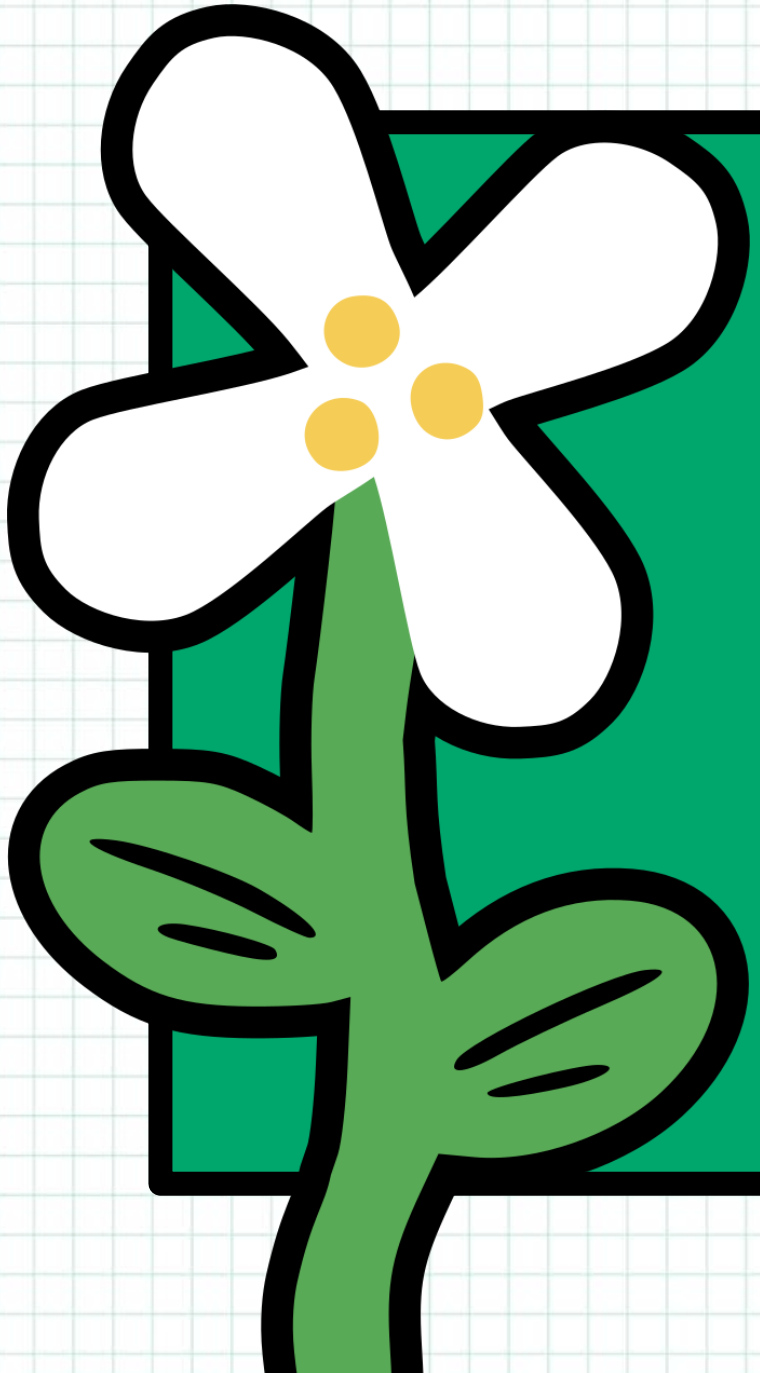
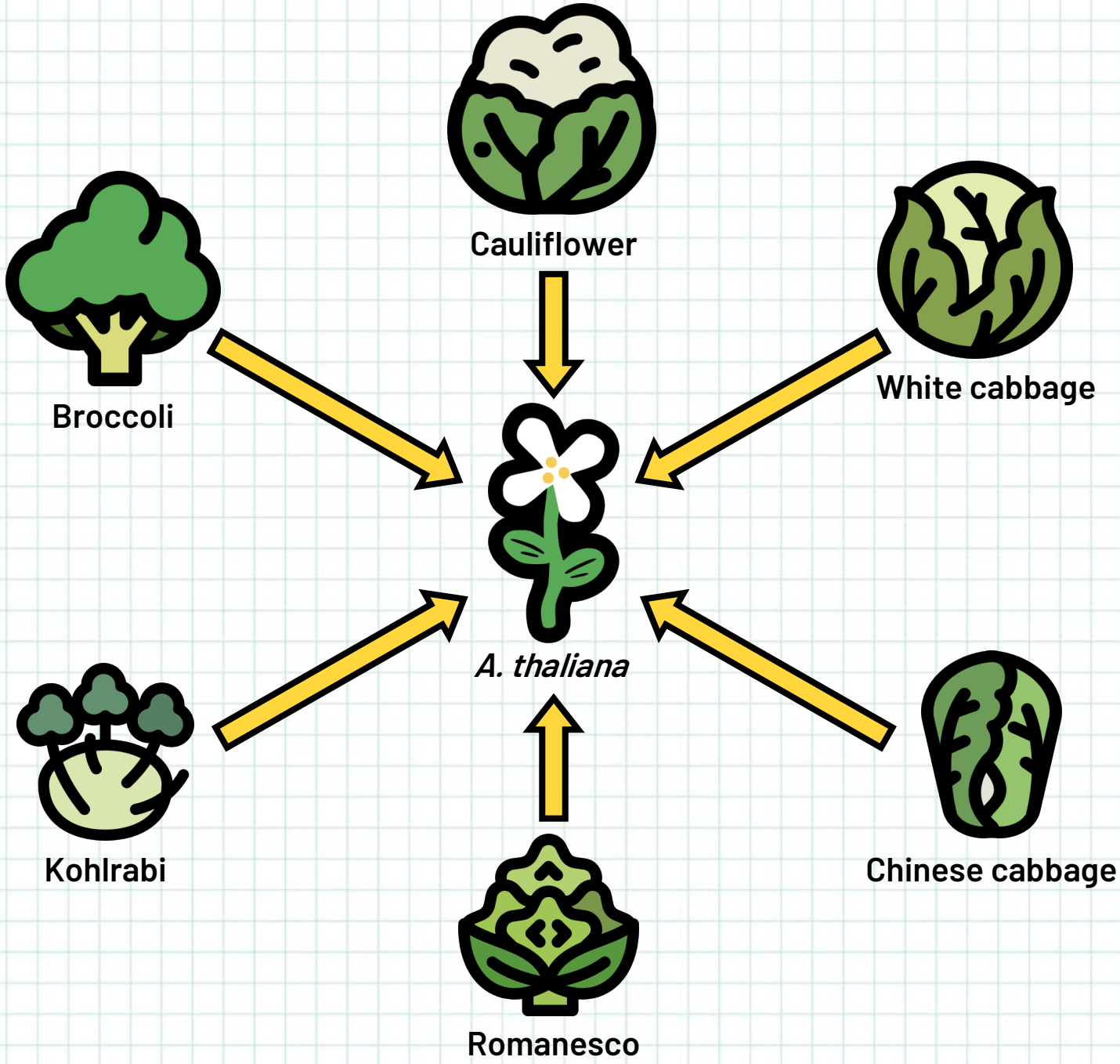
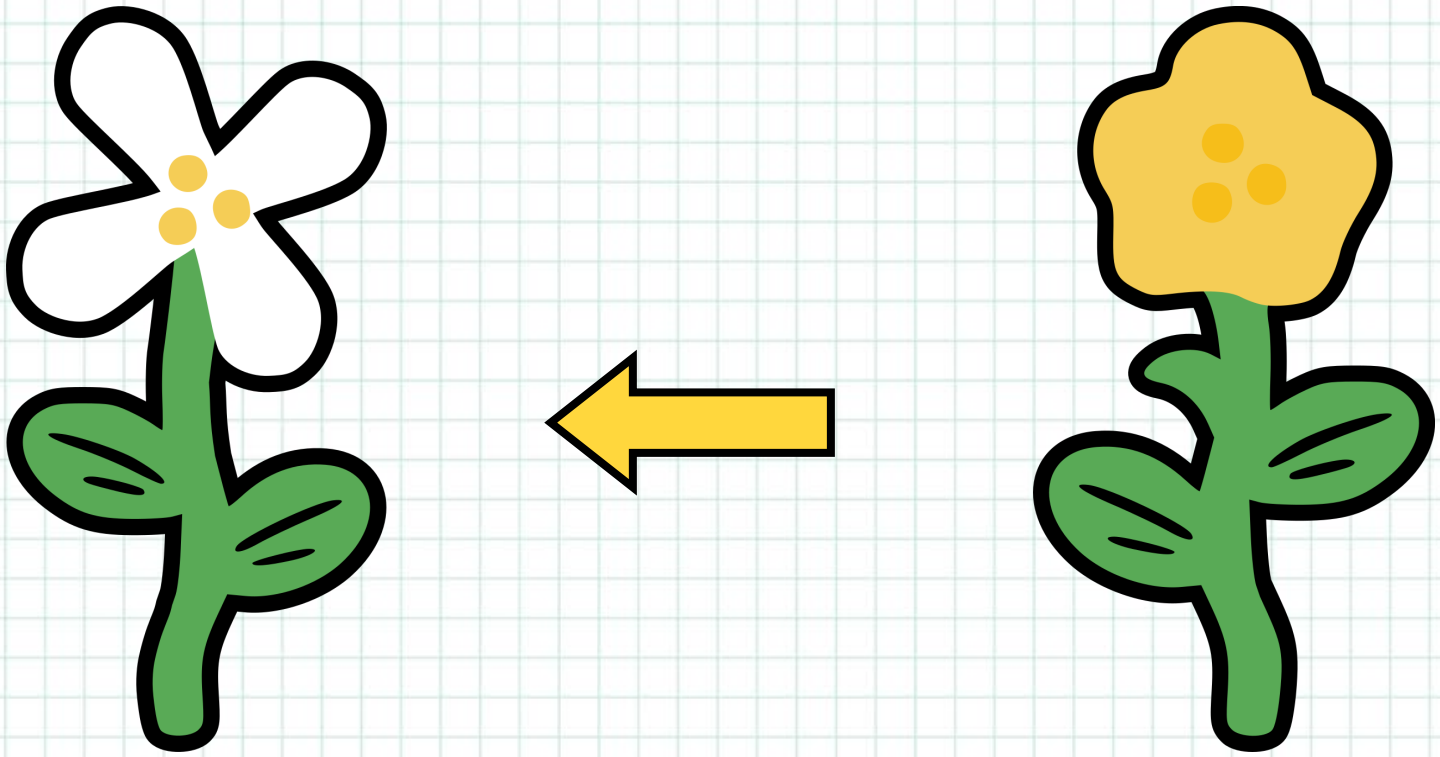


