Hypothesis Group

Plants & Python, 2021

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Collaboration

- **Generate Hypothesis:**
  - Discussing with computational groups available methods and data
- **Requirements for computational groups**
  - Heavily annotated data and code
  - What are the values for each column
  - Consistent names for everything
    - Resource of name/nomenclature
    - Consistent structure for comments/notes
  - What is each group testing?

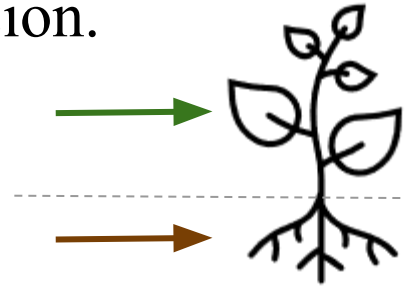
Hypothesis Generation

- **Broad Topics**
  - Examining homogeneity of experiment types in database
  - Above/below ground differences (non-transition)
  - Changes in regulatory and coding potential gene expression
  - Housekeeping genes - control

Hypotheses explanation

- Examining homogeneity of experiment types in database - treating experiment types as repeats of each other to test the robustness of the data set.

- Above/below ground differences (non-transition) - classifying tissue types into the subgroups of above ground/below ground growth with mutually exclusive gene expression.



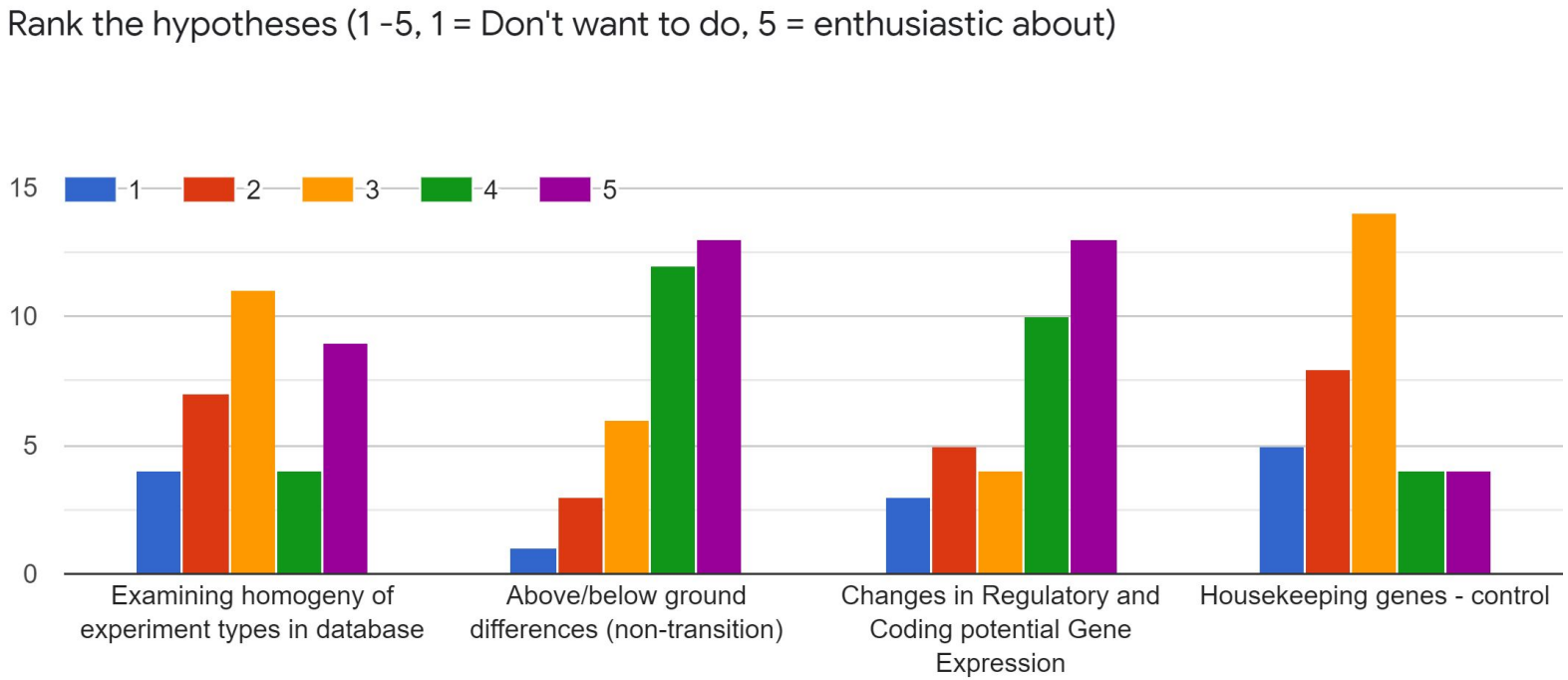
Hypotheses explanation

- Changes in regulatory and coding potential gene expression - using the classifiers of coding/noncoding to investigate how transcription profiles differ in different tissues/genotypes/stress conditions depending on the transcript type (coding or not, regulatory or functional protein).

- Housekeeping genes - control - examining the efficiency of common housekeeping genes in the background of WT gene expression vs. mutants gene expression with treatment type and tissue as random factors.

