Longitudinal modelling of crop root physiology as a breed-specific spatial response to environmental conditions

Grace S. Chiu,[1,2,3] Anton P. Wasson,[4] Alec B. Zwart[5]

[1] ANU Research School of Finance, Actuarial Studies and Statistics

[2] University of Washington, Department of Statistics
[3] University of Waterloo, Department of Statistics and Actuarial Science
[4] CSIRO Agriculture and Food
[5] CSIRO Data61

Outline

1. Why model root architecture?
2. Data visualization
3. Inference approach: Pre-Chiu vs. Chiu
4. Key insights:
   - Multiresolution heritability
   - Root system's bulk vs. exploration

1. Why model root architecture?

Above ground. . .

Damage to bumper global whe ×

www.reuters.com/article/us-global-wheat-feed-idUSKCN1000B1

REUTERS Damage to bumper global wheat crop spurs use as animal feed

COMMODITIES | Wed Jul 20, 2016 | 1:14am EDT

Damage to bumper global wheat crop spurs use as animal feed

A combine drives over stalks of soft red winter wheat during the harvest on a farm in Dixon, Illinois, July 16, 2013. REUTERS/Jim Young/File Photo

Above ground. . .

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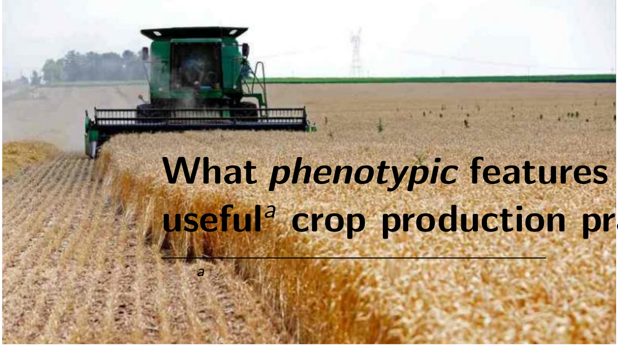

A combine drives over stalks of soft red winter wheat during the harvest on a farm in Dixon, Illinois, July 16, 2013. REUTERS/Jim Young/File Photo

What *phenotypic* features can identify useful[a] crop production practices?[b]

---

[a]

Above ground. . .

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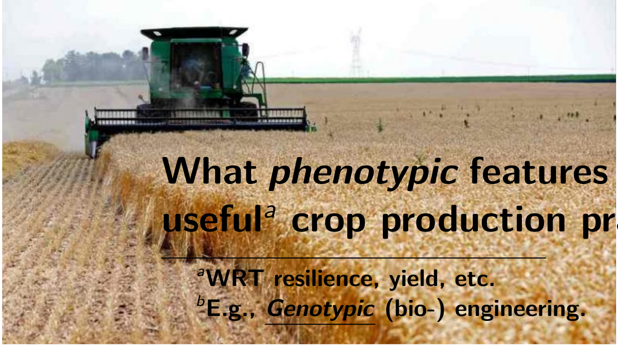

A combine drives over stalks of soft red winter wheat during the harvest on a farm in Dixon, Illinois, July 16, 2013. REUTERS/Jim Young/File Photo

What *phenotypic* features can identify useful[a] crop production practices?[b]

[a] WRT resilience, yield, etc.

[b] E.g., *Genotypic* (bio-) engineering.

Heritability

Heritability - Wikipedia

Secure https://en.wikipedia.org/wiki/Heritability

Definition [edit]

Any particular phenotype can be modeled as the sum of genetic and environmental effects:[4]

Phenotype (P) = Genotype (G) + Environment (E).

Likewise the phenotypic variance in the trait – Var (P) – is the sum of effects as follows:

Var(P) = Var(G) + Var(E) + 2 Cov(G,E).

$$h^2 = \frac{\sigma_G^2}{\sigma_P^2}$$

Heritability

In a planned experiment Cov(G,E) can be controlled and held at 0. In this case, heritability is defined as:

$$H^2 = \frac{\mathrm{Var}(G)}{\mathrm{Var}(P)}.$$

H^2 is the broad-sense heritability. This reflects all the genetic

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Heritability

Q: What phenotypic features result in a high h^2?

Heritability

Q: What phenotypic features result in a high h^2?

Age-old industry standard:

What above-ground phenotypic features result in a high h^2?

Getting to the ROOT of the issue. . .