Transferring knowledge of the floral transition from Arabidopsis to *B. oleracea* using gene expression dynamics

{greatR} - an R package for identifying similar transcript dynamics using curve registration

Ruth Kristianingsih
PhD student, Morris lab
John Innes Centre, Norwich, UK
@rutkr

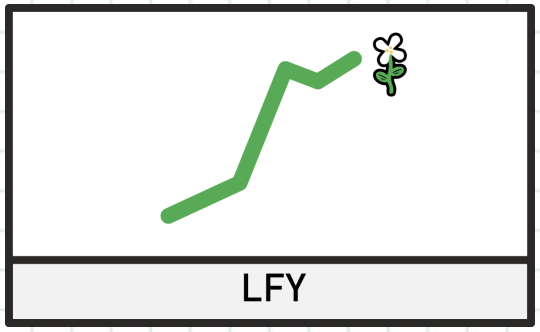

Cauliflower
Broccoli
White cabbage
A. thaliana
Kohlrabi
Chinese cabbage
Romanesco



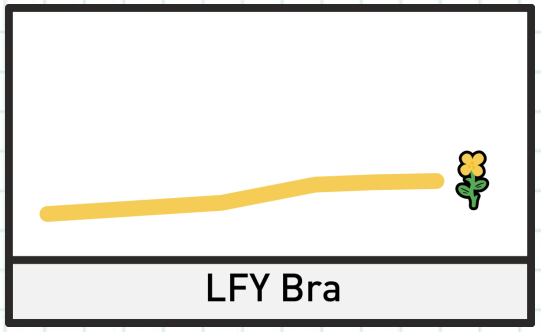
A. thaliana

B. oleracea

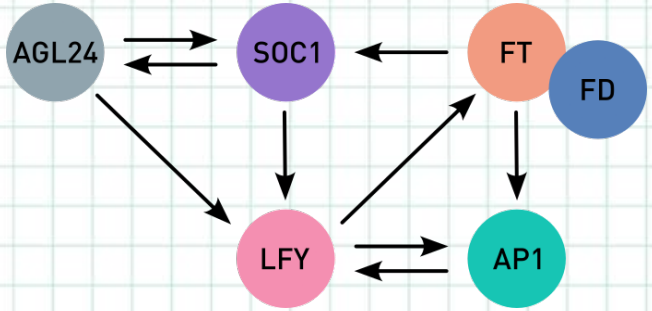
Transferring knowledge of floral transition regulatory networks of *A. thaliana* to *B. oleracea* is not an easy task

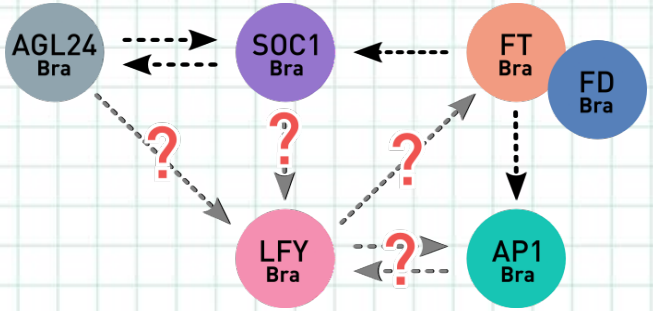


A. thaliana

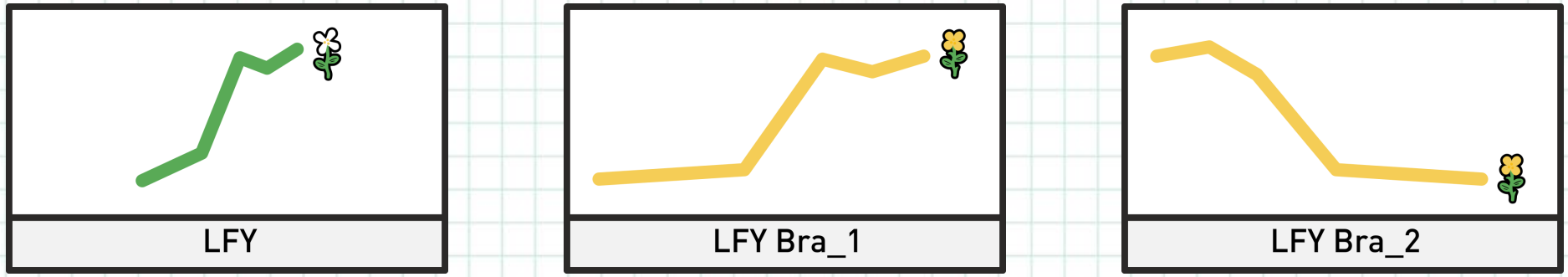


B. oleracea

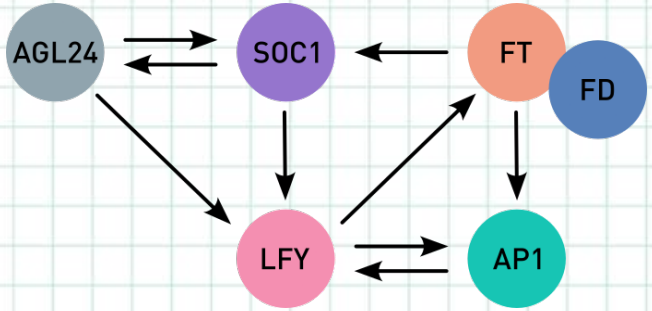




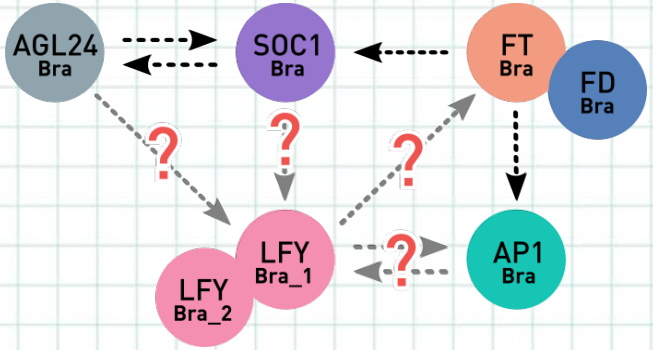
Transferring knowledge of floral transition regulatory networks of *A. thaliana* to *B. oleracea* is not an easy task

