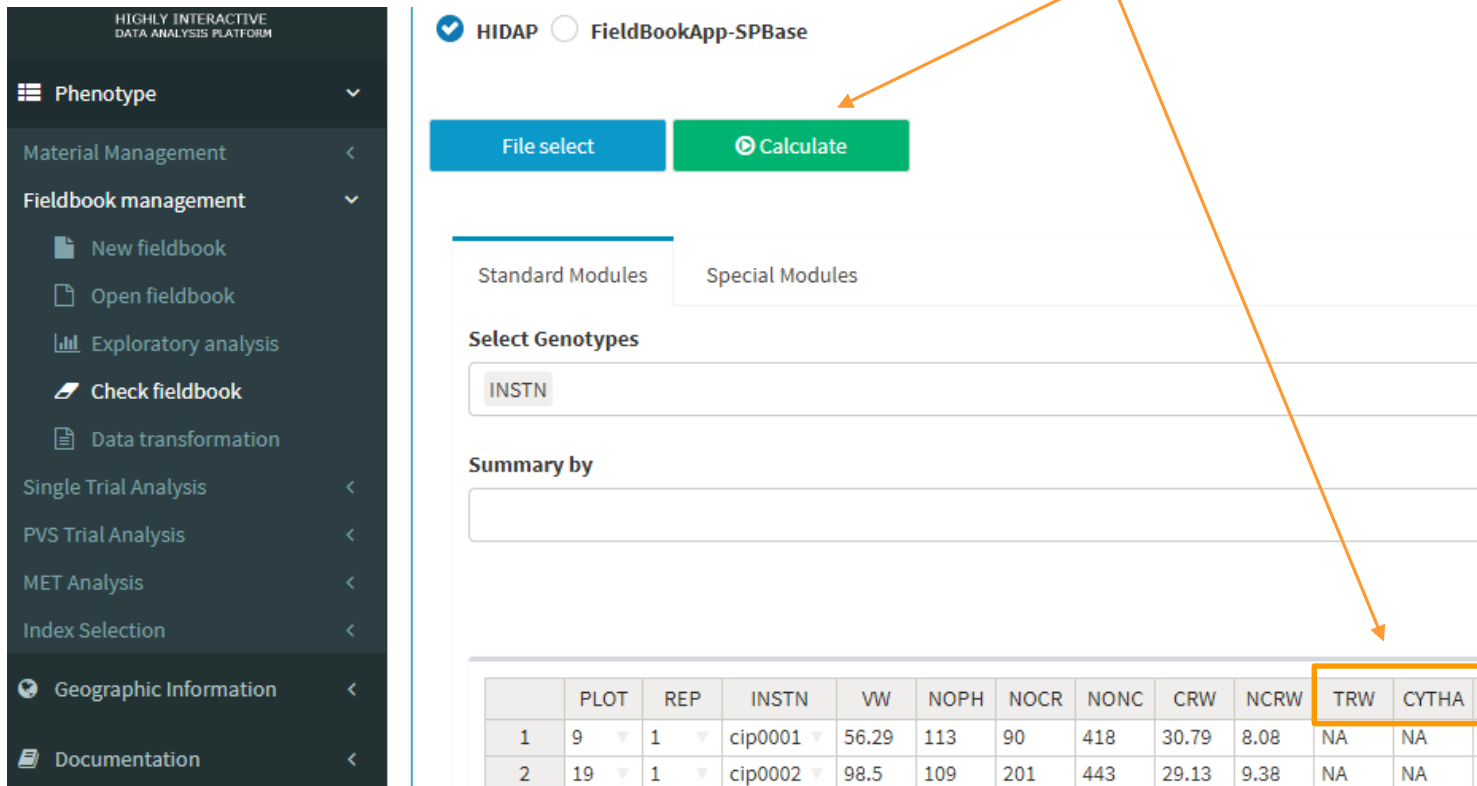
FieldBookApp

Check fieldbooks and compute derived traits

There are two kinds of checks:

- Yellow cells: Outliers (detected using interquartile range).
- Red cells: Out of range values.

All derived traits are computed (for instance TRW from CRW and NCRW) as long as they are in the fieldbook.



