

Optimising Canola Production in Diverse Australian Growing Environments

Project Team

Shannon Dillon
Chris Helliwell
Alex Boyer
Andrew Gock
Emmett Leyne
Bangyou Zheng
Ian Greaves

Julianne Lilley
Matt Nelson
Bill Bovill
Susie Sprague
Jeremy Whish
Brett Cocks
Ari Verbyla

Jing Wang
Rob Coe
Geoff Bull
Jamie Scarrow

Optimising canola phenology

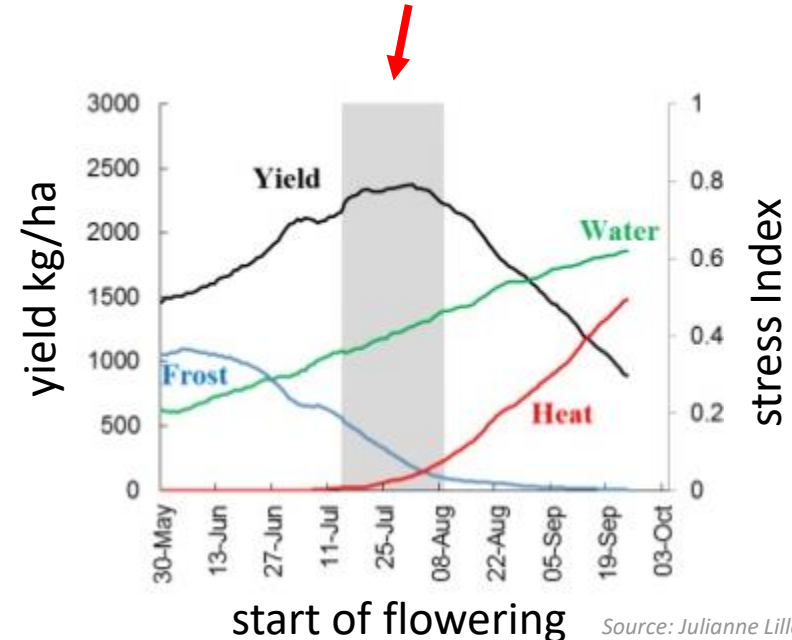
Timing canola phenology to the optimal flowering window is essential to productivity

Challenge to predict optimal sowing time for varieties in different environments

- driven by genetics and environment
- field based screening required
- compounded by rapid variety turnover



Optimal Start of Flowering



Genomic based tools – for crop management

Genomic based models for phenology prediction

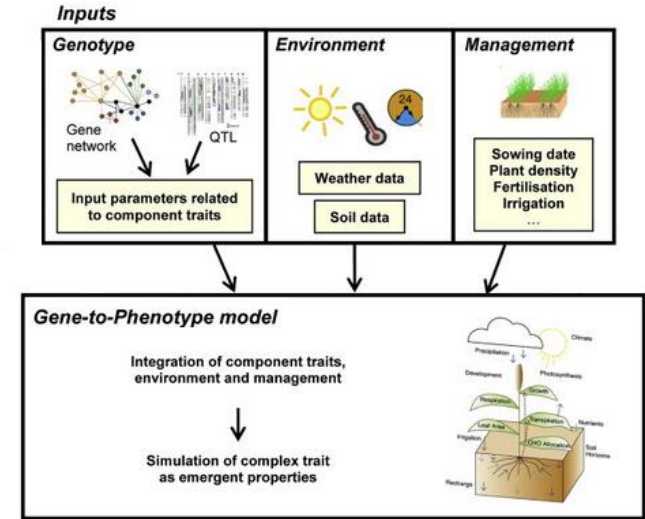
- Crop modelling
 - 'omics to inform phenology parameters (vernal, thermal time)
- Predict phenology directly
 - 'omic and environmental inputs



