**GitHub Repository:** <a href="https://github.com/jnsantos123/irri">https://github.com/jnsantos123/irri</a> **Web Application:** <a href="https://jsantos1.shinyapps.io/preTrialApp/">https://jsantos1.shinyapps.io/preTrialApp/</a>

Merge Function: Merges metadata and plot-level data of a trial based on identified variables.

- 1. Make sure that extracted data are stored in a single folder and that metadata and plot level data of each trial are next to each other.
- 2. Set "x" object as the directory of the folder containing the extracted data.
- 3. Set "y" object as the directory where the merged data will be stored.
- 4. Run "Merge" function with parameters "x" and "y".

**Traits List Function:** Identifies traits that appeared in at least one trial from a collection of trials.

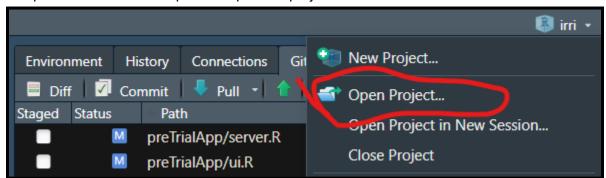
- 1. Make sure that you have completed merging the data before proceeding to this step.
- 2. Set "x" object as the directory where the merged data are stored.
- 3. Set "y" object as the directory where the traits list will be stored.
- 4. Run "traits" function with parameters "x" and "y"

**Traits Summary Function:** Identifies which of the listed traits are present per trial and checks the completeness of data per trait.

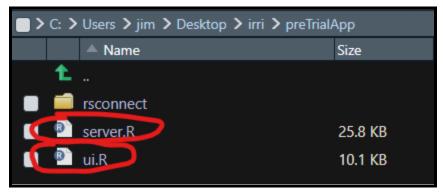
- 1. Make sure that you have completed merging and identifying traits before proceeding to this step.
- 2. Set "x" object as the directory where the merged data are stored.
- 3. Set "y" object as the directory where the trait summary will be stored.
- 4. Set "z" object as the directory of the traits list file.
- 5. Run "traitSummary" function with parameters "x", "y", and "z".

## **Pre-Trial App**

- 1. Retrieving scripts for the web application
  - a. Download the scripts from the GitHub repository <a href="https://github.com/jnsantos123/irri">https://github.com/jnsantos123/irri</a>.
  - b. Unzip the downloaded scripts and open the project *irri-master* in RStudio.



c. Open the *ui.R* and *server.R* from the *preTrialApp folder*. (Double click on the file to open it)



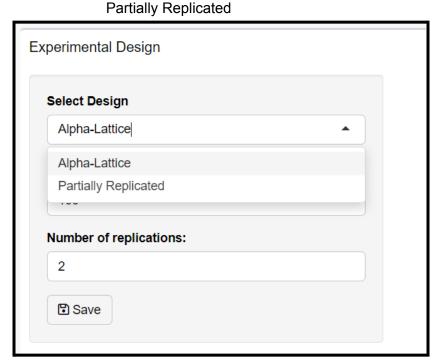
d. Run app. If the current R and package versions are not compatible with the app, install the versions used in creating the app found at the top of the scripts.



## 2. Experimental Design

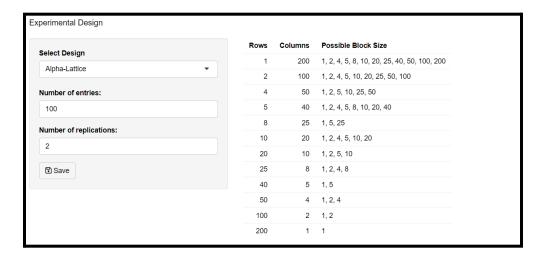
a. Choose an experimental design to be implemented

Options: Alpha-Lattice

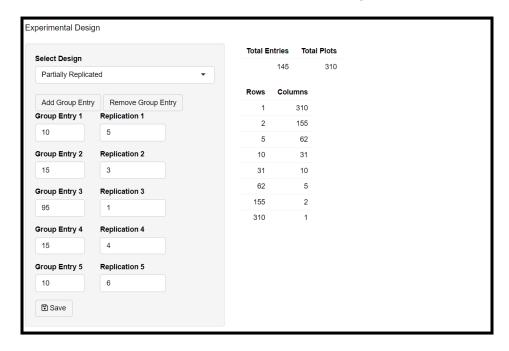


- b. If the design is alpha-lattice,
  - i. Input: Number of entries and replications

- ii. **Output:** Possible field row and column combinations; Block sizes for a given column.
- iii. Click "Save" to view the output or make changes.

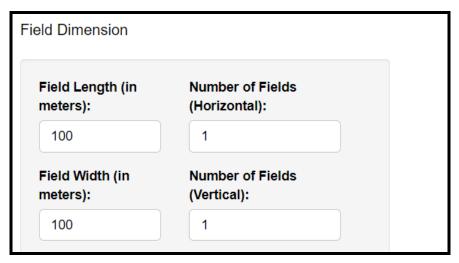


- c. If the design is partially replicated,
  - i. **Input:** Add the number of groups first. Then, populate the entries and replications per group.
  - ii. Output: Possible field row and column combinations.
  - iii. Click "Save" to view the output or make changes.