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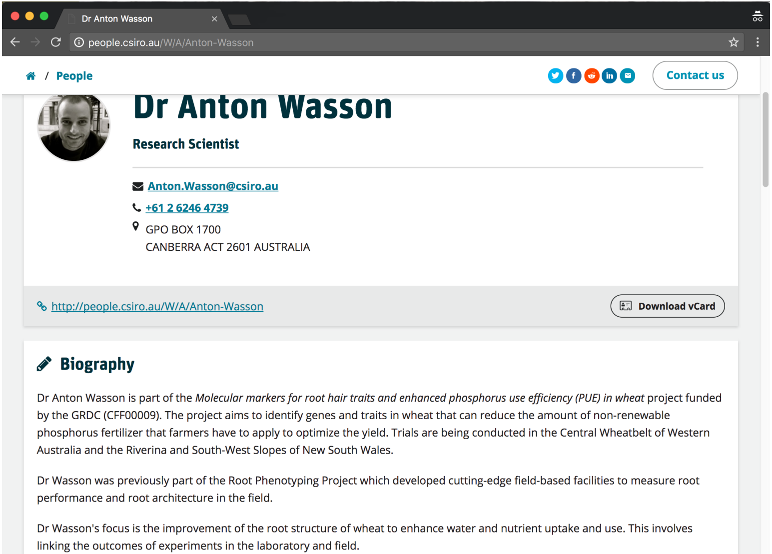

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Biography

Dr Anton Wasson is part of the *Molecular markers for root hair traits and enhanced phosphorus use efficiency (PUE) in wheat* project funded by the GRDC (CFF00009). The project aims to identify genes and traits in wheat that can reduce the amount of non-renewable phosphorus fertilizer that farmers have to apply to optimize the yield. Trials are being conducted in the Central Wheatbelt of Western Australia and the Riverina and South-West Slopes of New South Wales.

Dr Wasson was previously part of the Root Phenotyping Project which developed cutting-edge field-based facilities to measure root performance and root architecture in the field.

Dr Wasson's focus is the improvement of the root structure of wheat to enhance water and nutrient uptake and use. This involves linking the outcomes of experiments in the laboratory and field.

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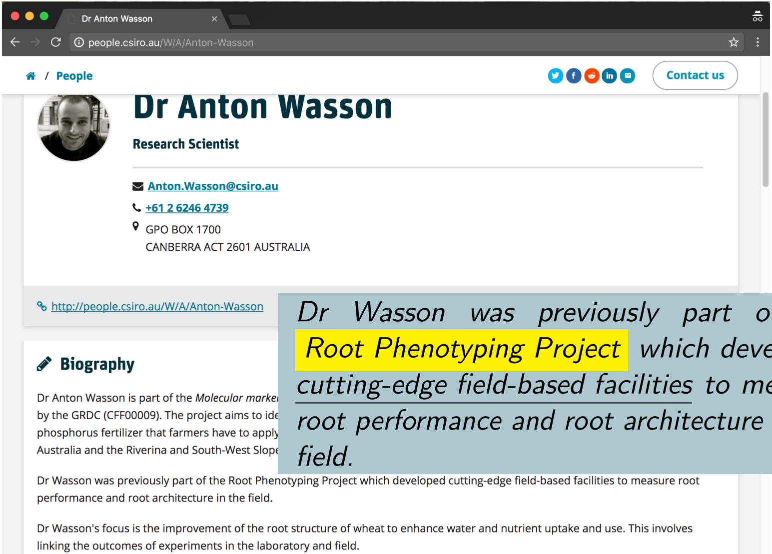

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Cutting-edge root system imaging

portable fluorescence spectro ×

Secure https://academic.oup.com/jxb/article-lookup/doi/10.1093/jxb/erv570

Journal of Experimental Botany

SEB

Article Navigation

A portable fluorescence spectroscopy imaging system for automated root phenotyping in soil cores in the field

Anton Wasson ✉, Leanne Bischof, Alec Zwart, Michelle Watt

J Exp Bot (2016) 67 (4): 1033-1043. **DOI:** https://doi.org/10.1093/jxb/erv570

Published: 29 January 2016

Cutting-edge root imaging

up/doi/10.1093/jxb/erv570

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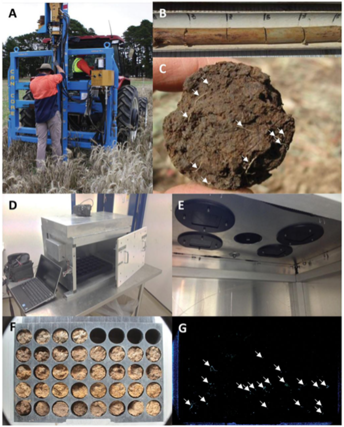
Fig. 1.