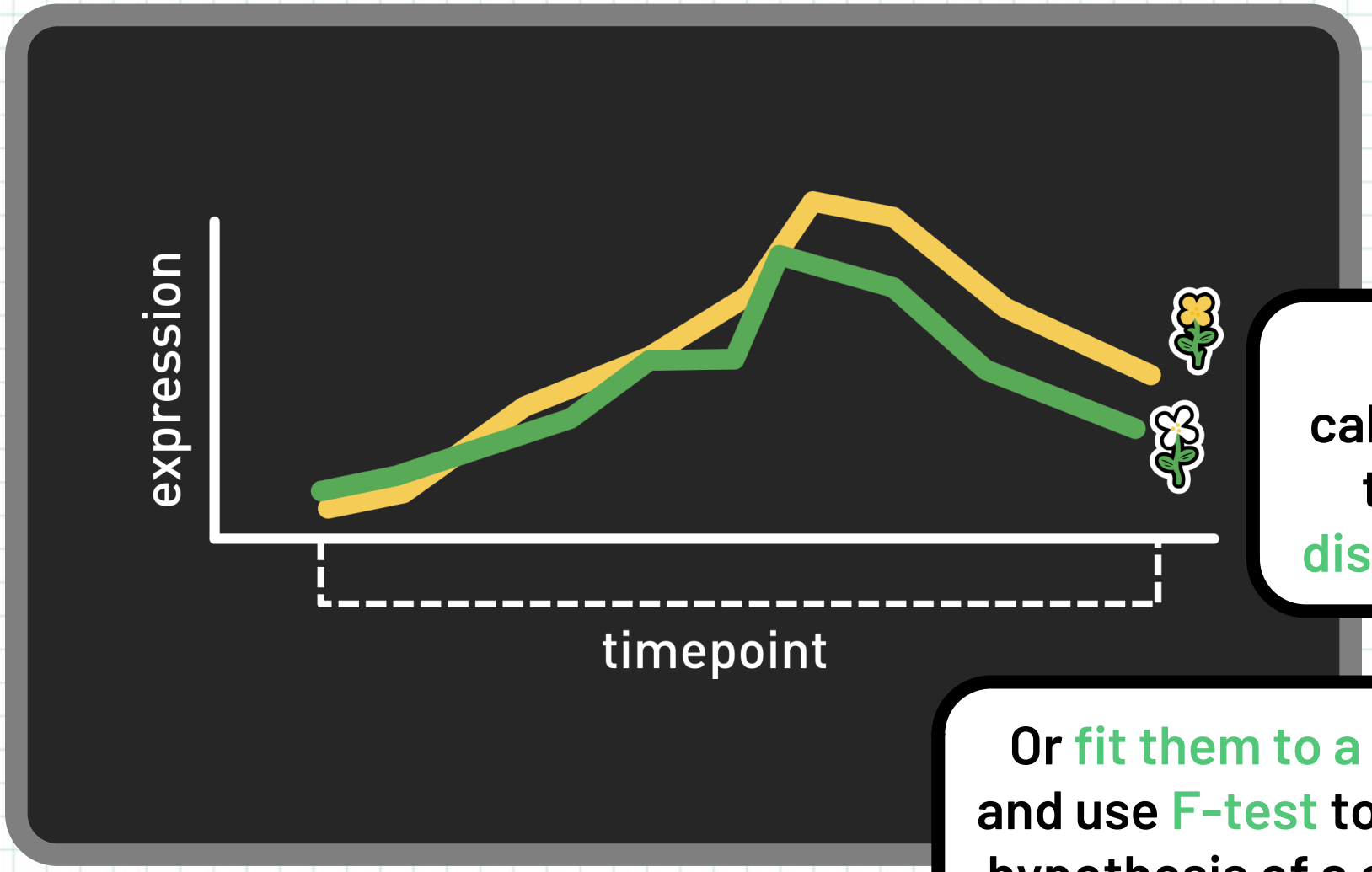


A. thaliana



B. oleracea

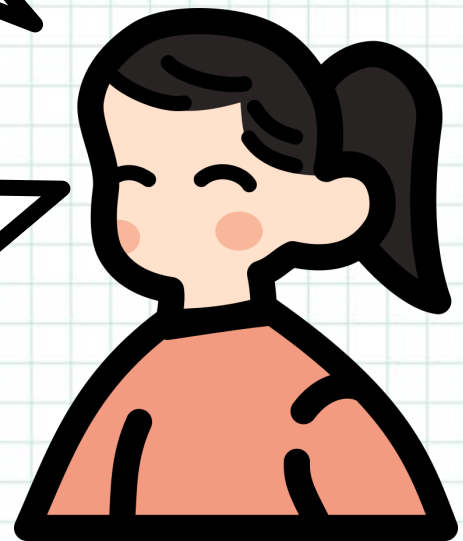


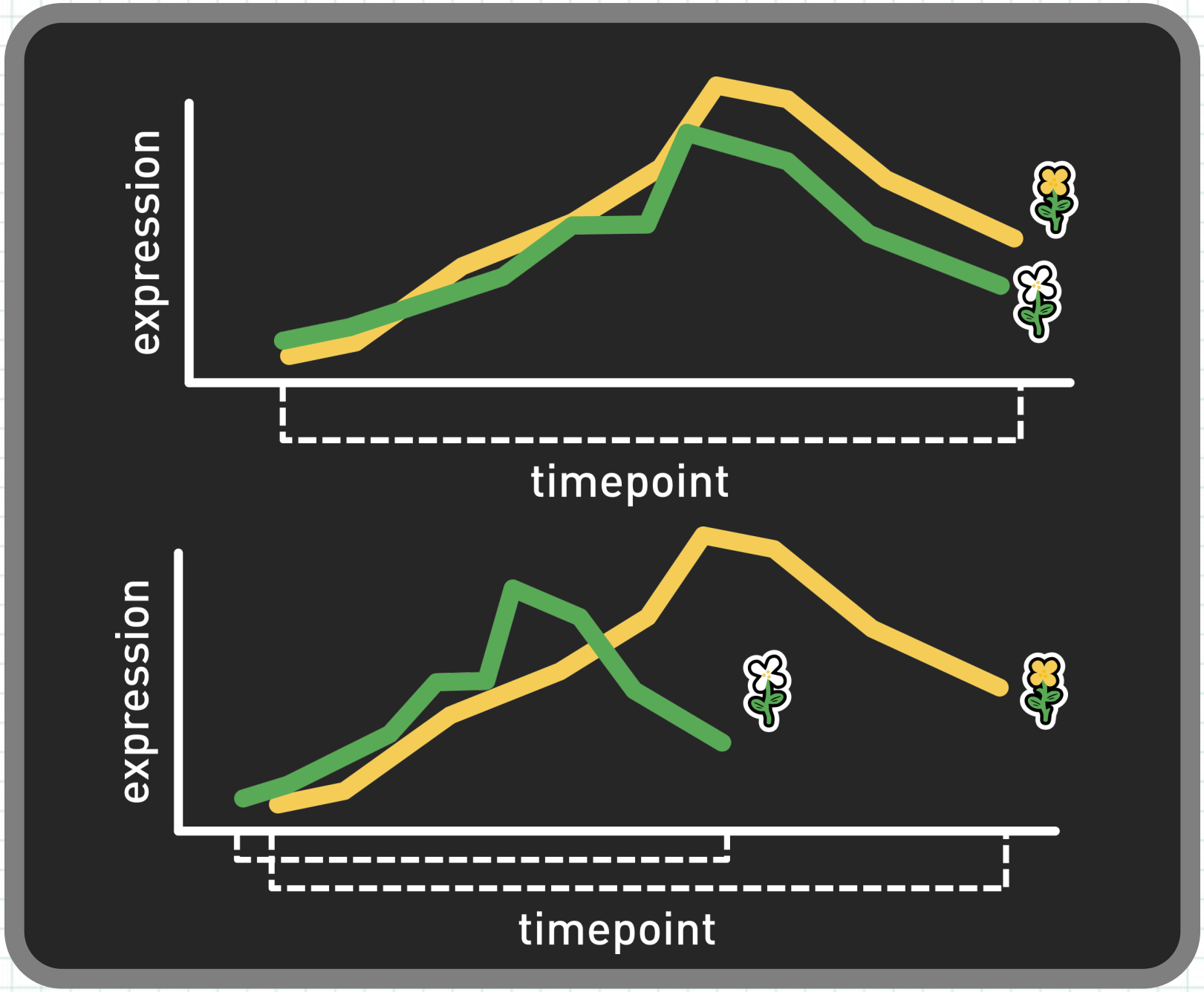


After plotting them, then find the correlation?