Growers able to determine optimal sowing date

- maximise yield
- phenology app

APSIM plant models



Adapted from Holzworth et al 2014, *Environmental Modelling and Software*

Genomic based tools – for breeding

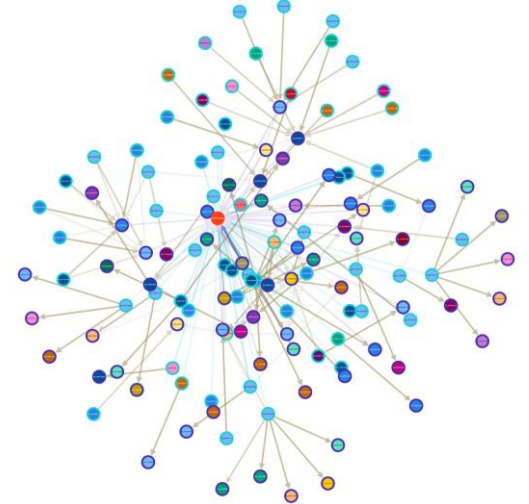
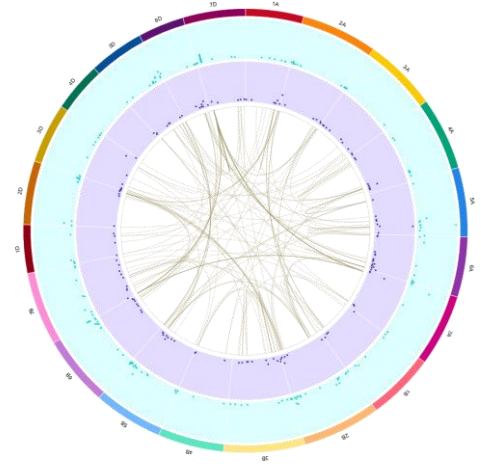
Characterise genomic variation in phenology

- Genomic variants (SNP, transcript)
- Interactions (GxE, GxG)
- Pathways

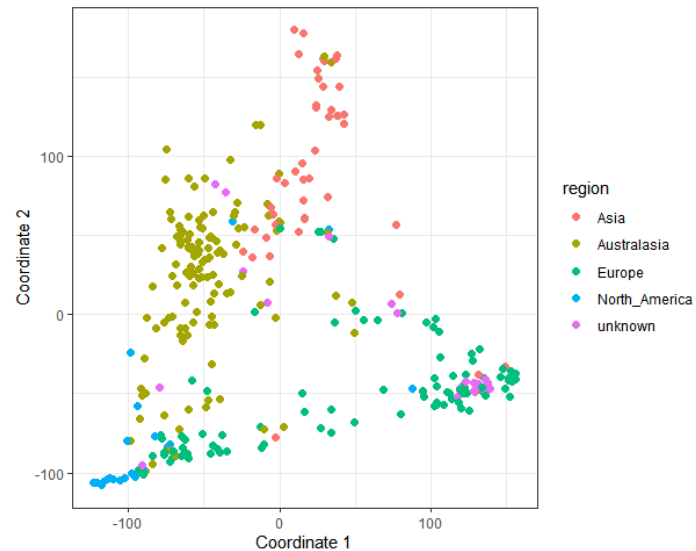
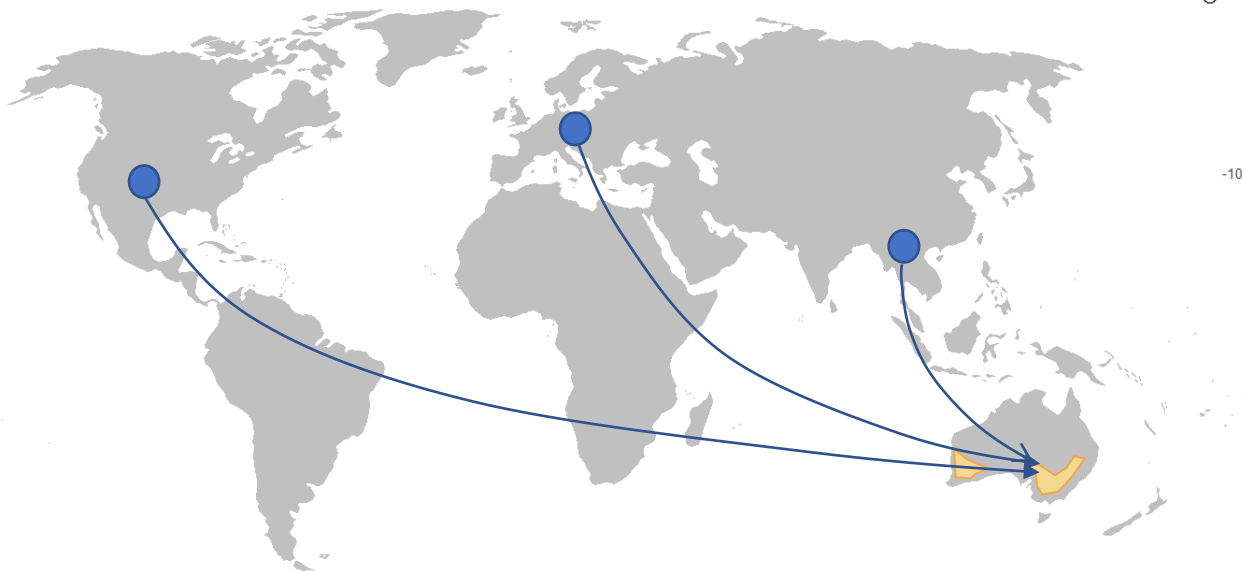