## 3. Field Dimension

a. Input: Field dimension (length and width in meters) and frequency.

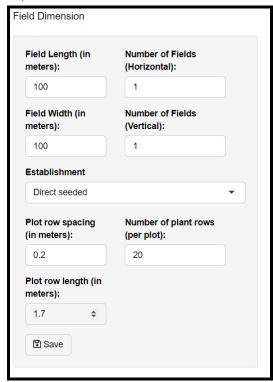


b. Choose what planting method will be used

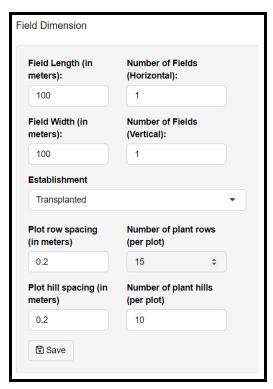
Options: Direct-seeded

Transplanted

- c. If direct-seeded will be used,
  - i. Input: Spacing within rows of a plot; Number of plant rows per plot; Length of plot rows in meters.



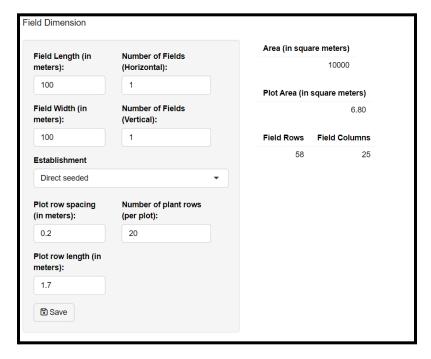
- d. If transplanted will be used,
  - i. Input: Spacing within rows and hills of a plot; Number of plant rows and hills per plot.



e. Click "Save" to view the output or make changes.

Output: Field and Plot Areas (in square meters)

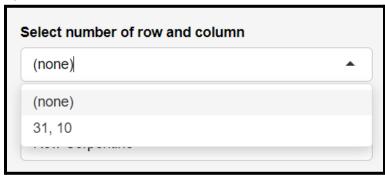
Number of rows and columns that could fit in the field



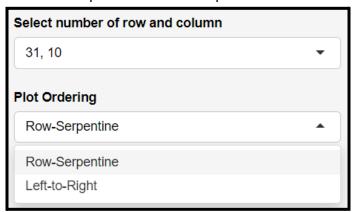
## 4. Field Layout

a. If the design is partially replicated,

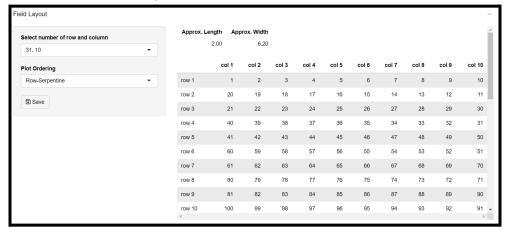
i. Select the number of row and column combination to be used for the layout.



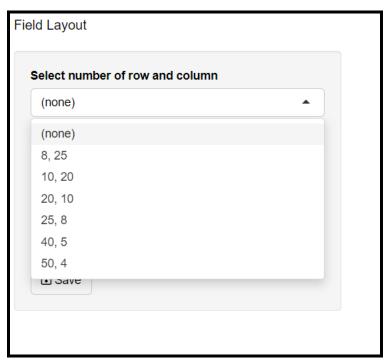
ii. Select which plot order will be implemented



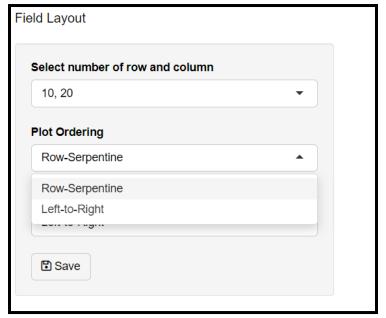
iii. Click "Save" to view the output or make changes.Output: Approximate measure for the field length and width Field Layout



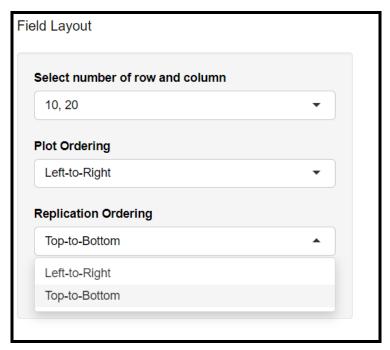
- b. If the design is alpha-lattice
  - i. Select the number of rows and columns combination to be used for the layout



ii. Select which plot order will be implemented



iii. Select which replication order will be implemented



iv. Click "Save" to view the output or make changes.Output: Approximate measure for the field length and width Field Layout

