

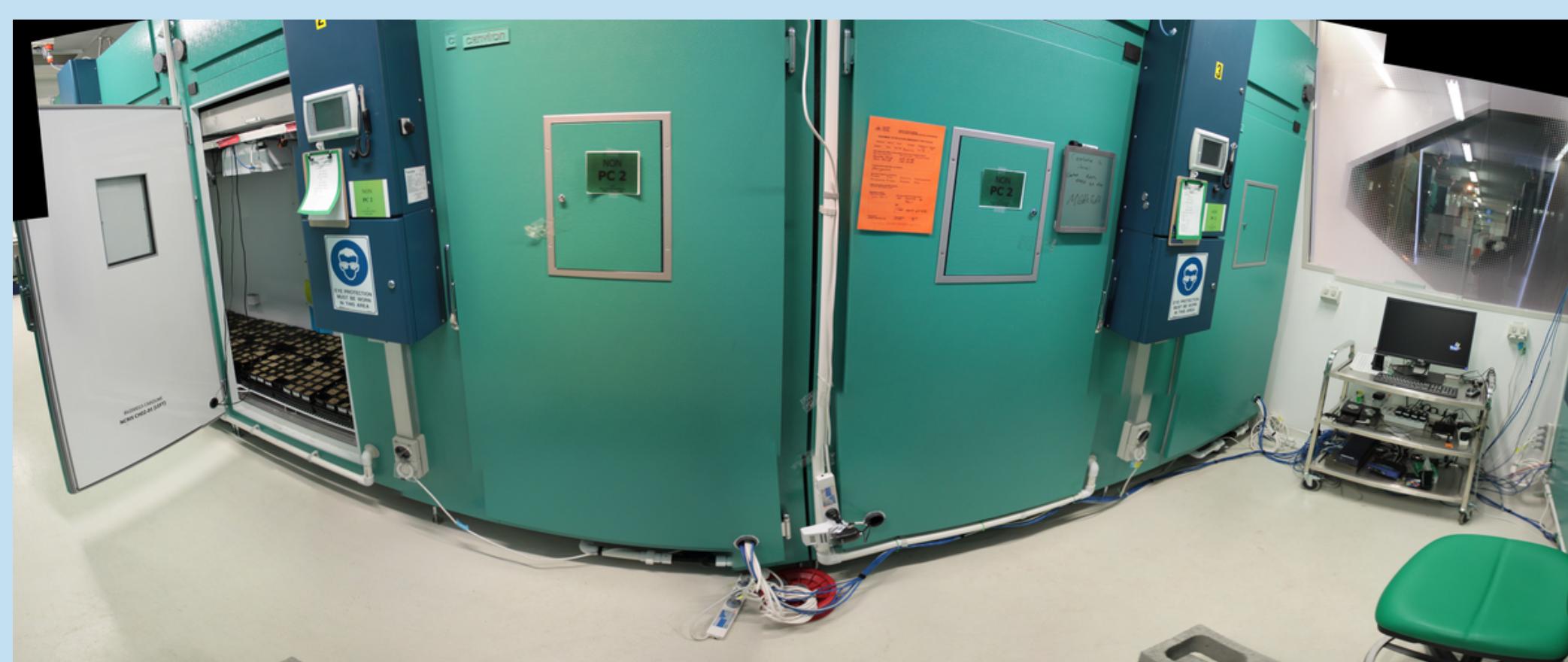
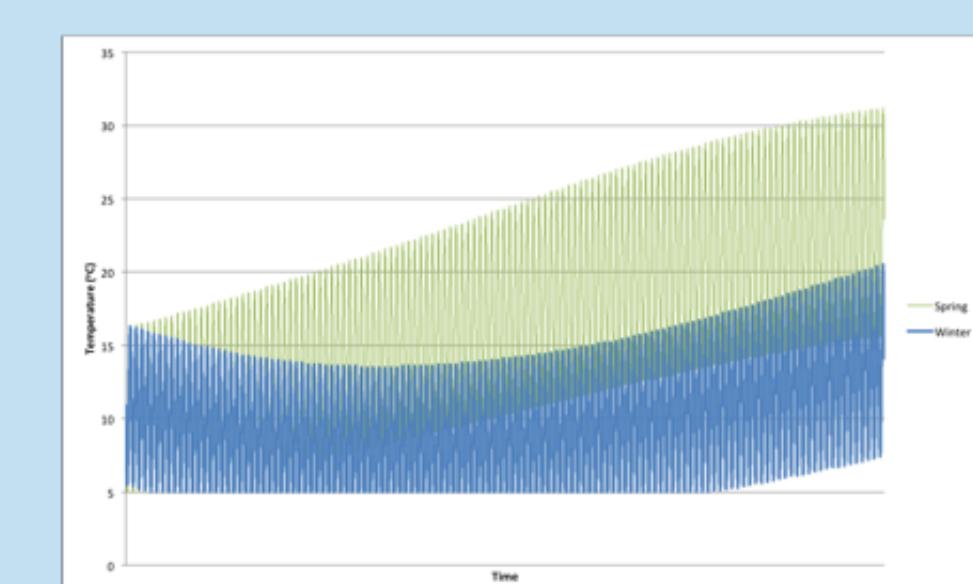