Breeders able to select for allele combinations
to target optimum start of flowering in
different environments

- marker based interventions
- integrated multi-omic prediction methods



Canola Diversity Panel



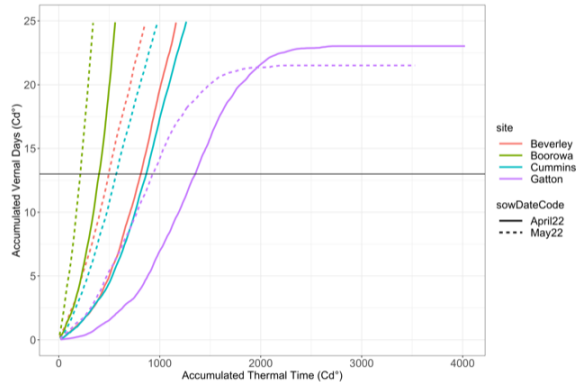
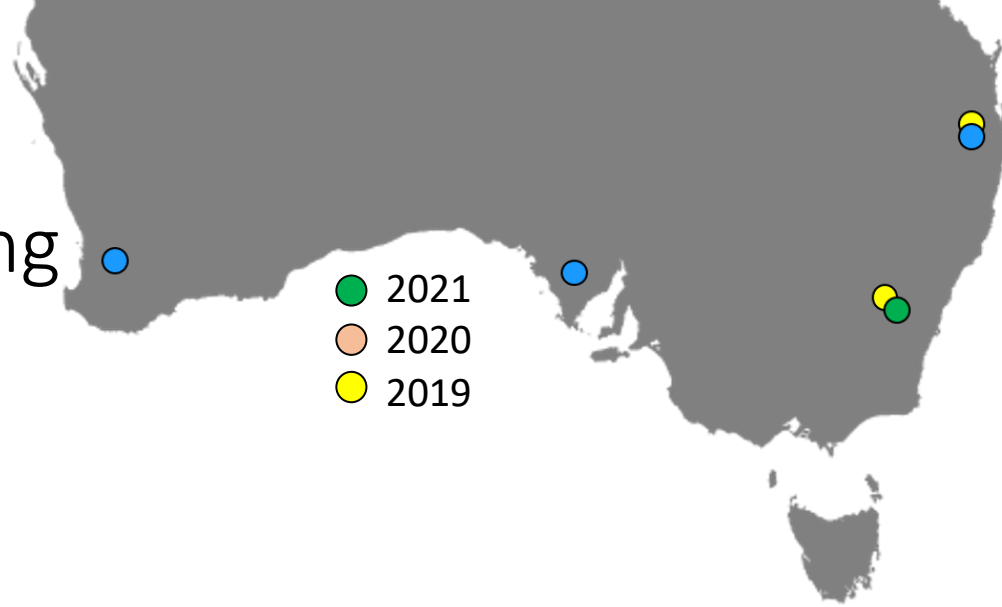
690 varieties

- Modern AUS
- Global:
 - BRAVO
 - ASSYST

Core set of 350 varieties
underpin data collection

Agronomy, crop modelling & phenology

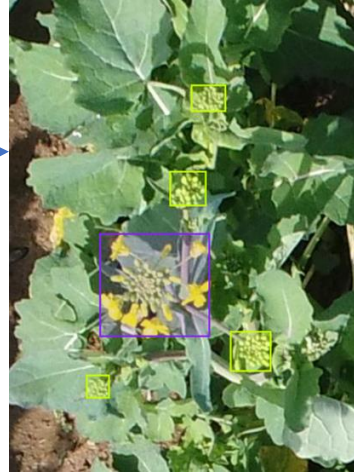
- Field trials
- Controlled environments
 - daylength
 - vernalization



