Ara-BOX-cis v2: A G-box regulatory network for a single cell developmental atlas

Daphne Ezer

Check-in code: 227956

Outline of this term's material

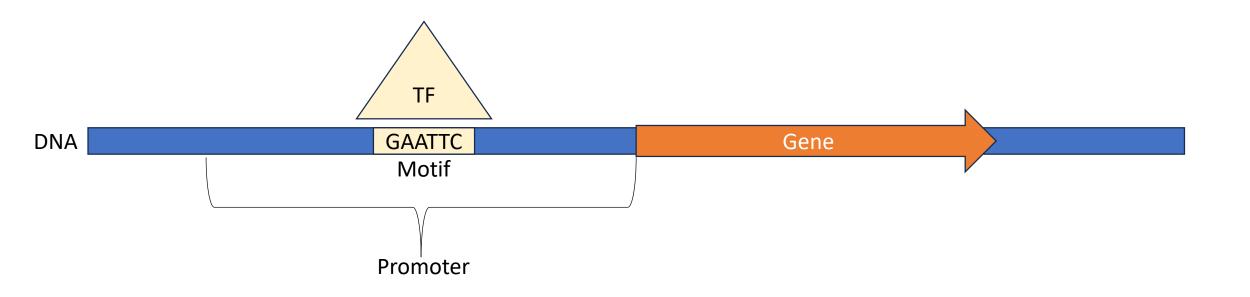
- 1. Overview of project: what is the main aim?
- 2. Background on G-box regulatory networks
 - 1. What is a gene network?
 - 2. What is machine learning?
- 3. Background on the data set
 - 1. What is special about single cell RNA-seq?
 - 2. What are some exploratory analyses and visualisations we can do?
- 4. Background on method
 - 1. How do we infer gene networks using single cell gene expression data?
 - How do we evaluate if we've done a good job?

Questions for you:

• What is your background?

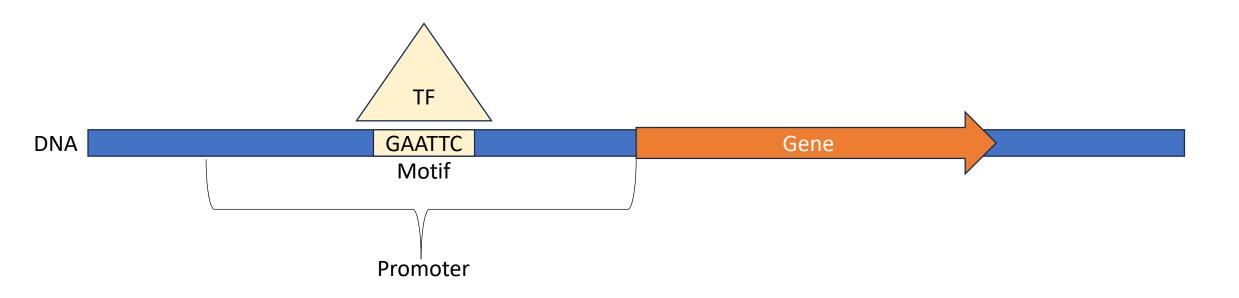
What do you hope to gain from this degree?

What is a transcription factor (TF)?



- Transcription factors bind to specific **motifs**. In plants (but NOT animals) these tend to be near the genes that they regulate.
- Transcription factor binding can lead to increased or decreased transcription

A fundamental question in biology:



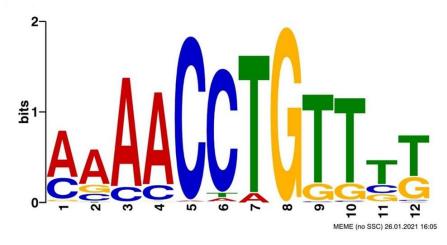
Promoter sequence

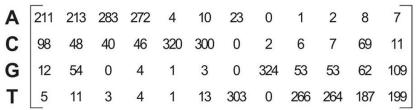


How do changes in DNA sequence in the promoter lead to changes in gene regulation?

What are transcription factor binding motifs like in plants?