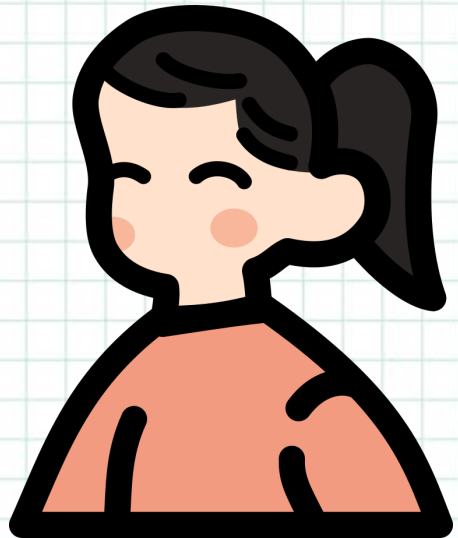
Or calculate their distance?

Or fit them to a model, and use F-test to test the hypothesis of a common set of parameters?

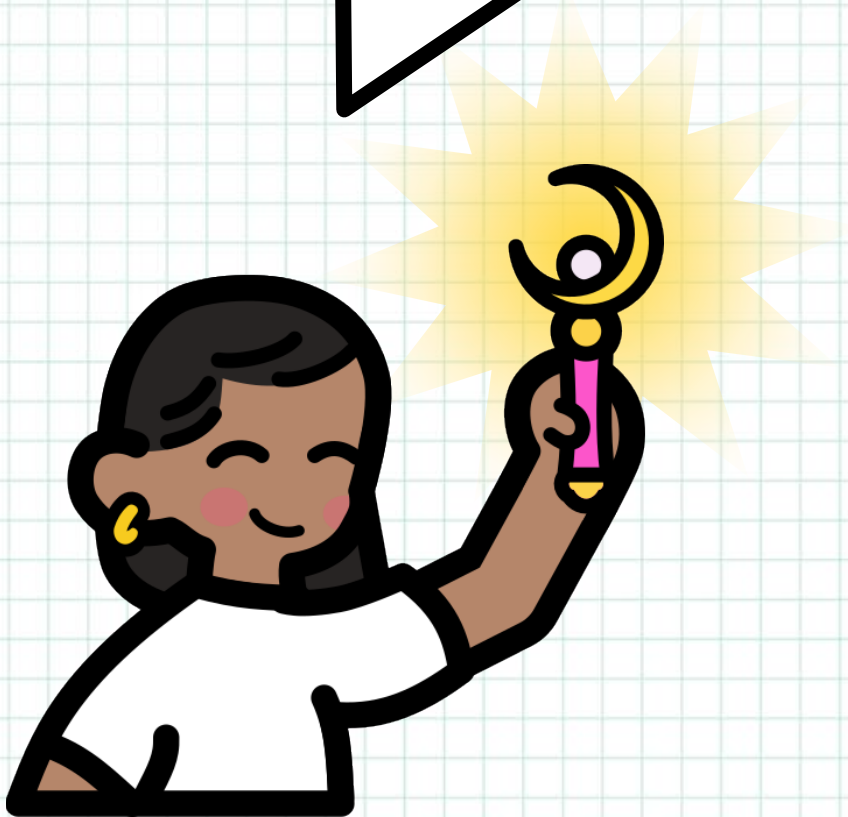



expression
timepoint
expression
timepoint

????



Don’t worry, we found a way to do this robustly and accurately!! 💡



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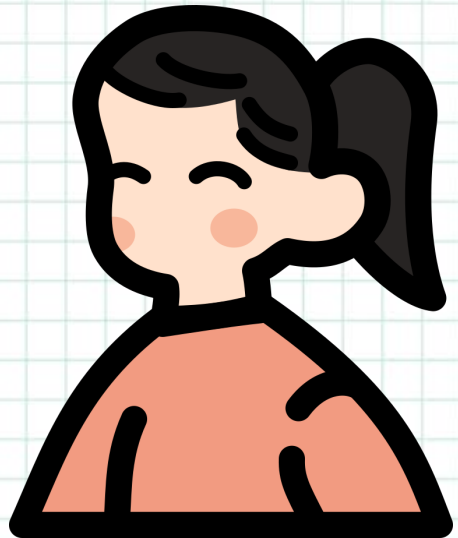
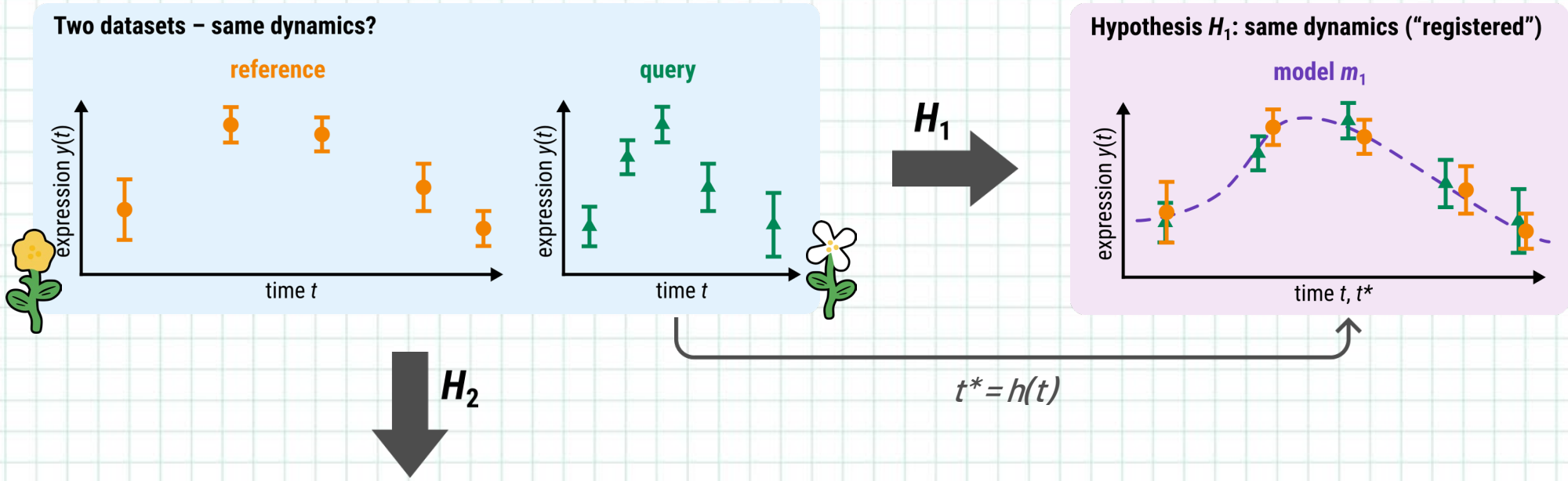
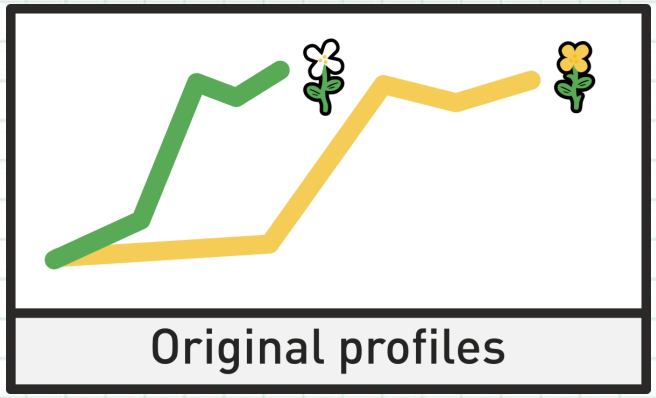