The screenshot displays the HIDAP (Highly Interactive Data Analysis Platform) interface. On the left is a dark sidebar menu with the following items: Phenotype, Material Management, Fieldbook management (with sub-items: New fieldbook, Open fieldbook, Exploratory analysis, Check fieldbook, Data transformation), Single Trial Analysis, PVS Trial Analysis, MET Analysis, Index Selection, Geographic Information, and Documentation. The 'Check fieldbook' option is highlighted with an orange arrow. The main panel shows the 'HIDAP' application selected, with a 'Calculate' button highlighted in green and also pointed to by an orange arrow. Below the buttons are tabs for 'Standard Modules' and 'Special Modules', a 'Select Genotypes' field containing 'INSTN', and a 'Summary by' field. At the bottom, a data table is shown with columns: PLOT, REP, INSTN, VW, NOPH, NOCR, NONC, CRW, NCRW, TRW, and CYTHA. The TRW and CYTHA columns are highlighted with an orange box.


	PLOT	REP	INSTN	VW	NOPH	NOCR	NONC	CRW	NCRW	TRW	CYTHA
1	9	1	cip0001	56.29	113	90	418	30.79	8.08	NA	NA
2	19	1	cip0002	98.5	109	201	443	29.13	9.38	NA	NA

Check fieldbooks and compute derived traits - Exercise

Open the fieldbook **SPAgronomic042017_ICA_exp1**.

Click on **Calculate** to get derived traits.

Check the fieldbook for outliers.



	PLOT	REP	INSTN	Observed traits						Calculated traits						
				VW	NOPH	NOCR	NONC	CRW	NCRW	TRW	CYTHA	RYTHA	CI	HI	BIOM	FYTHA
1	9	1	cip0001	56.29	113	90	418	30.79	8.08	38.87	9.5031	11.9969	17.7165	40.847	29.3704	17.3735
2	19	1	cip0002	98.5	109	201	443	29.13	9.38	38.51	8.9907	11.8858	31.2112	28.1074	42.287	30.4012
3	4	1	cip0003	56.24	103	25	124	12.93	2.37	15.3	3.9907	4.7222	16.7785	21.3866	22.0802	17.358
4	12	1	cip0004	64.51	107	78	373	26.77	6.74	33.51	8.2623	10.3426	17.2949	34.1869	30.2531	19.9105
5	8	1	cip0005	145.95	114	91	170	11.45	1.61	13.06	3.534	4.0309	34.8659	8.2133	49.0772	45.0463
6	18	1	cip0006	15.71	64	19	207	21.52	2.96	24.48	6.642	7.5556	8.4071	60.9107	12.4043	4.8488

Check fieldbooks – FieldBookApp / SPBase

FieldBookAPP

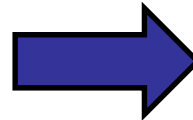


Data Quality and Processing

Radio buttons

HIDAP FieldBookApp-SPBase

	A	B	C	D	E	F	G
1	plot_name	trait	value	timestamp	person	location	number
2	17PPTS24SCTT_1016_1_NCP06-0020_G3	SEASON CO_331:0000794		15 02/11/2017 10:53			1
3	17PPTS24SCTT_1015_1_NCP14-0099	SEASON CO_331:0000794		15 02/11/2017 11:00			1
4	17PPTS24SCTT_1015_1_NCP14-0099	RTFLESH1 CO_331:0000782		15 02/11/2017 11:00			1
5	17PPTS24SCTT_1015_1_NCP14-0099	RTFLESH2 CO_331:0000783		15 02/11/2017 11:00			1
6	17PPTS24SCTT_1015_1_NCP14-0099	RTSTALK CO_331:0000777		15 02/11/2017 11:02			1
7	17PPTS24SCTT_1015_1_NCP14-0099	RTATTACH CO_331:0000778		15 02/11/2017 11:02			1
8	17PPTS24SCTT_2013_1_NCP13-0030	SEASON CO_331:0000794		15 02/11/2017 11:11			1
9	17PPTS24SCTT_2013_1_NCP13-0030	RTFLESH1 CO_331:0000782		15 02/11/2017 11:11			1
10	17PPTS24SCTT_2013_1_NCP13-0030	RTFLESH2 CO_331:0000783		15 02/11/2017 11:12			1
11	17PPTS24SCTT_2013_1_NCP13-0030	RTSTALK CO_331:0000777		15 02/11/2017 11:12			1
12	17PPTS24SCTT_2013_1_NCP13-0030	RTATTACH CO_331:0000778		15 02/11/2017 11:13			1
13	17PPTS24SCTT_2013_1_NCP13-0030	RTSHP1 CO_331:0000774		15 02/11/2017 11:13			1
14	17PPTS24SCTT_2013_1_NCP13-0030	RTSHP2 CO_331:0000775		15 02/11/2017 11:13			1
15	17PPTS24SCTT_2013_1_NCP13-0030	RTSHPU CO_331:0000776		15 02/11/2017 11:14			1
16	17PPTS24SCTT_2013_1_NCP13-0030	LDR CO_331:0000779		15 02/11/2017 11:14			1
17	17PPTS24SCTT_2013_1_NCP13-0030	SKINCOLOR CO_331:0000780		15 02/11/2017 11:15			1
18	17PPTS24SCTT_2013_1_NCP13-0030	RTSKNTEX CO_331:0000781		15 02/11/2017 11:16			1