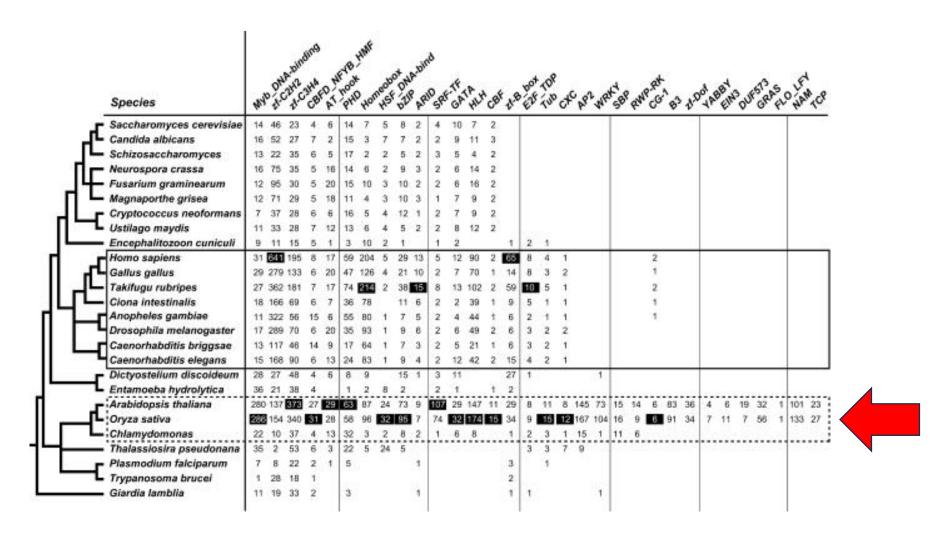
(A) Position weight matrix



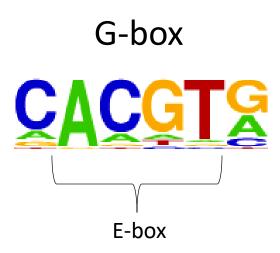


- Many transcription factors arose through historic gene duplication events (paralogs).
- Similar transcription factors are part of the same "family"
- Transcription factors in the same family tend to bind to similar motifs.

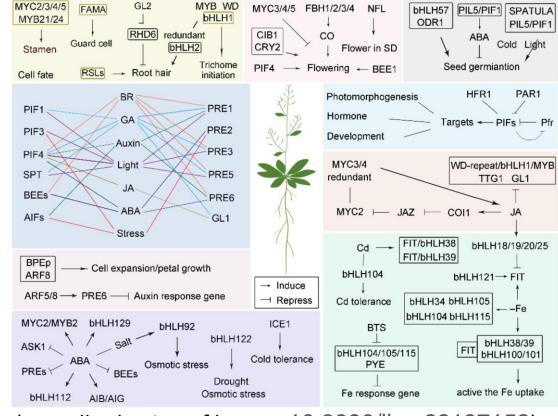
This is hard in plants because of the expansion of transcription factor families



What is a G-box?



 Many bHLH and bZIP transcription factors can bind to them and are involved in many processes



(a small selection of bHLHs, 10.3390/ijms22137152)

Mysterious G-boxes have been an issue for many Arabidopsis researchers

A **G-box**-like motif is necessary for transcriptional regulation by circadian pseudo-response regulators in **Arabidopsis**

TL Liu, L Newton, MJ Liu, SH Shiu, EM Farré - Plant physiology, 2016 - Am Soc Plant Biol

[HTML] W-box and G-box elements play important roles in early senescence of rice flag leaf L Liu, W Xu, X Hu, H Liu, Y Lin - Scientific reports, 2016 - ncbi.nlm.nih.gov

[HTML] The regulation of the Z-and **G-box** containing promoters by light signaling components, SPA1 and MYC2, in **Arabidopsis**

SN Gangappa, JP Maurya, V Yadav, S Chattopadhyay - PloS one, 2013 - journals.plos.org

Role of the **G-box** element in regulation of chlorophyll biosynthesis in **Arabidopsis** roots <u>K Kobayashi, T Obayashi, T Masuda</u> - Plant signaling & behavior, 2012 - Taylor & Francis

The **Arabidopsis** JAZ2 promoter contains a **G-Box** and thymidine-rich module that are necessary and sufficient for jasmonate-dependent activation by MYC ...