Hypothesis Survey

Hypothesis Survey

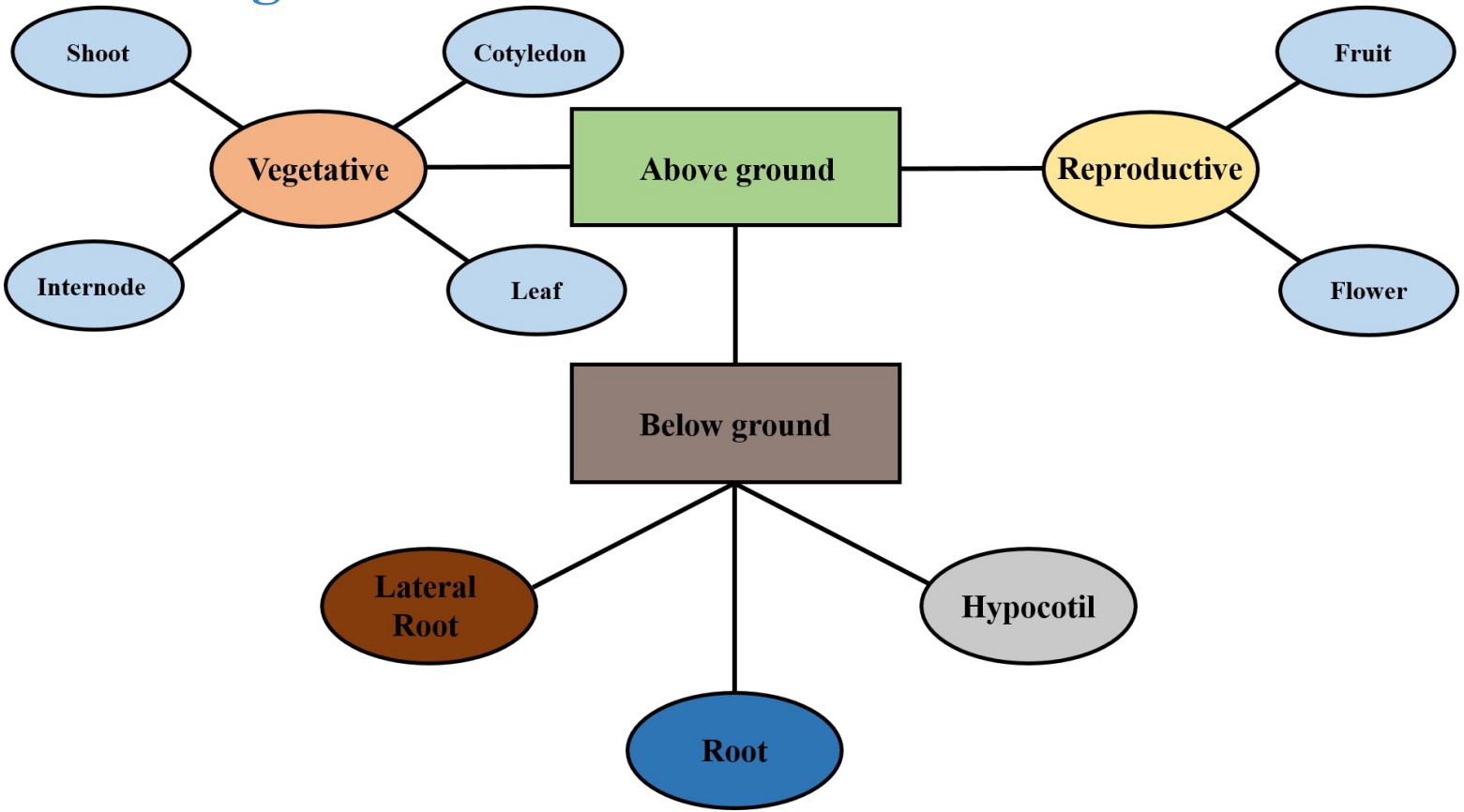


Wrap up from survey

- Above ground/Below ground are the most supported