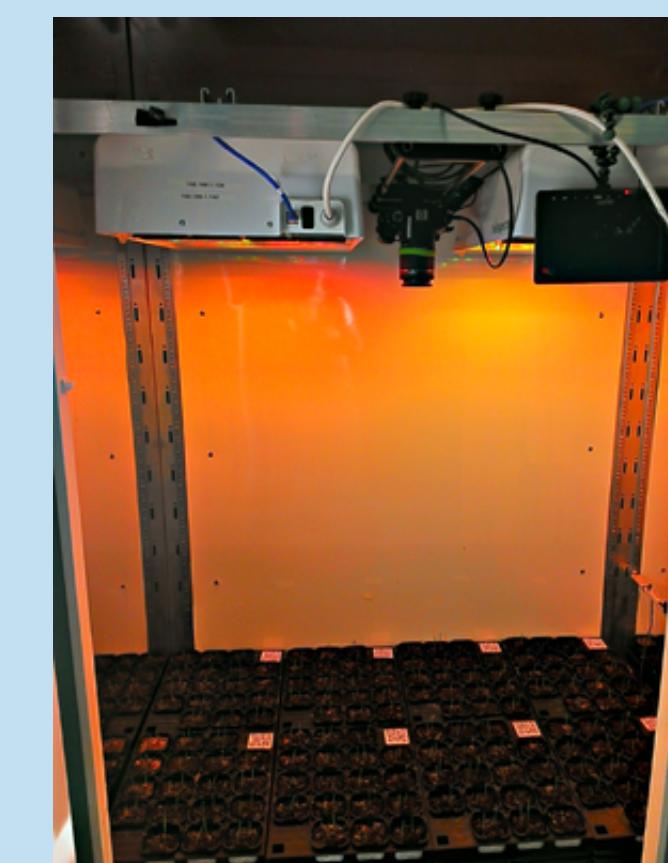
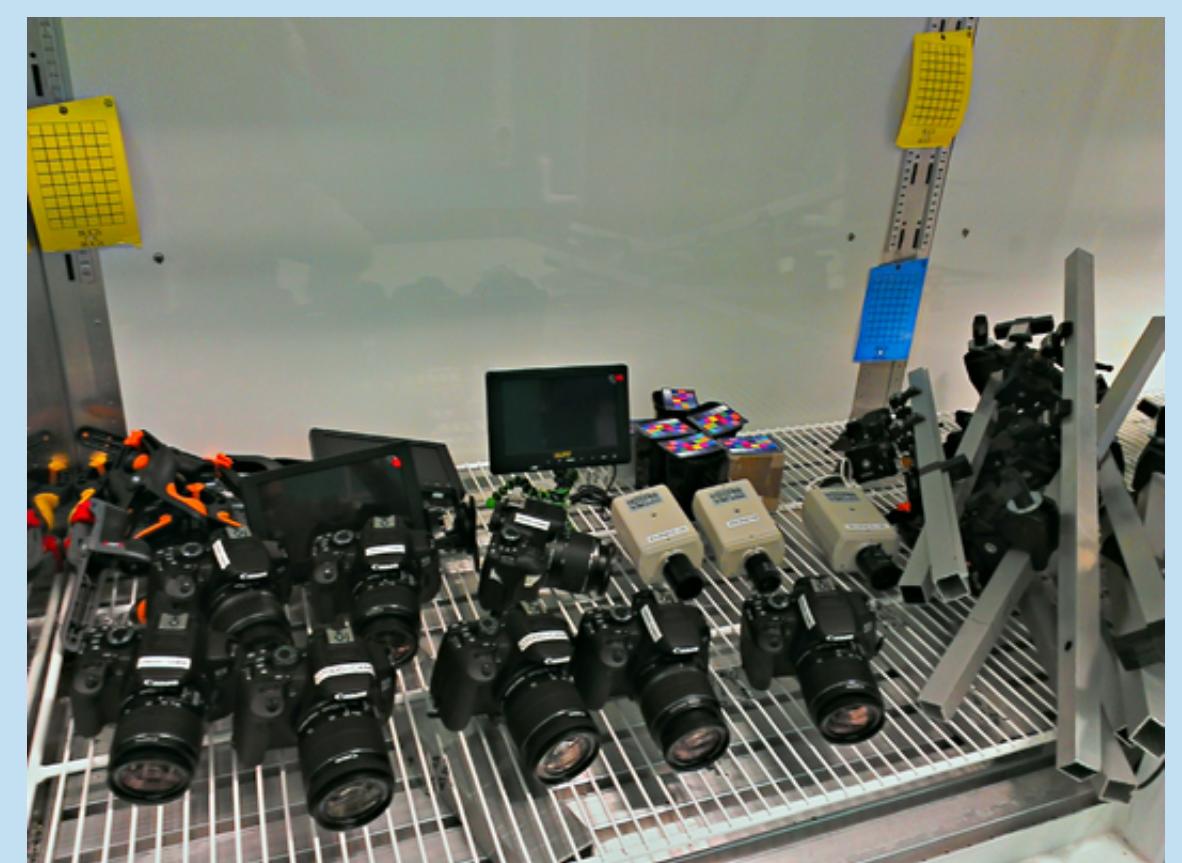
TraitCapture:

Tools for Adaptation: Integrating Environment, Genotype and Phenotype

Kevin Murray¹, Tim Brown¹, Riyan Cheng¹, Steve Eichten¹, Norman Warthmann¹, Xavier Sirault², Justin Borevitz^{1*}

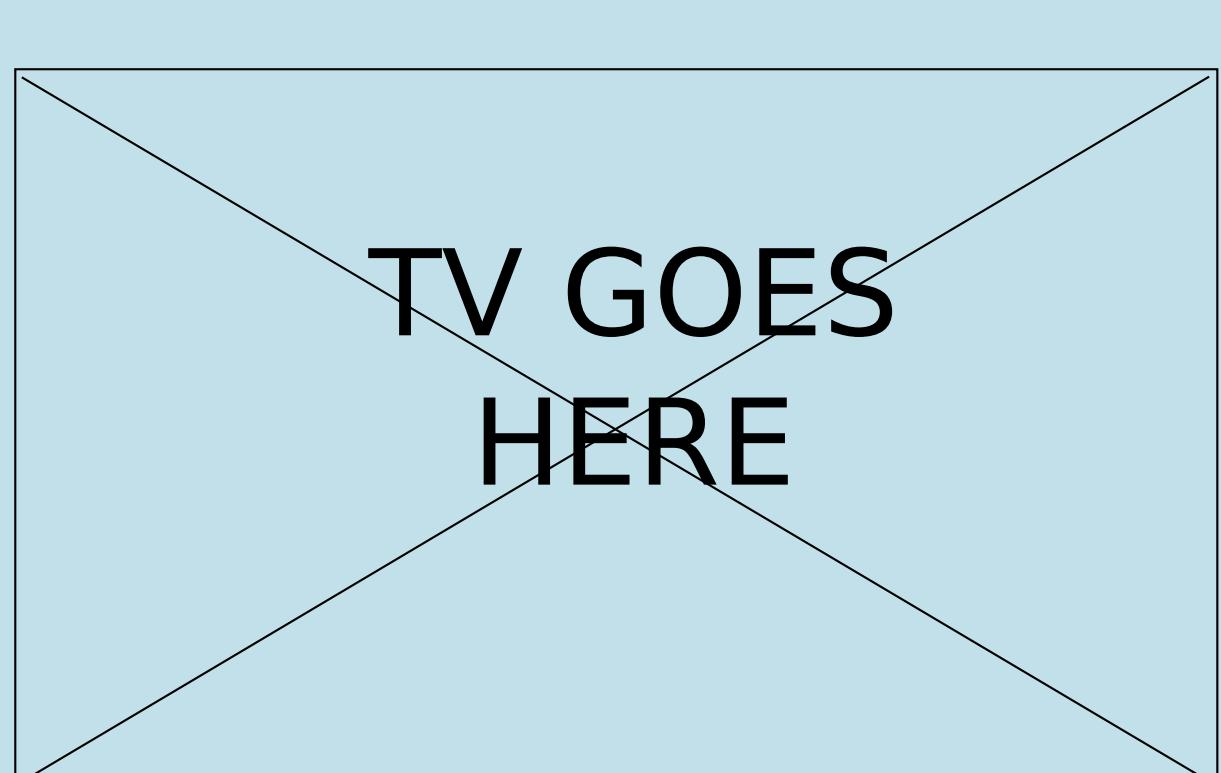
What is it?