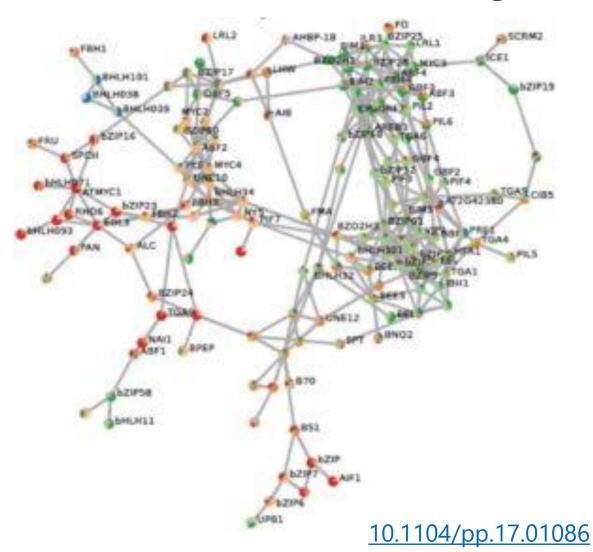
P Figueroa - Plant and Cell Physiology, 2012 - Jpn Soc Plant Physiol

Functional elements of the **Arabidopsis** Adh promoter include the **G-box** WL McKendree Jr, RJ Ferl - Plant molecular biology, 1992 - Springer

Mutation of either **G box** or I box sequences profoundly affects expression from the **Arabidopsis** rbcS-1A promoter.

RG Donald, AR Cashmore - The EMBO Journal, 1990 - ncbi.nlm.nih.gov

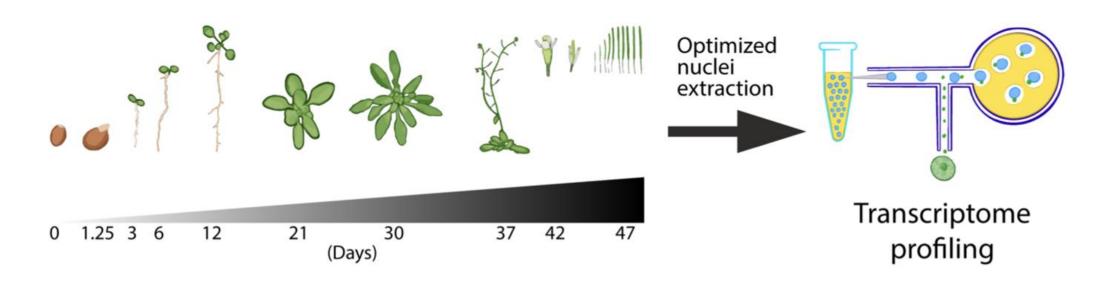
Ara-BOX-cis: the G-box regulatory network



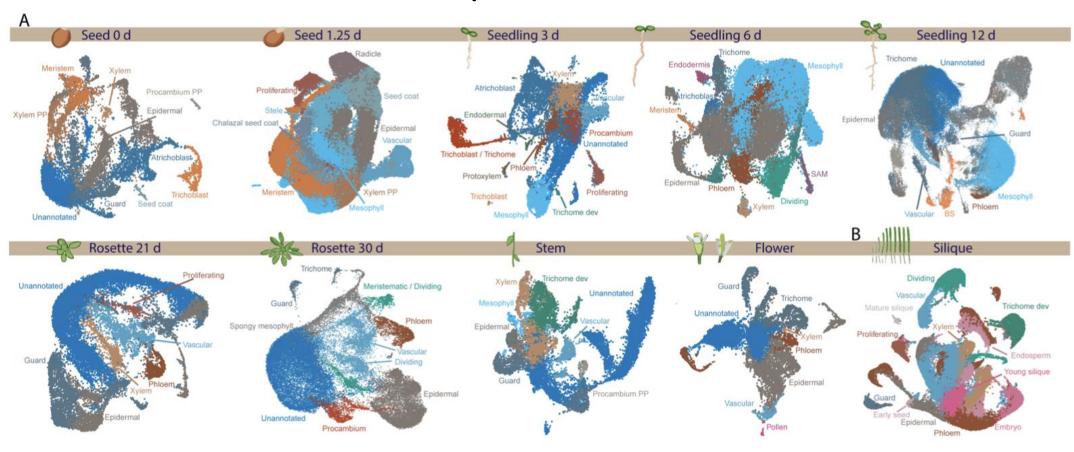
 We will discuss how this network was constructed in Project Meeting 2

Does Ara-BOX-cis need an update?

- Ara-BOX-cis was trained using a database of whole seedling RNA-seq
- Does it apply to different cell types?
- Does it apply to different developmental stages?
- New data available: a single nucleus developmental atlas (just released!)