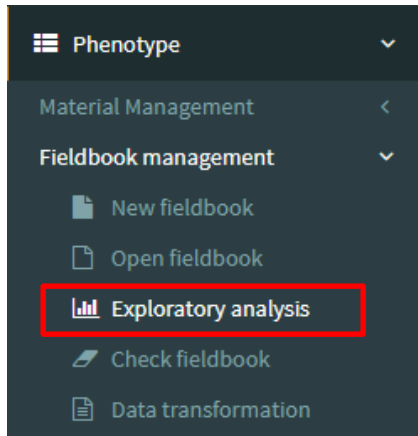


	PLOT	REP	INSTN	NTP	Plant_Vigor	SE	NPH	PPH	NMTP	MTWP	MTWPL	MTYNA	MTYA	Tuber_Apper	ATMW	A
1	1	1	CIP397006.18	10	7	7	10	100	36	4.7	0.47	17.4074	17.4074	5	130.5556	18
2	2	1	CIP397012.22	10	9	7	10	100	76	14.6	1.46	54.0741	54.0741	7	192.1053	20
3	3	1	CIP397030.31	10	9	5	10	100	110	8.4	0.84	31.1111	31.1111	5	76.9636	18
4	4	1	CIP397065.28	10	9	5	10	100	104	17.45	1.745	64.6296	64.6296	7	167.7885	21
5	5	1	CIP397079.26	10	9	2	10	100	66	130.45	13.045	483.1481	483.1481	7	1976.5152	21
6	6	1	CIP397100.9	10	5	7	10	100	56	7.45	0.745	27.5926	27.5926	5	133.0357	14
7	7	1	CIP397060.19	10	9	5	10	100	50	7.7	0.77	28.5185	28.5185	3	154	21
8	8	1	CIP397069.11	10	7	7	10	100	86	14.7	1.47	54.4444	54.4444	7	170.9302	19
9	9	1	CIP397099.6	10	9	5	10	100	90	19.2	1.92	71.1111	71.1111	9	213.3333	20
10	10	1	CIP397065.2	10	7	5	10	100	43	8.7	0.87	32.2222	32.2222	7	202.3256	21
11	11	1	CIP397073.7	10	9	5	10	100	81	12	1.2	44.4444	44.4444	7	148.1481	21
12	12	1	CIP397078.12	10	9	3	10	100	149	15.95	1.595	59.0741	59.0741	7	107.047	19
13	13	1	CIP397079.6	10	9	5	10	100	100	13.35	1.335	49.4444	49.4444	7	133.5	21
14	14	1	CIP397012.20	10	9	5	10	100	87	12.8	1.28	47.4074	47.4074	7	147.1264	19
15	15	1	CIP397077.16	10	7	7	10	100	50	7.5	0.75	27.7778	27.7778	7	150	20
16	16	1	CIP397073.15	10	9	5	10	100	79	9.1	0.91	33.7037	33.7037	5	115.1899	21
17	17	1	CIP397067.2	10	9	7	10	100	51	9.15	0.915	33.8889	33.8889	5	178.4118	23
18	18	1	CIP397035.26	10	9	5	10	100	63	11	1.1	40.7407	40.7407	7	174.6032	19
19	19	1	CIP397029.21	10	9	7	10	100	103	14.5	1.45	53.7037	53.7037	5	140.7767	18

Exploratory analysis

Exploratory graphs:

- Boxplot
- Scatterplot
- Histogram
- Density plot



Phenotype

Material Management

Fieldbook management

- New fieldbook
- Open fieldbook
- Exploratory analysis**
- Check fieldbook
- Data transformation

Choose a fieldbook

Browse... SPAgronomic042017_ICA_exp1.xlsx

Upload complete

Choose a graph

boxplot

Grouped by

Choose

X label

Select trait

Choose

Orientation of the label (Degrees °)

none

Y label

Exploratory analysis - Exercise

Open the fieldbook ***SPAgronomic042017_ICA_exp1***. Make the following graphs:

- Boxplot of CRW.
- Boxplot of CRW by replication.
- Scatterplot of NOCR and CRW.
- Histogram of VW.
- Density plot of VW.