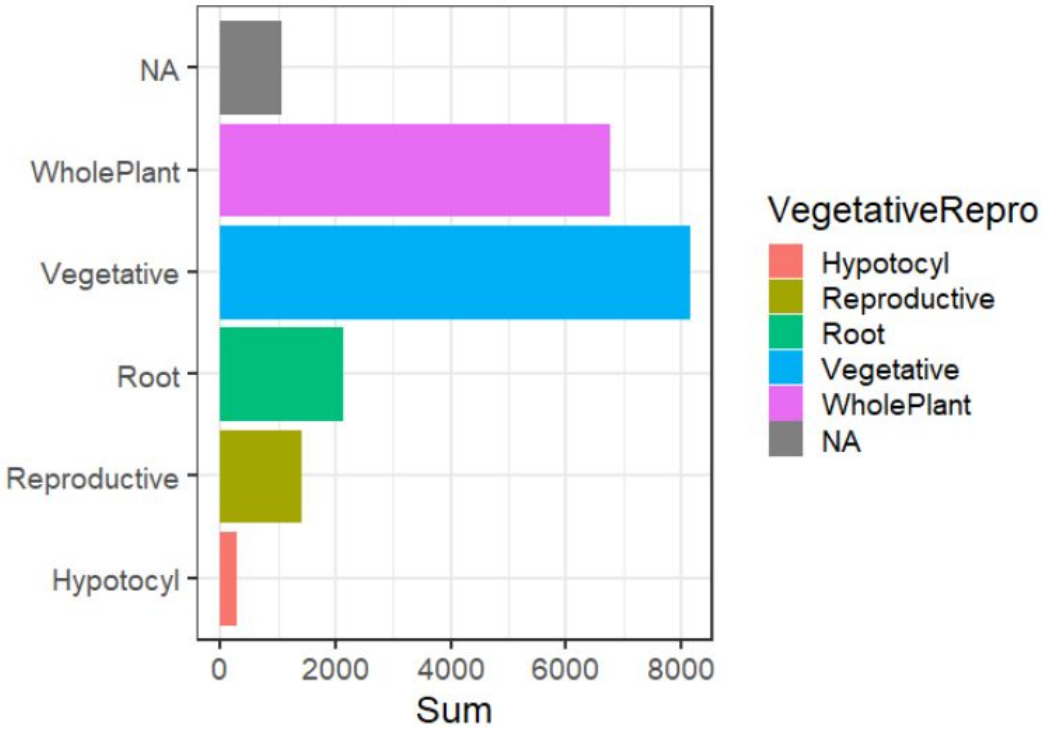
- Issues:
  - Messy datasets
  - Missing data
  - Large number of possible categorical variables