- Integrated plant growth facility, sample tracking, genomics, phenomics and statistical analysis
- Free/Open-source software computational pipelines for cross-scale genome analysis and image analysis for automated phenotyping
- >30k lines of code, >15 software projects, > 1500 git commits
- Project outline published in Current Opinions^[1]



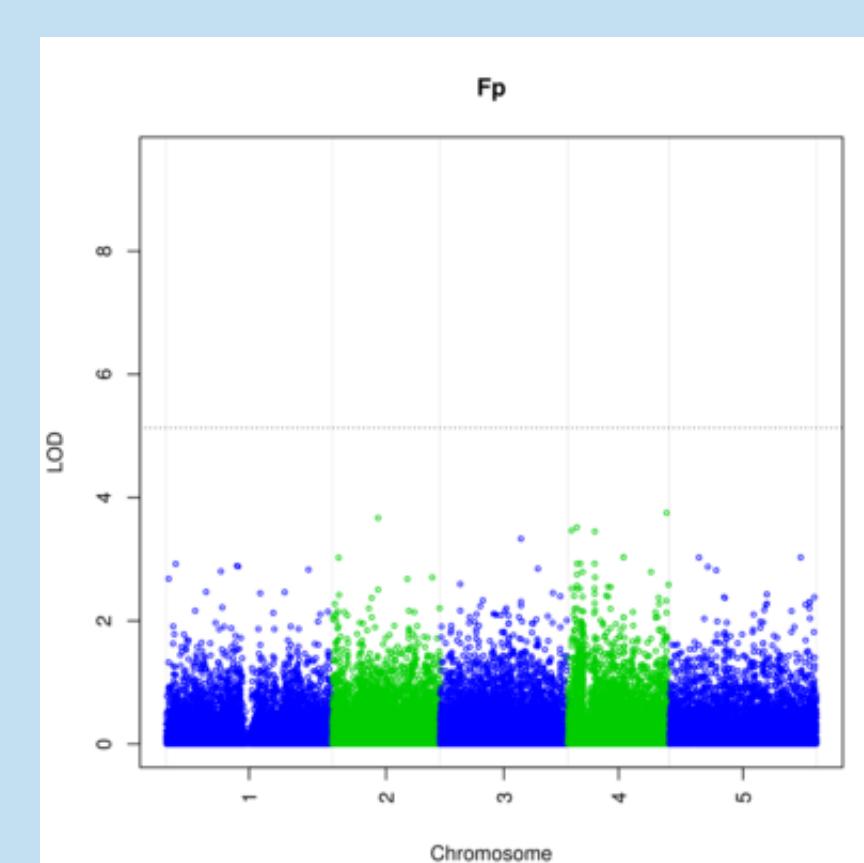
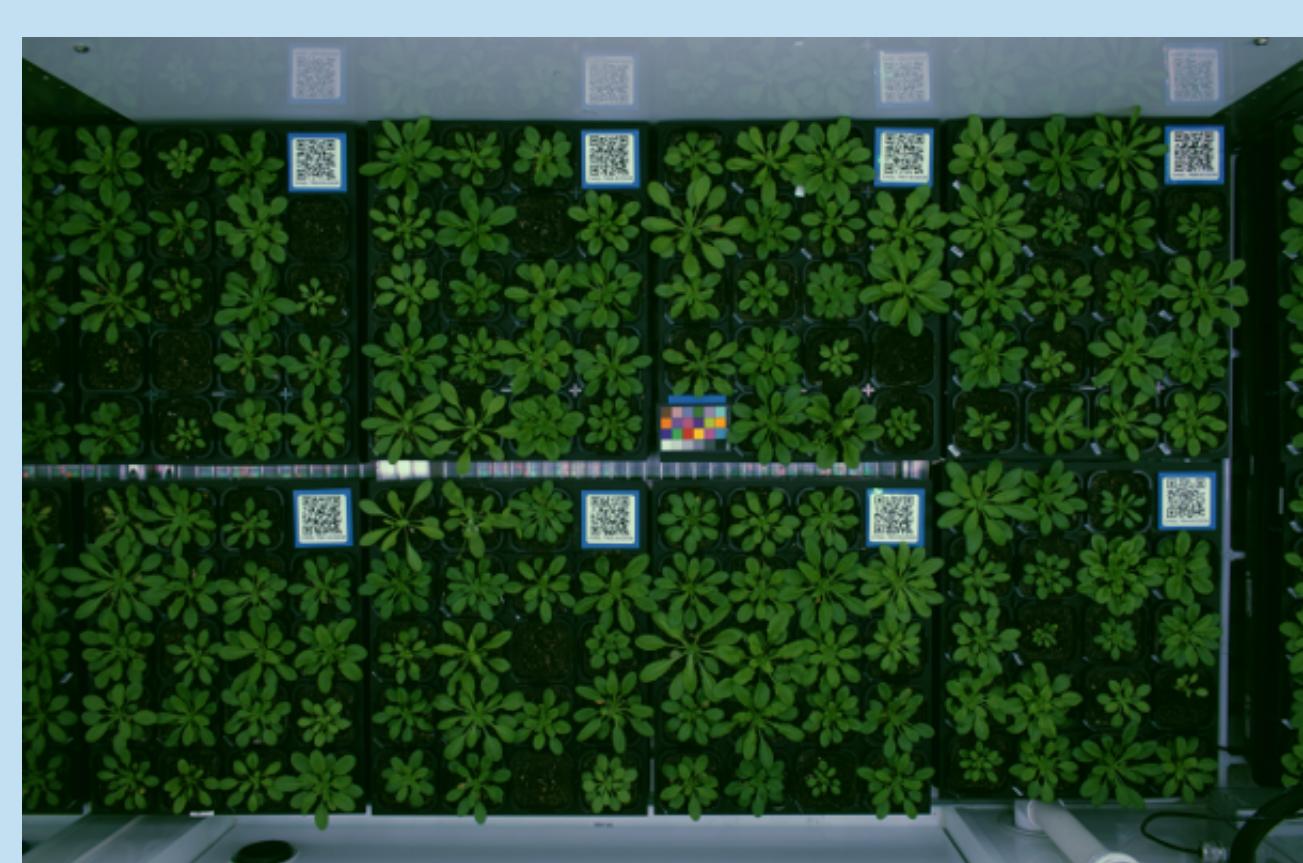
Automated, Real-time Phenomics

- *EyePi*^[v]: Raspberry Pi-based image acquisition hardware & software
- *Timestreamlib*^[6]: time-series image format and manipulation library
- Colour correction, rectification, segmentation, derandomisation
- Automated batch image analysis
- GUI and web interface for interactive analysis and visualisation
- Python 2.7 & 3.3+, cross platform, Open Source (GPL licensed)