Two curves can be compared by fitting them to a joint model

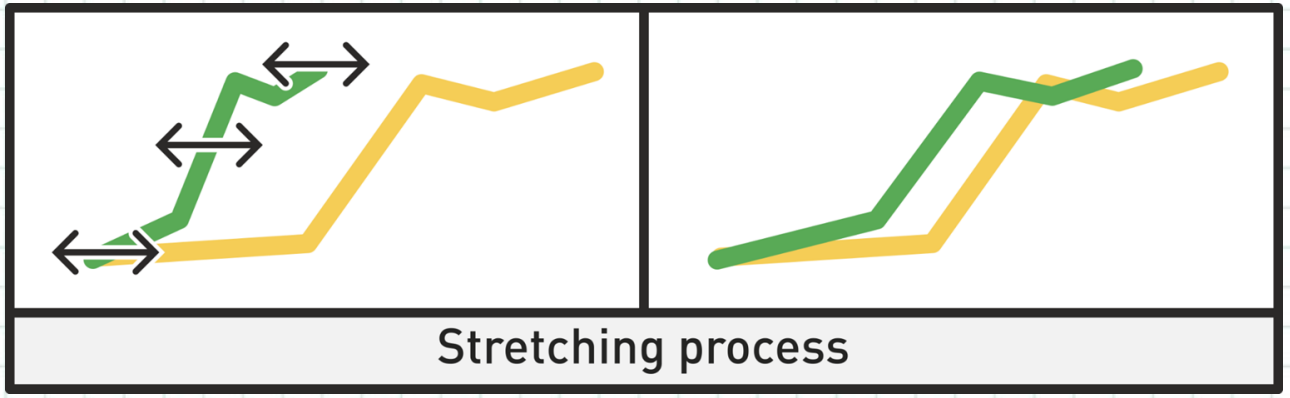


Curve registration method resolves differences in expression states

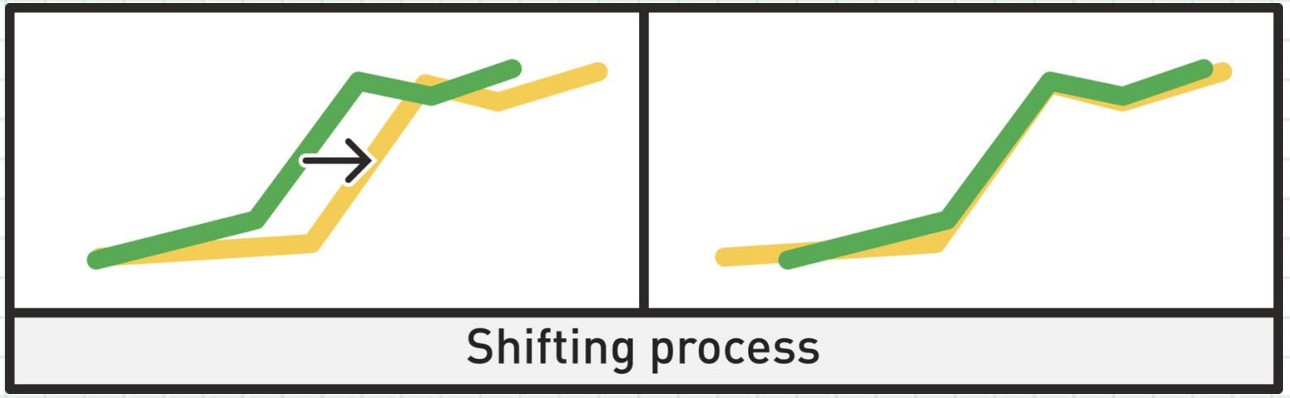
$t^* = h(t)$



Original profiles



Stretching process



Shifting process

$$P(H_1|D) = P(m_1|r,q) = P(r,q|m_1)P(m_1)/P(r,q)$$

$$\Lambda_{H_1}(\theta) \propto \exp\{-d(m_1,r)^2/2\sigma_r^2\} \exp\{-d(m_1,q)^2/2\sigma_q^2\}$$

$$d(m_1,r) = \left[\sum_{i=1}^{N_r} \left(m_1(\theta,t_i) - y_{r,i}\right)^2\right]^{1/2}$$

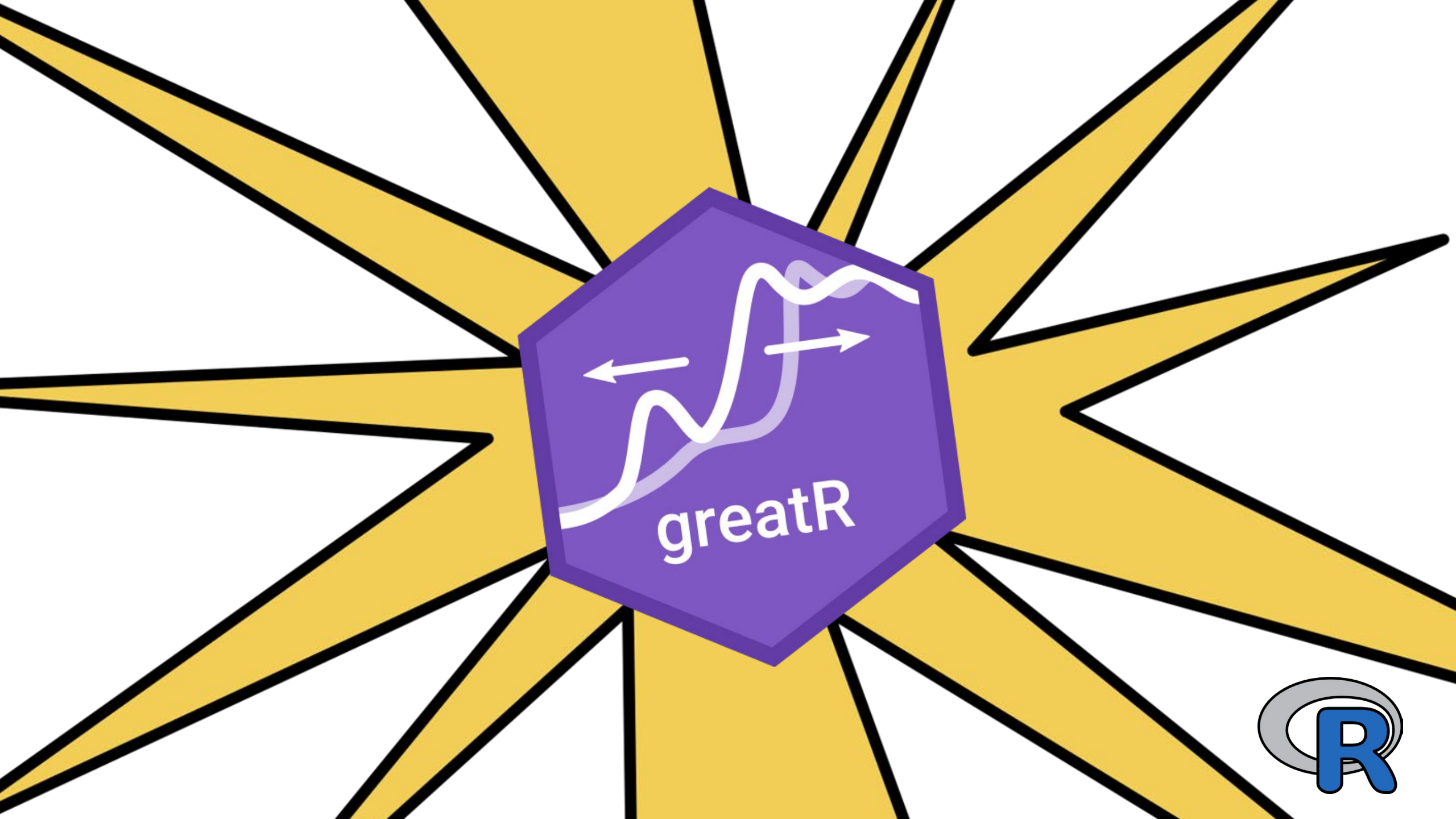
$$d(m_1,q) = \left[\sum_{j=1}^{N_q} \left(m_1(\theta,t_j) - y_{q,j}\right)^2\right]^{1/2}$$

$$\Lambda_{H_2}(\theta_r,\theta_q) \propto \exp\{-d(m_r,r)^2/2\sigma_r^2\} \exp\{-d(m_q,q)^2/2\sigma_q^2\}$$