Possible categorical variables



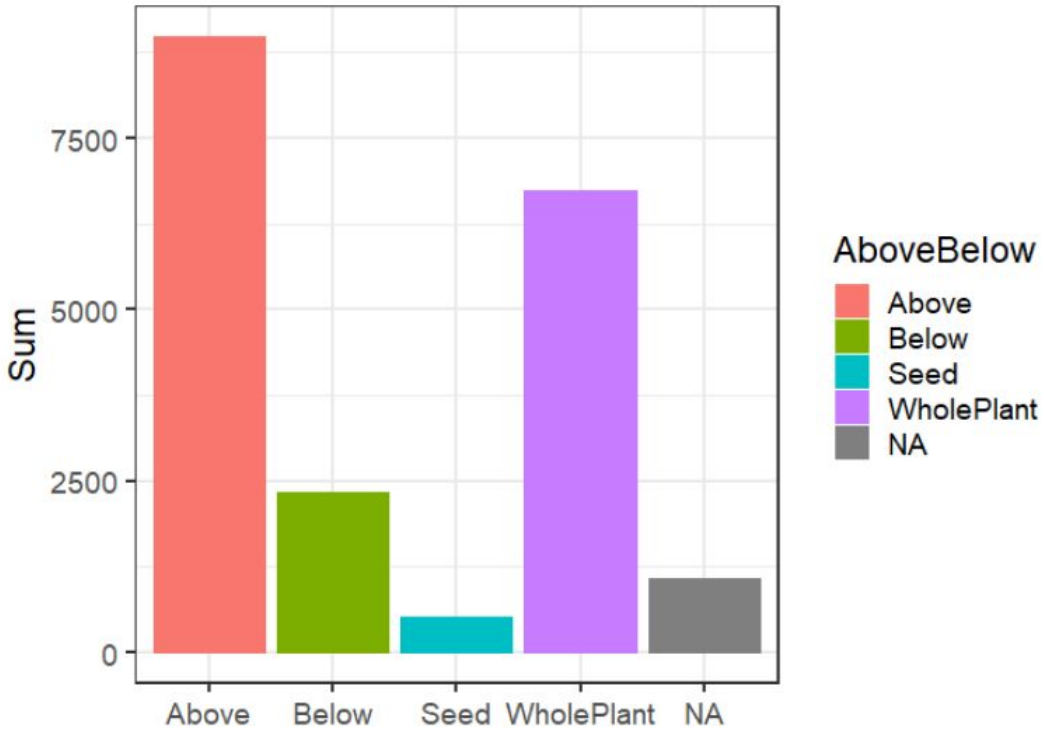
Above ground/Below ground classifications

- 19642 data points
  - 95% categorized, 5% uncategorized
- 23 tissue types
- 5 vegetative/reproductive types
  - 41% vegetative
  - 34% whole plant
  - 11% root
  - 7% reproductive
  - 1% hypotocyl
  - 5% uncharacterized



Above ground/Below ground classifications

- 19642 data points
  - 95% categorized, 5% uncategorized
- 4 above/below types
  - 46% above ground
  - 12% below ground
  - 34% whole plant
  - 3% seed
  - 5% uncategorized



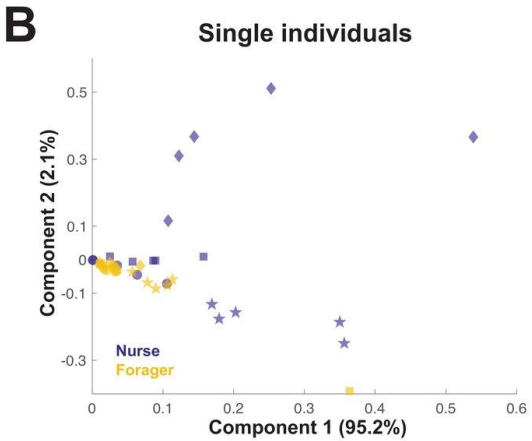
Transposase and transcription factor classifications

- 745 transposases
- 2967 transcription factors

Treatment categories

- Abiotic, biotic, and control
- Work in progress - 1075 categories
- Wildtype/control
- UV, shade, dark
- Water, dehydration, drought
- Temperature
- Wounding
- Oxidative
- Gene regulation/expression
- Growth regulation