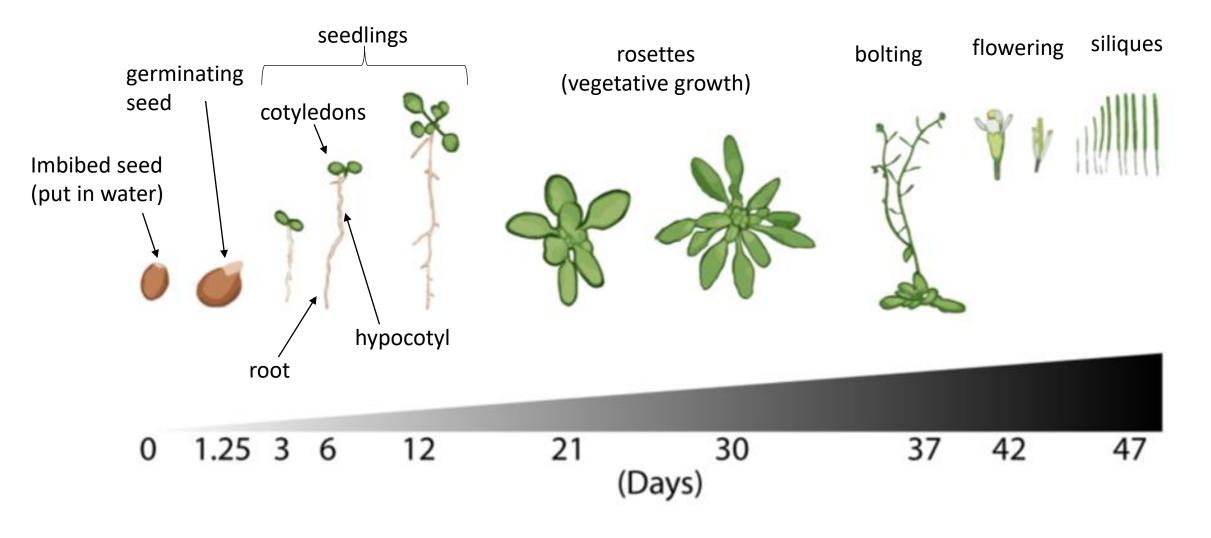


What data was produced by the single cell developmental atlas?

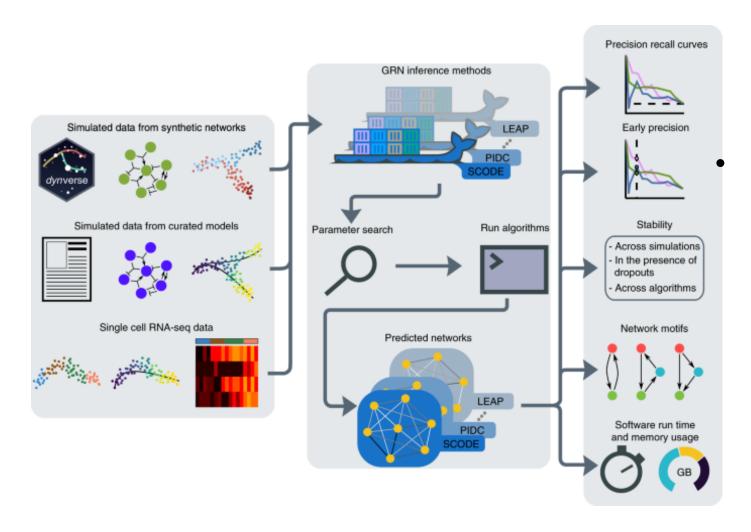


We will discuss this dataset in depth in Project Meeting 3

Plant development overview:



How do we use single cell RNA-seq data to infer a gene regulatory network?



We will discuss how to build a network in **Project Meeting 4**

Aims of research project

• Is the existing Ara-BOX-cis G-box network consistent with the new single cell RNA-seq data?

 Do different G-box networks exist in different cell types or in different developmental stages?

Can we construct Ara-BOX-cis version 2.0?

Outline of this term's material

- 1. Overview of project: what is the main aim?
- 2. Background on G-box regulatory networks
 - 1. What is a gene network?
 - 2. What is machine learning?
- 3. Background on the data set
 - 1. What is special about single cell RNA-seq?
 - 2. What are some exploratory analyses and visualisations we can do?
- 4. Background on method
 - 1. How do we infer gene networks using single cell gene expression data?
 - 2. How do we evaluate if we've done a good job?

Discussion questions:

• How does bioinformatics research differ from wet lab research?

 What are the similarities between bioinformatics and wet lab research?

Group work

• What makes a collaboration successful?

• What are some reasons why a collaboration might fail?