High-throughput RNAseq & epigenomics

- High-throughput RNAseq and Bisulphite-seq library prep protocols in development
- Fast, accurate RNAseq differential expression pipeline^[e]
- Developing protocols & methods for population epigenomics
- High-throughput library prep
- Robust differential methylation analysis pipelines in development



Future Projects

- Functional Structural Plant Models: Allow statistical prediction of phenotypes from genetics and environment
- Advanced visualisation of time-series imagery
- Scale computational infrastructure from single servers to supercomputer facilities

List of software

- [α] SolarCalc: <http://1.usa.gov/1o0tq0d>
- [β] SPCCControl: <http://git.io/2DtcwQs>
- [γ] EyePi: <http://git.io/tsutgg>
- [δ] Timestreamlib: <http://git.io/OCPQ8A>
- [ε] RNAseq Pipeline: <http://git.io/0v40KA>
- [ζ] QTLRel: <http://bit.ly/ZRJlmL>

Poster Homepage:
<http://git.io/qH3C9A>



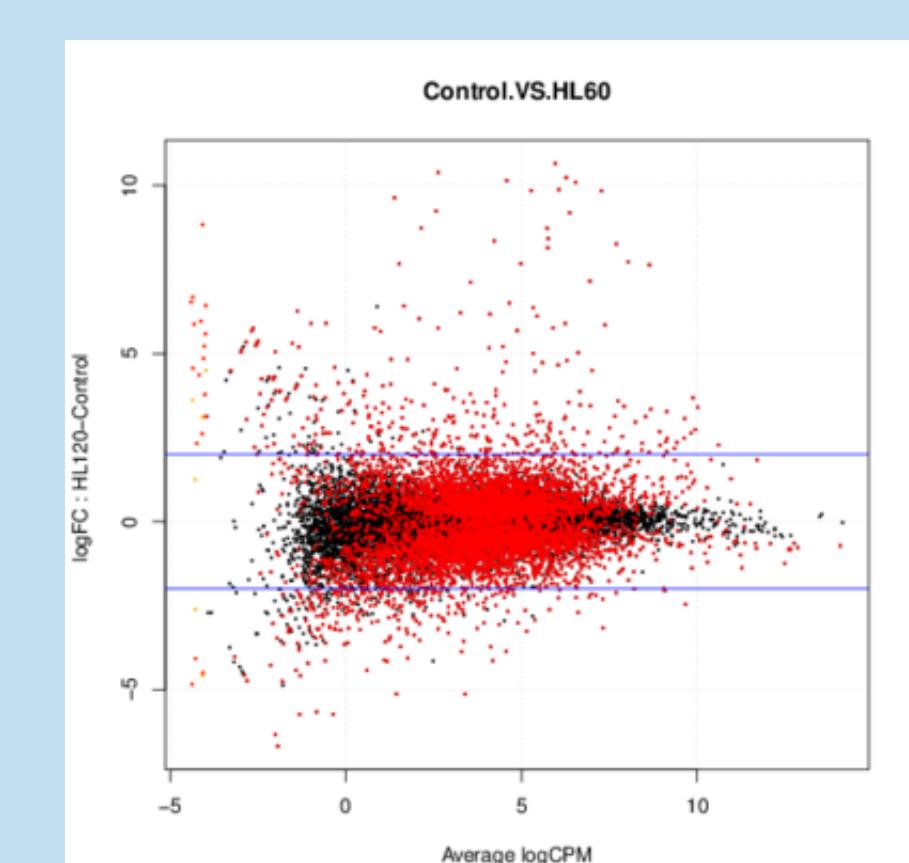
The SpectralPhenoClimatron

- Controlled environment plant growth facility fitted with Multispectral LED lamps
- DSLR cameras, 15min frequency in daylight, ~300x300px/plant
- *SolarCalc*^[a] simulates regional climates without weather^[2]
- *SPCCControl*^[β] controls multispectral lamps, temperature, humidity and cameras every minute