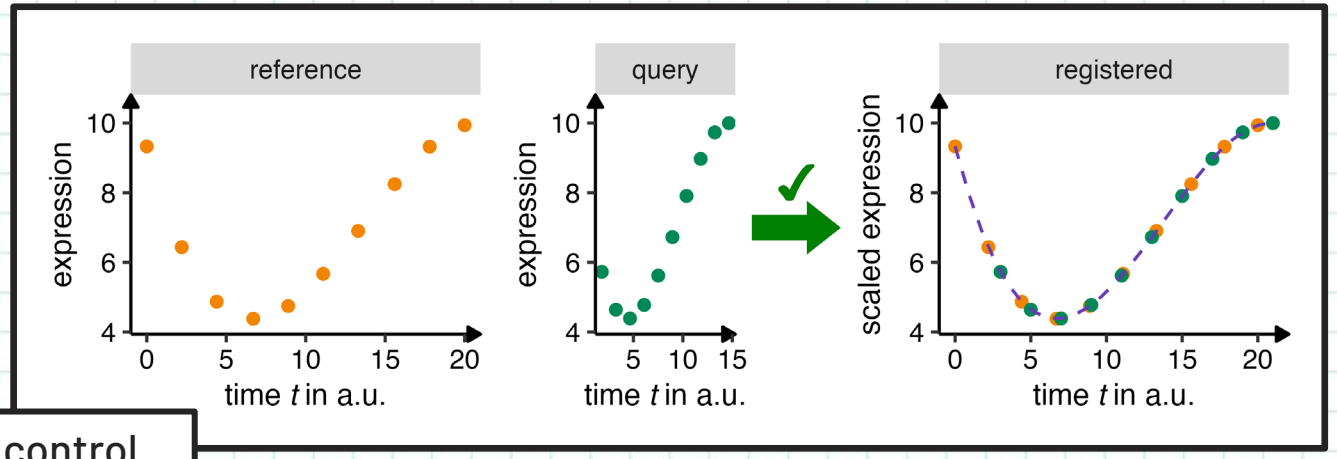
$$f(a,t) = a_1\,t + a_2\,t^2 + a_3\,t^3 + a_4\,(t-\tau_1)^3$$

$$\mathrm{BIC} = -2\mathcal{L} + k\log N_D$$

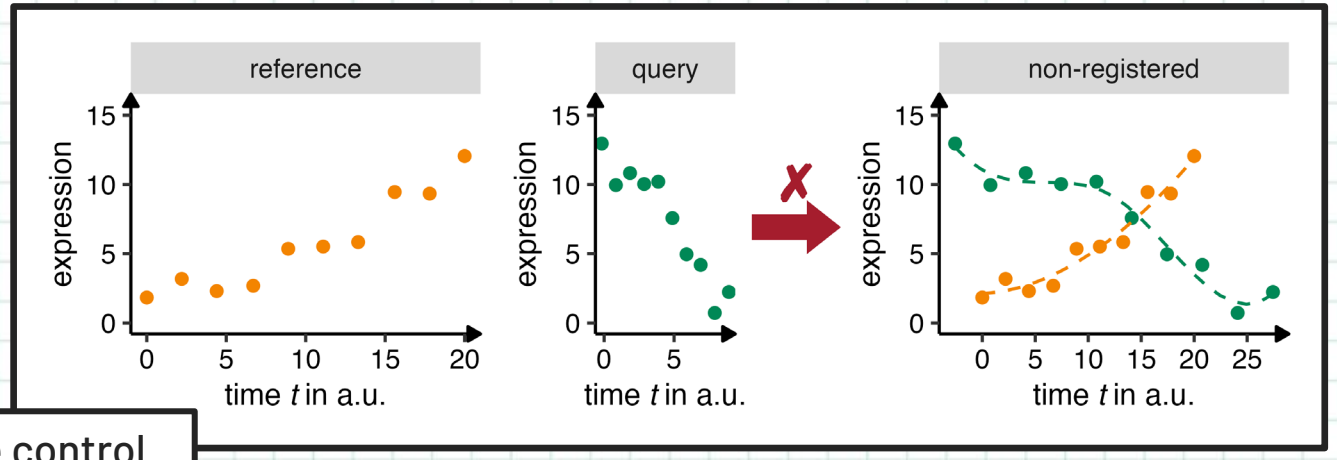
Simulated Annealing **L-BFGS-B** **Nelder-Mead**


greatR

{greatR} successfully registered simulated data with the same dynamics

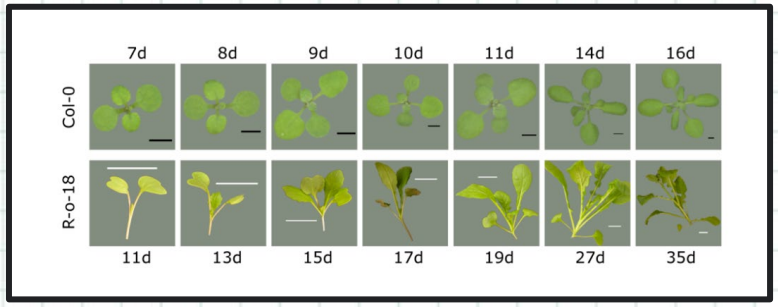


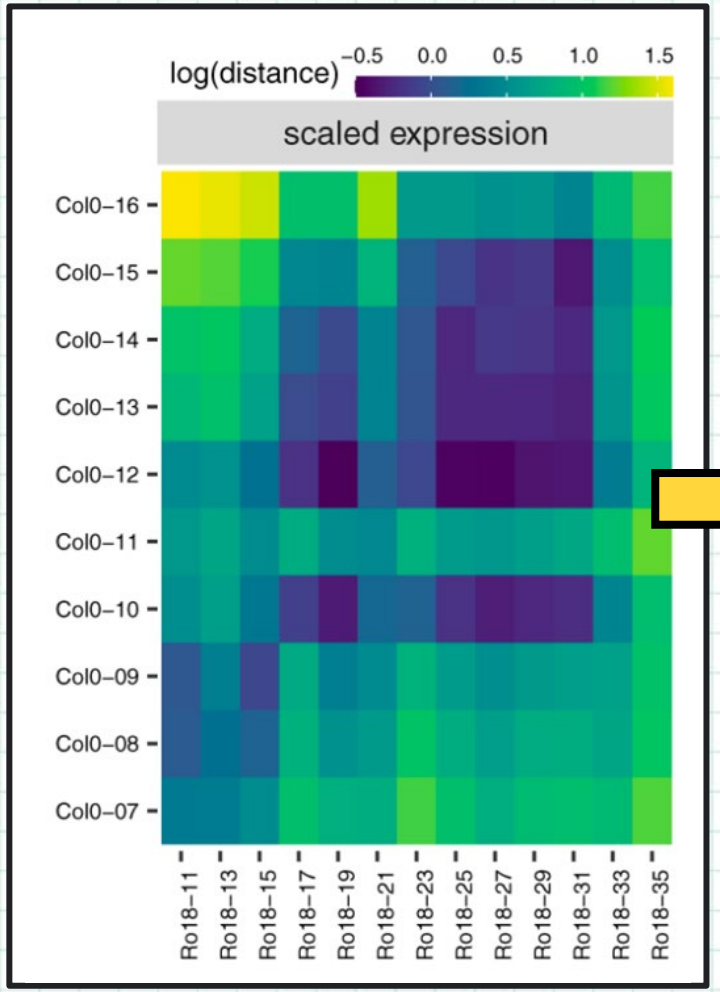
Positive control

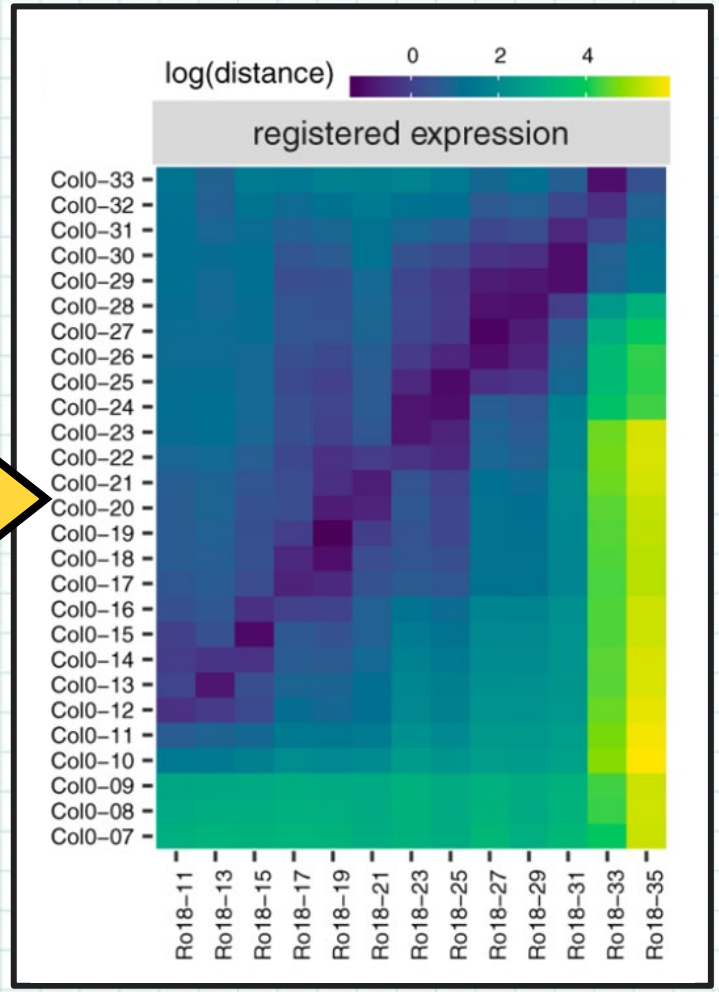


Negative control

Curve registration resolves differences in expression states between *A. thaliana* and *B. rapa* (yellow mustard)