ML computer vision – Post Doctoral Fellow



Drone
images

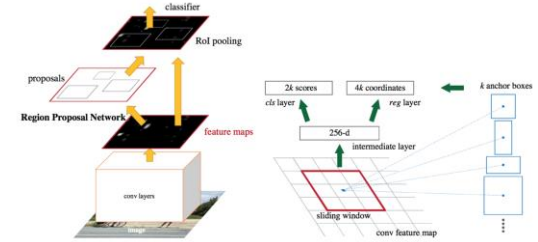


Annotation

2021 Boorowa
phenology trial:
350 varieties

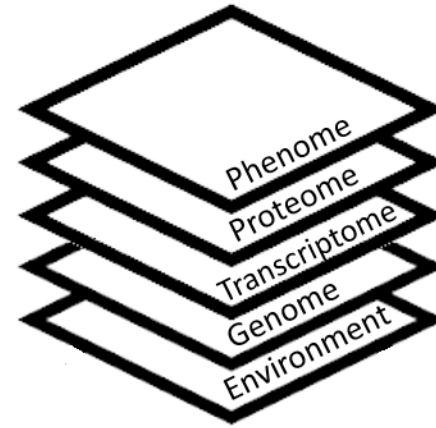
Manual phenology
scores

Train a deep learning model

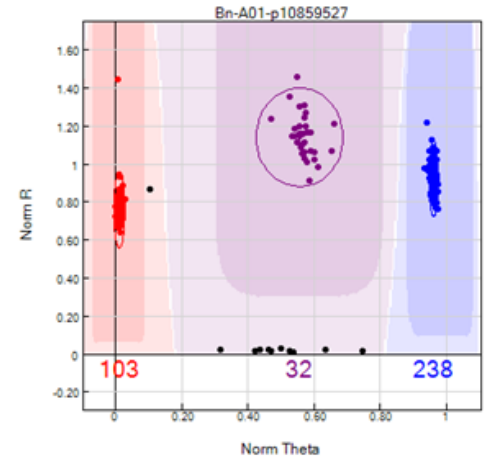
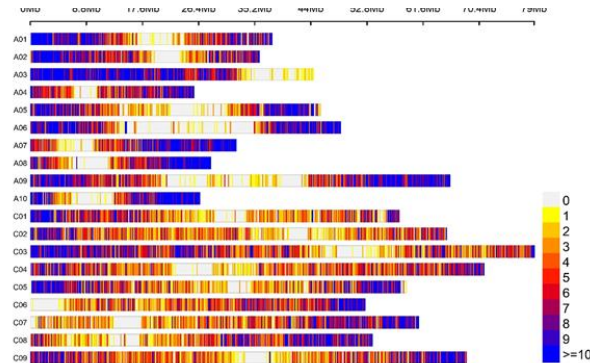