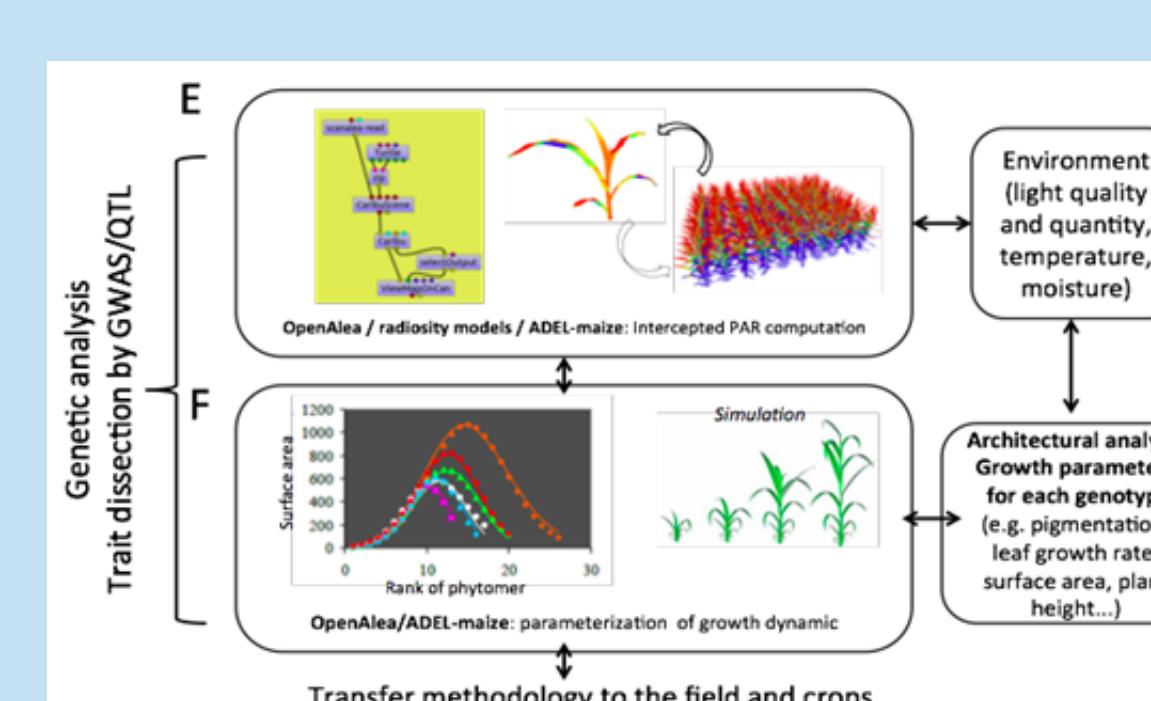
Cross-scale Genomics

- Reduced representation sequencing method
 - Custom optimised library preparation protocol; 576-1152 samples per lane
 - Custom variant calling pipeline build on TASSEL^[3]
- Low-coverage Whole-genome Sequencing
 - Low-cost library preparation protocol, customised from^[4]
 - Advanced robotics providing tissue grinding, liquid handling, SPRI.
 - Novel alignment-free variant calling algorithms (in initial development)



Advanced Statistical Association Analysis

- *QTLRel*^[ζ]: Statistical methods to map QTLs in complex populations^[5]
- QTL/GWAS analysis with increased statistical power by combining traits in joint analysis^[6]
- Real-time QTL mapping, allowing interactive adjustment of experimental conditions



References:

- [1]: Brown et al., 2014, DOI: 10.1016/j.pbi.2014.02.002
- [2]: Spokas et al. 2006, DOI: 10.1614/WS-05-098R.1
- [3]: Glaubitz et al. 2014, DOI: 10.1371/journal.pone.0090346
- [4]: Elshire et al. 2011, DOI: 10.1371/journal.pone.0019379
- [5]: Cheng et al. 2011, DOI: 10.1186/1471-2156-12-66
- [6]: Cheng et al. 2011, DOI: 10.1534/genetics.113.155937

[*] Corresponding author:
justin.borevitz@anu.edu.au

Author Affiliations:

- 1: ARC Centre of Excellence in Plant Energy Biology, ANU
Website: <http://plantenergy.edu.au/>
- 2: High Resolution Plant Phenomics Centre, CSIRO Canberra
Website: <http://www.plantphenomics.org.au/>