Single trial report

1. Model specification and data description.
2. ANOVA and CV.
3. Plots to check assumptions.
4. Genotype means.
5. LSD and Tukey test (only if ANOVA turns out significant for genotypes).
6. Dotplot for genotypes (only if number of genotypes < 10).
7. Variance components estimation.

Single trial report - Exercise

Create a report for the **SPAgronomic042017_ICA_exp1** fieldbook.
This is under a RCBD

The screenshot displays a web application interface for generating a report. On the left, a dark sidebar contains a navigation menu with the following items: Phenotype, Material Management, Fieldbook management, Single Trial Analysis (with a sub-item 'Single report' highlighted in a red box), PVS Trial Analysis, MET Analysis, Index Selection, Geographic Information, Documentation, and About. The main content area on the right features a 'Select File' button at the top. Below it is a green success banner with a white checkmark icon and the text 'GREAT! Fieldbook selected: SPAgronomic042017_ICA_exp1.xlsx'. The interface then presents a series of configuration options, each with an orange arrow pointing from the sidebar to the corresponding field: 'Select statistical design of your experiment' (dropdown menu showing 'Randomized Complete Block Design (RCBD)'), 'Select Replications' (dropdown menu showing 'REP'), 'Select Genotypes' (dropdown menu showing 'INSTN'), and 'Select Trait(s)' (input field containing 'VW' and 'TRW'). At the bottom, the 'Report format' section includes radio buttons for 'html' (selected) and 'word', followed by an 'Analyze' button.

MET report

1. Model specification and data description.
2. Means by genotype, environment, and GxE interactions.
3. ANOVA and CV.
4. Plots to check assumptions.
5. LSD and Tukey test (only if ANOVA turns out significant for genotypes).
6. Variance components and broad sense heritability estimation.
7. Stability analysis (only if ANOVA turns out significant for interaction).

MET report - Exercise

Create a report for all the **SPAgronomic042017** fieldbooks (6 files).

The screenshot displays a web-based interface for generating a MET report. On the left, a dark sidebar contains a navigation menu with the following items: Phenotype, Material Management, Fieldbook management, Single Trial Analysis, PVS Trial Analysis, MET Analysis, **MET report** (highlighted with a red box), Index Selection, Geographic Information, Documentation, and About. An orange arrow points from the 'MET report' menu item to the main content area.

The main content area features a 'Select Files' button at the top. Below it is a large green notification box with a white checkmark icon and the text: "ALL FIELDBOOKS READY FOR MET". The notification lists six files: "Combined fieldbooks SPAgronomic042017_CIPSRM-1_exp1.xlsx, SPAgronomic042017_CIPSRM-1_exp2.xlsx, SPAgronomic042017_ICA_exp1.xlsx, SPAgronomic042017_ICA_exp2.xlsx, SPAgronomic042017_SATIPO_exp1.xlsx, SPAgronomic042017_SATIPO_exp2.xlsx".

Below the notification, there are several selection options:

- Select genotypes:** A dropdown menu showing "INSTN".
- Select environments:** A dropdown menu showing "ENVIRONMENT".
- Select replications:** A dropdown menu showing "REP".
- Select trait(s):** A multi-select field containing "VW" and "CRW".
- Report format:** Radio buttons for "html" (selected) and "word".
- Analyze:** A button with a play icon.

Orange arrows on the right side of the interface point from the sidebar menu items to their corresponding selection fields: "Index Selection" to the genotype dropdown, "Geographic Information" to the environment dropdown, "Documentation" to the replication dropdown, and "About" to the trait selection field.

Final Exercise

1. Create a list of 8 genotypes (give them any name) plus two checks (select the checks from the institutional list).
2. Create a RCBD with 2 blocks. Include the following traits: VW, CRW, NCRW, FYTHA, RYTHA, BIOM, HI.
3. Enter some data for VW, CRW and NCRW.
4. Check the fieldbook and compute the derived traits: FYTHA, RYTHA, BIOM, HI.
5. Get a report for these data.

Thanks!