'omics platforms

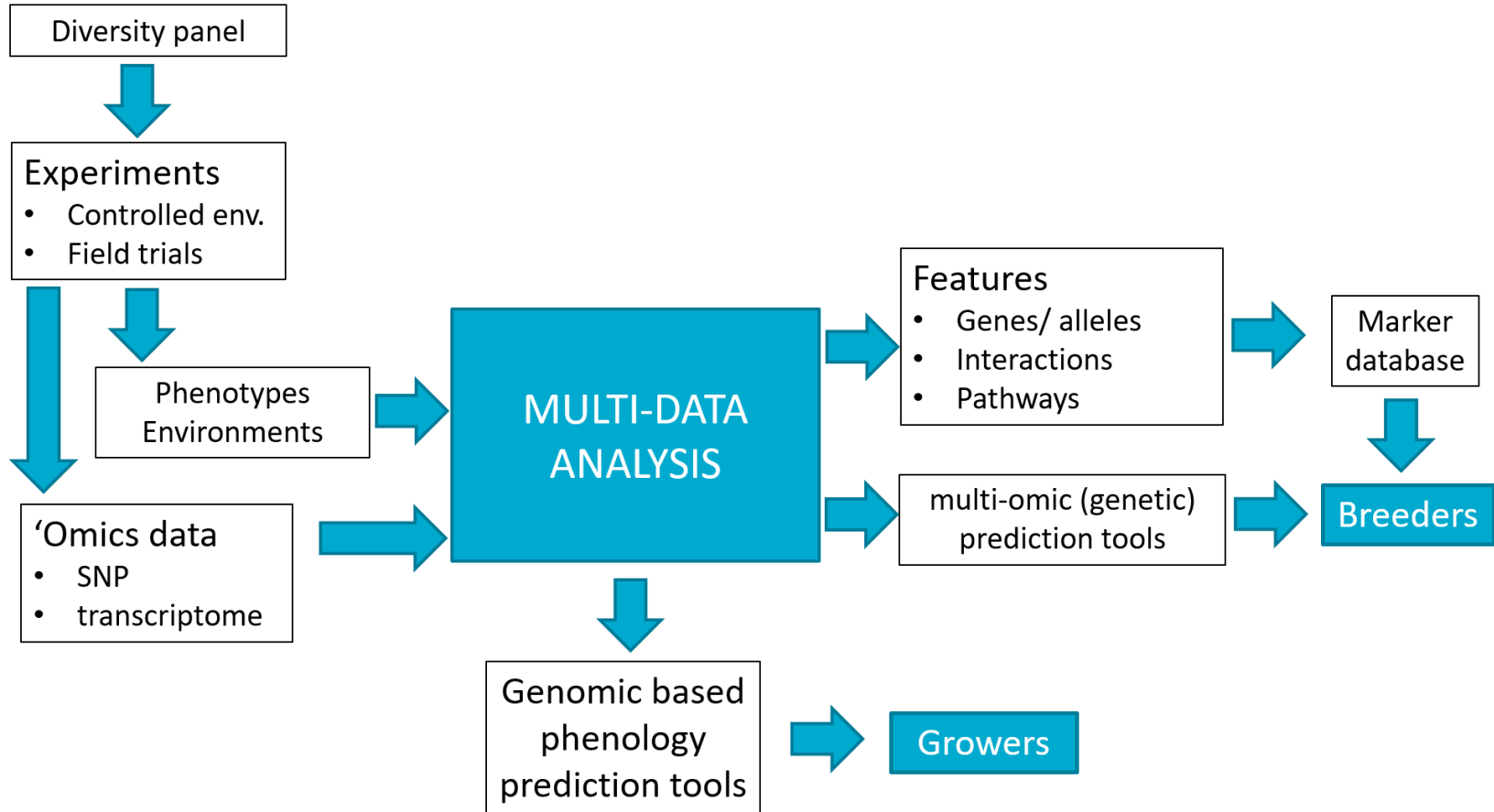
- Transcriptomes – low cost
 - Transcripts (~50K)
- Genome wide SNPs
 - 90K brassica array (~30K)
 - Transcript SNPs (~30K)
- Proteomes (wheat)



Transcript distribution



Integrative analytics



Model refinement and validation

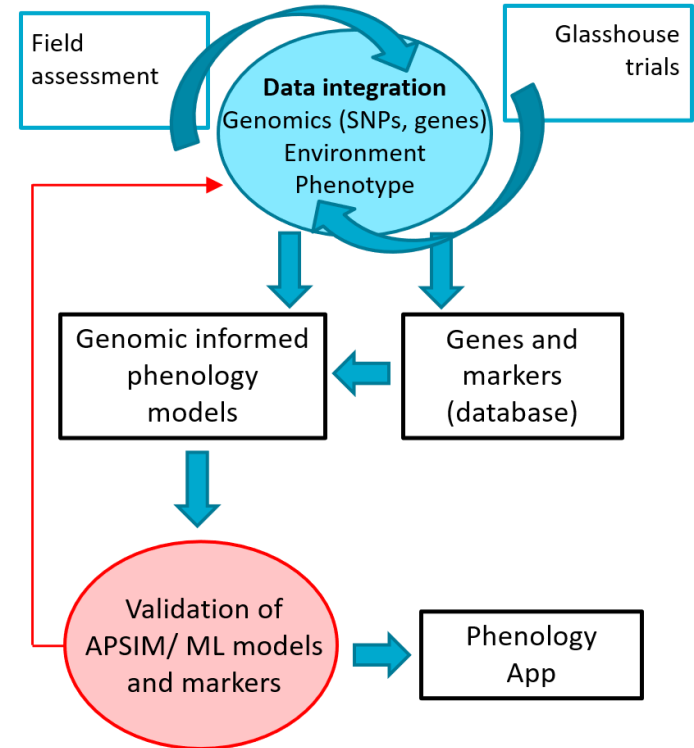
Confidence in any phenology model will depend on...
> robust model validation in 'real-world' setting

Possible options for this project include

- > historical data - where genotypes are available or can be generated
- > new trial data

Use NVT sites (2022)

- > Expand environment range
- > Validate and refine model
- > Inviting breeding companies including varieties in NVT to collaborate



Thankyou

Contacts:

Chris Helliwell: chris.helliwell@csiro.au

Shannon Dillon: shannon.dillon@csiro.au