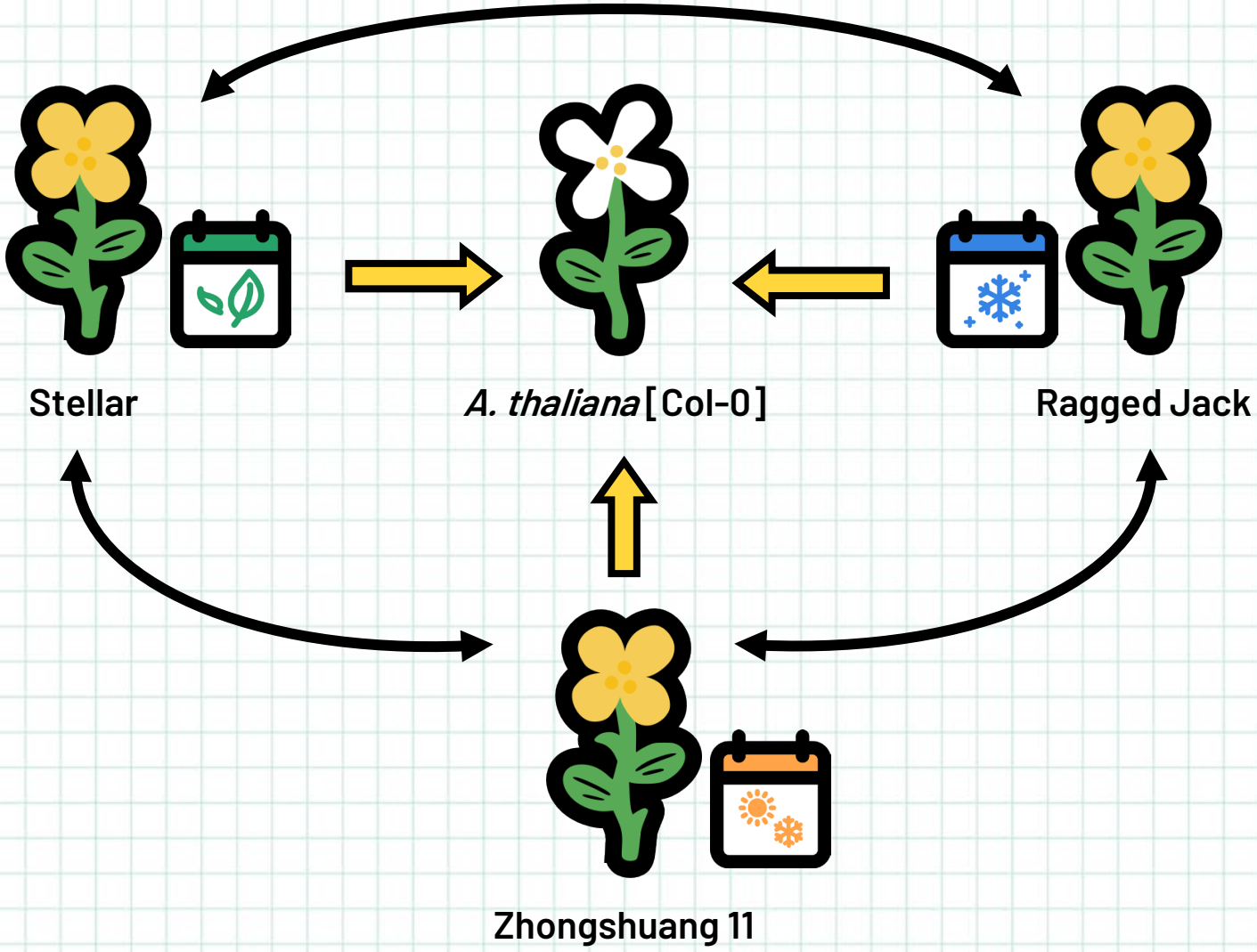




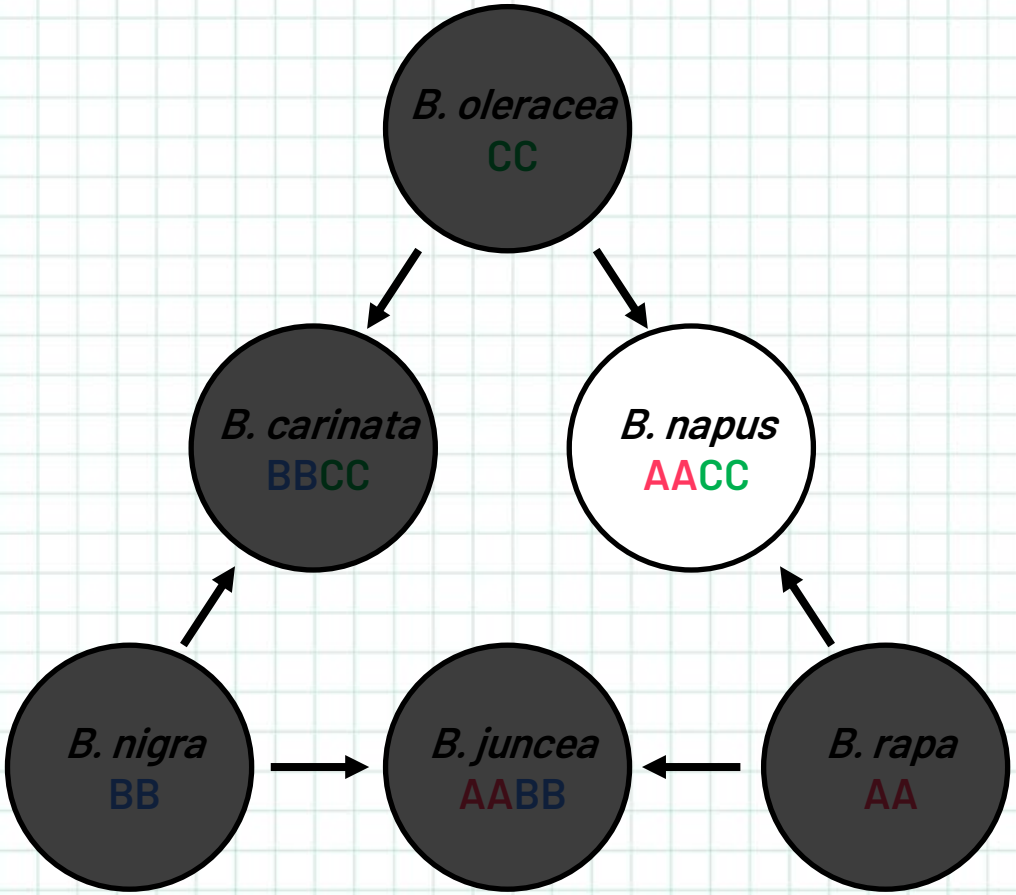


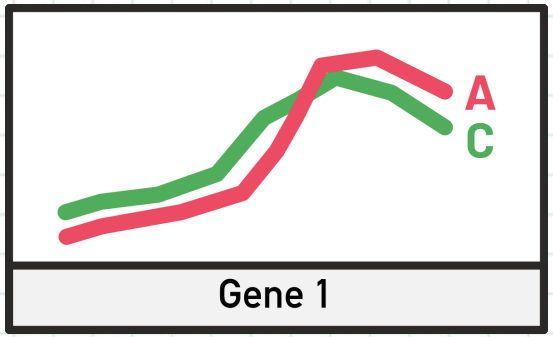
Calderwood *et al.* 2021

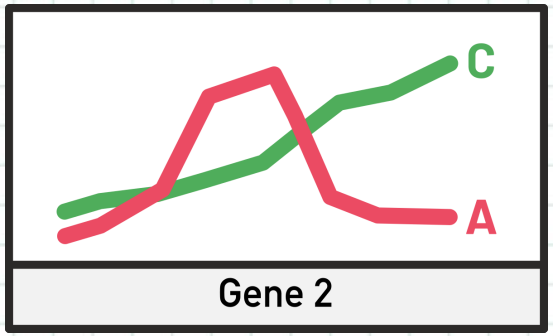
{greatR} for comparing different *B. napus* cultivars



