A Wiki-like document of the project

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INHERSEED's wiki

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- LaTeXand its class memoir (http://www.ctan.org/pkg/memoir).
- R (http://www.r-project.org/) and RStudio (http://www.rstudio.com/)
- bookdown (http://bookdown.org/) and memoiR (https://ericmarcon.github.io/memoiR/)

Name of the owner of the logo

http://www.company.com

An explanatory sentence. Leave an empty line for line breaks.

Contents

Introduction

Plant microbial INHERitance across generations through SEEDs: impact of this primary inoculum on plant fitness and microbiota assembly

This document acts as a wiki-like platform regarding all protocols and data treatment within the INHERSEED project. The project is lead by Marie Simonin (PI - INSERT WEBSITE), Tristan Lafont Rapnouil is a post-doc in charge of monitoring the project progress and data acquisition and, Mathilde Brunel is a technician involved in greenhouse managing and wetlab experimentations.

While not all data and protocols can be hosted on Github, links to where they are actually findable are persented in this document.

For any questions related to this project, you can contact marie.simonin@inrae.fr and/or tristan.lafontrapnouil@gmail.com.

CHAPTER 1

Data framework

INHERSEED aims to respect the FAIR principles for open science. To do so we share in the present document protocols, raw data, processing scripts/procedures and, processed data as used in resulting articles 1.1.

Figure 1.1: Shared info regarding acquisition, raw data, processing and published data in the INHERSEED project

To ensure reproducibility data standard processing (bioinformatic pipeline and diagnostics) were embbeded in snakemake pipeline. R session info were also stored as text files available here. The Data Management Plan is hosted here.

Deliverable of the project are:

1. Data, protocols and workflows:

- github hosted document. (Text)
- Metabarcoding dataset: amplicon sequencing dataset as .fastq for *gyrB* and *ITS1* markers. (Dataset)
- Seed and plant phenotype as .csv. (Dataset)
- Processing scripts and pipelines (Python, Bash and R). (Workflow)
- Protocols for all data acquisition (Text)

2. Results:

- **WP1**:
- Plant taxonomy and traits influence on seed microbiota
- Assessment of microbial transmission from plants to seeds
- Exploring phylosymbiosis on seed microbiota
- **WP2**:
- Evaluation of microbial transmission from seeds to seedlings
- Inherited and non-inherited taxa transmission success
- Exploring phylosymbiosis on seedling microbiota
- Identification of microbial taxa with potential effects on seedling phenotypes
- **WP3**:
- Experimental validation of vertical transmission of inherited taxa
- Identification of inherited taxa affecting plant fitness
- Identification of inherited taxa influencing microbiota assembly

#links to data info

- [Project proposal][document/full_proposal/aapg_20203-INHERSEED_full_proposal.pdf
- [Original seeds sources][]
  - [species list][]
  - [suppliers][]
- [Seed phenotype][]
  - [Seed pictures][]
  - [TRAITOR software][]
- [DNA extractions][]
  - [Seeds][]
  - [Leaves][]
  - [Roots][]
  - [Soil][]
- [Plant phenotype][]
- [R script to download all datasets][]

#References

List of Figures

Abstract

Keywords Keyword in English, As a list.