Omic atlases have elucidated complex biological questions

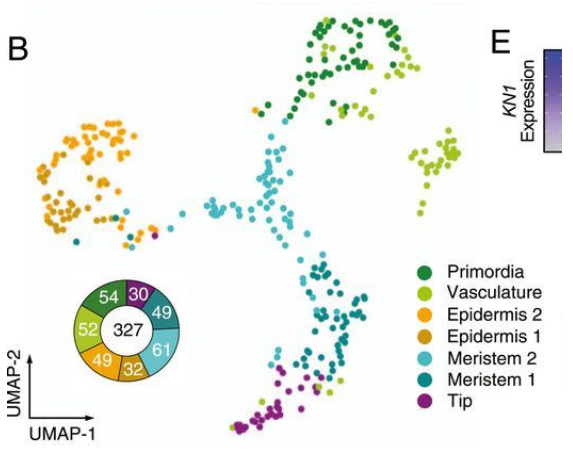


Ant social role

Hakala *et al.*, 2021

Human cell cycle

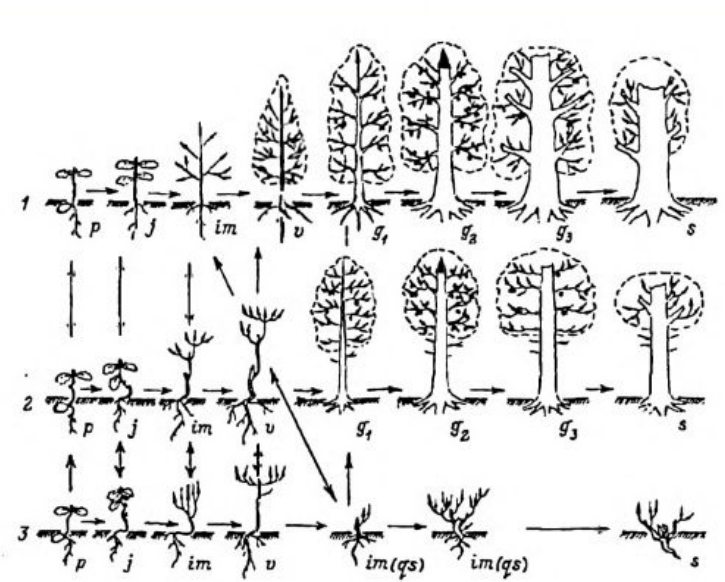
Stallaer *et al.*, 2021



Plant SAM

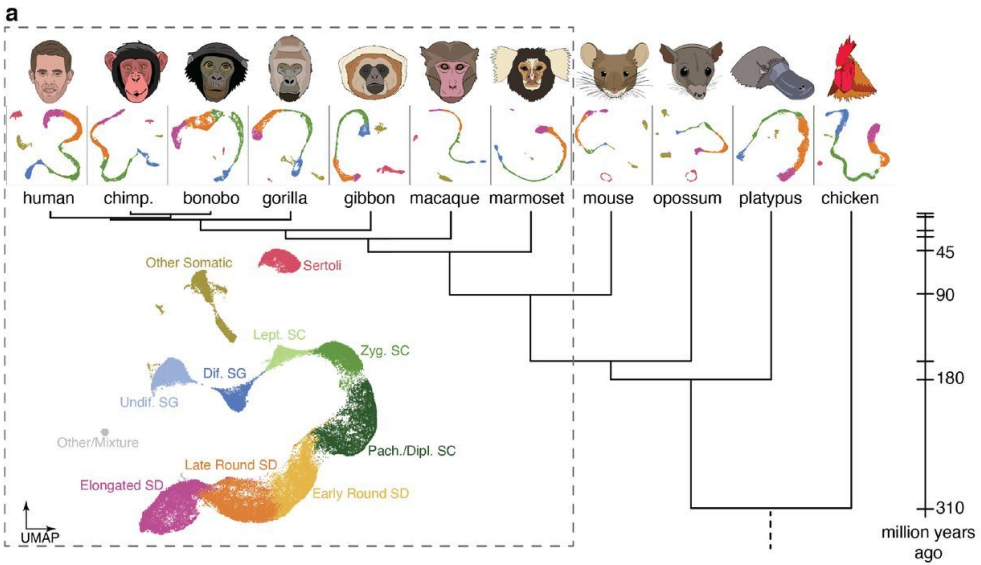
Satterlee *et al.*, 2021

Ontogeny could be explained using next-gen technologies



Ontogeny of a tree

Smirnova *et al.,* 1999