{greatR} for comparing gene expression between A, C subgenome in *B. napus*







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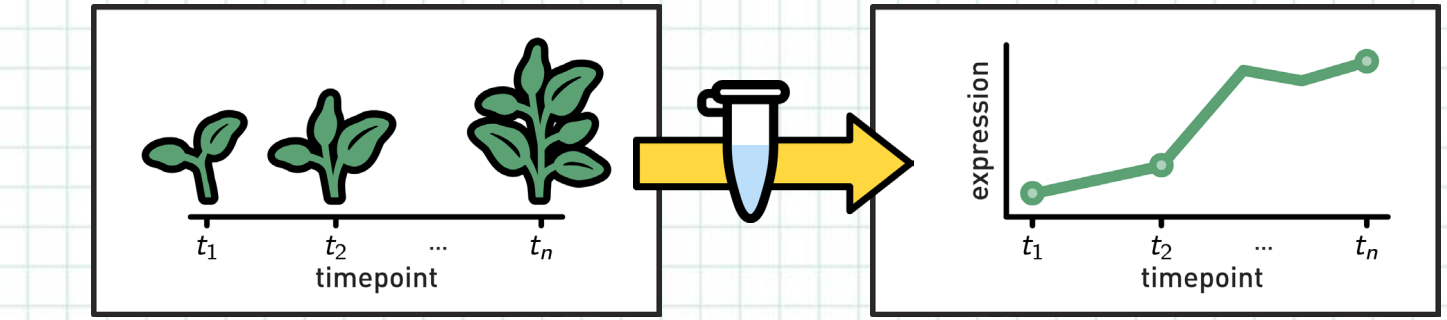
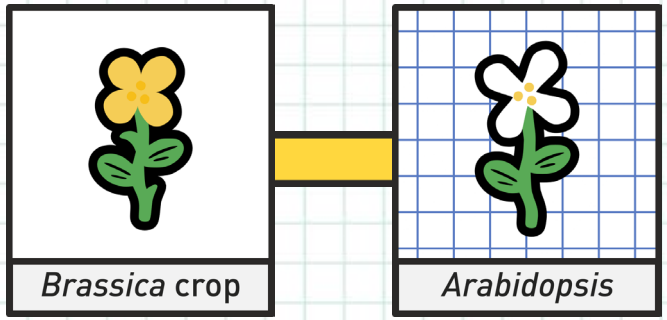
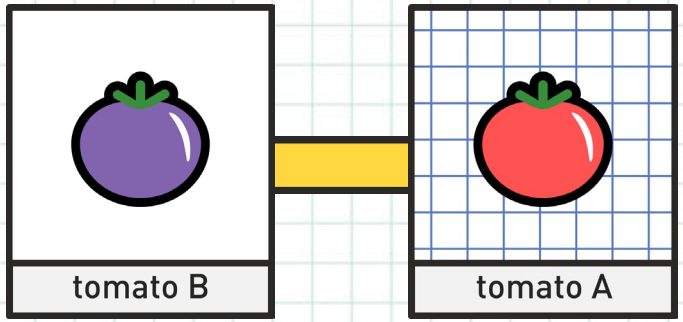
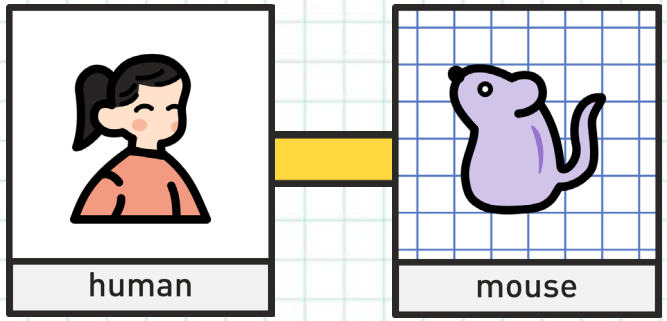
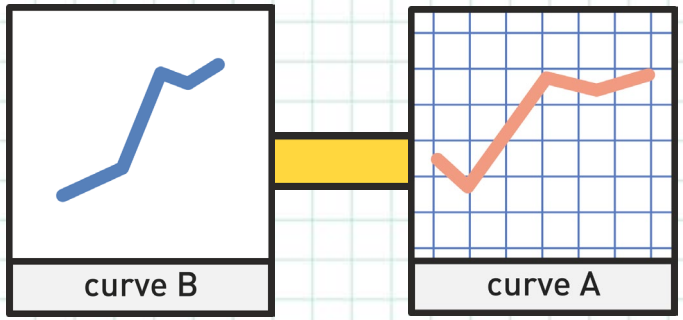
Different kind of data can be compared using {greatR}



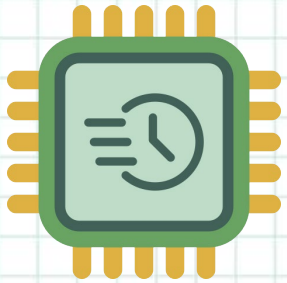


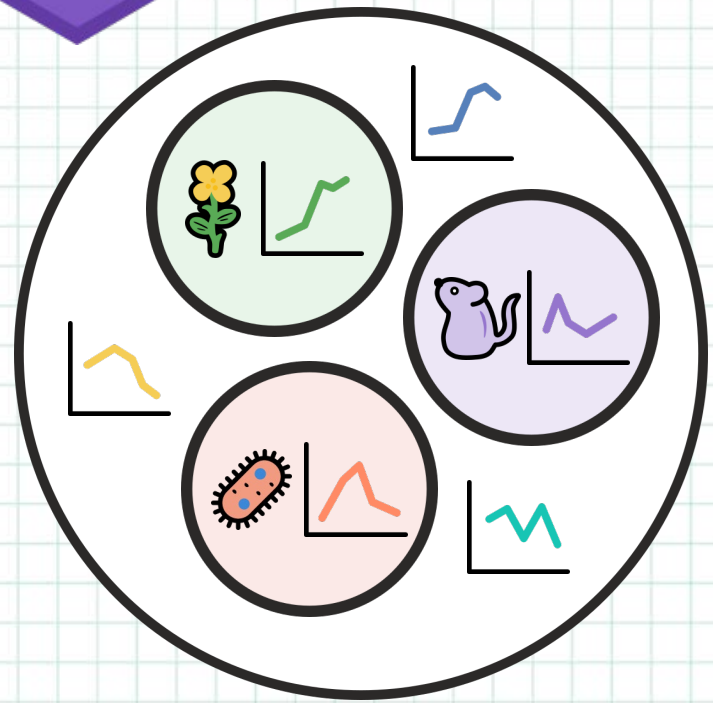




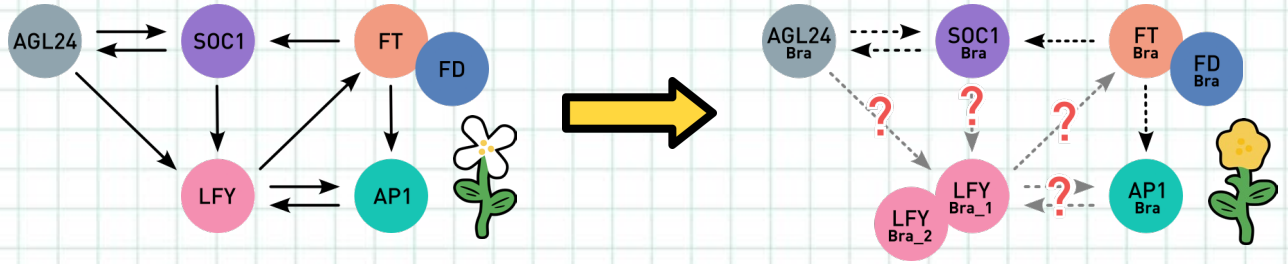


Summary





- knowledge transfer



- the identification of modules of co-regulated genes
- the discovery of condition-specific temporally differentially expressed genes

Morris lab

Supervisory team

References

{greatR}

BRAVO
Brassica Rapeseed And Vegetable Optimisation

John Innes Centre
Unlocking Nature's Diversity

John Innes Foundation