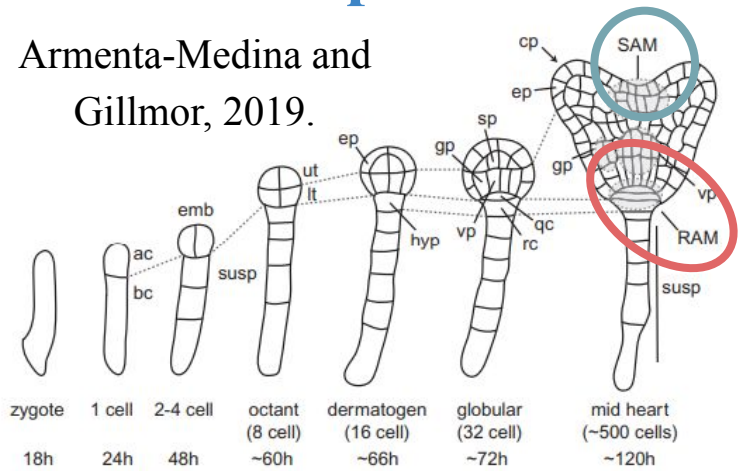


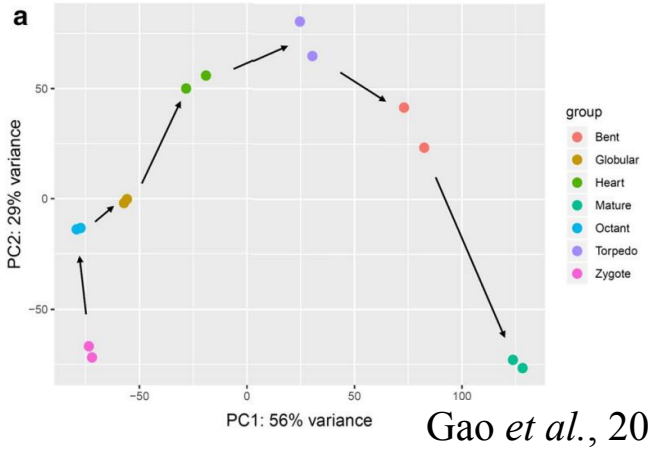
Evolution of spermatogenesis

Murat *et al.,* 2021

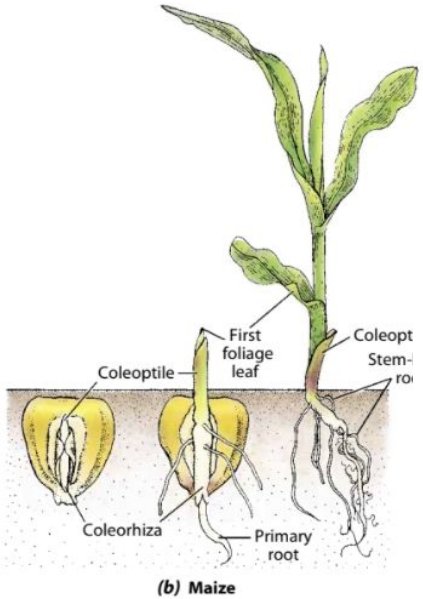
Plant development starts after fertilization

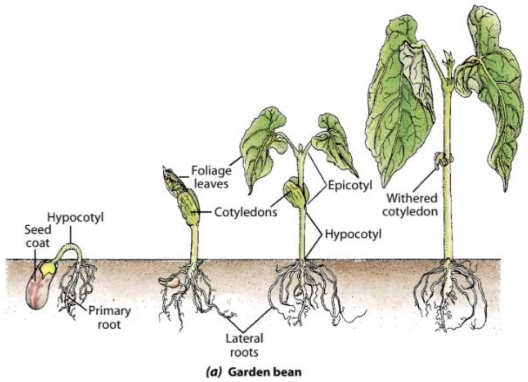
Armenta-Medina and Gillmor, 2019.





Gao *et al.*, 2019.





Literature (not formatted yet)

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