Steps in the BlueBox methodology. (A) An operator root sampling with a 2 m long stainless steel coring tube with a tapered tip (not visible). The tube was driven into the ground by a tractor-mounted push press. (B) A soil core emptied into a cradle in a manual root-counting method. The core has been scored with a knife every 10cm to facilitate breaking. (C) The broken face of a soil core segment as seen by a human operator. The number of visible roots (highlighted with white arrows) is assessed in a few seconds. (D) The fluorescence imaging box (in the laboratory; for field use this would typically be mounted on a utility vehicle). The access panel at the front is ajar and a cassette is visible within. The digital SLR camera is operated remotely from the laptop. The battery on the left powers the LEDs, installed underneath the top cover. (E) View of the ceiling of the interior of the box. The central aperture is face of the digital SLR camera lens. The other apertures are UV-emitting LEDs (inactive in this photo) behind black light filter glass. (F) A visible image of the cassette containing the soil core segments. The cassettes were flipped so that both faces of the segment were photographed (the underside is visible here). (G) The fluorescence image of the cassette shown in F. The roots are fluorescing blue; larger roots are highlighted with white arrows.

Cutting-edge root imaging

up/doi/10.1093/jxb/erv570

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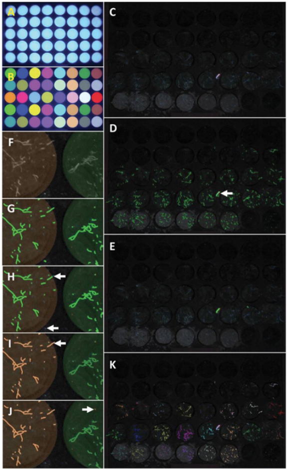
Fig. 3.



The image processing steps in the analysis software. (A) Image of cassette template. (B) Circular 'Well' labels (each label is overlaid as a separate colour). (C) RGB image of cores in wells. (D) Detected 'Linear structures' mask (overlaid in green on blue channel). (E) 'Debris' mask (overlaid in green on original image). (F–J) All subsets shown with 'Well' labels as transparent overlays: (F) blue channel image; (G) 'Debris-excluded root' mask (in green); (H) 'Roots within wells' mask (in green), with arrows indicating excluded roots; (I) labelled 'Reconstructed roots' (in 'Well' label colour), with arrow indicating a reconstructed root; (J) labelled 'Filtered roots' (in 'Well' label colour), with arrow indicating a root filtered by hue. (K) Labelled 'Filtered roots' (overlaid in 'Well' label colour on the RGB image).

2. Data visualization

"It's very important to see first hand how the data are collected. Like, the guy downstream sees a fish swoosh by, yells to the data entry guy 200 yards upstream: 'Fish! I think it was a G[???] Redhorse!' Could've been Greater or Golden or neither; data guy enters 'seahorse'."

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— (My dramatized version of) the greatest piece of advice from Peter Guttorp.

Soil coring at multiple field environments can directly quantify variation in deep root traits to select wheat genotypes for breeding

A. P. Wasson, G. J. Rebetzke, J. A. Kirkegaard, J. Christopher, R. A. Richards, M. Watt

J Exp Bot (2014) 65 (21): 6231-6249. **DOI:** https://doi.org/10.1093/jxb/eru250

Published: 24 June 2014

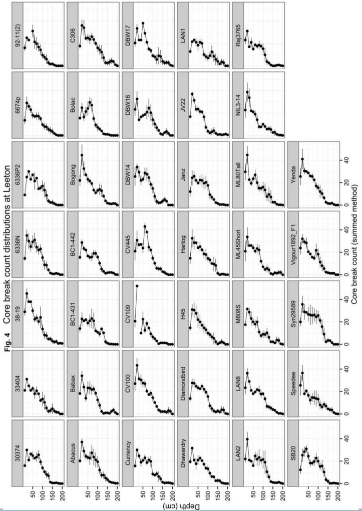

Fig. 4 Root distributions by depth at Leeton Experimental Station 2011. The error bars show the standard error of the mean for four replicated observations. [...]

Front. Plant Sci., 02 March 2017 | https://doi.org/10.3389/fpls.2017.00282

Differentiating Wheat Genotypes by Bayesian Hierarchical Nonlinear Mixed Modeling of Wheat Root Density

Anton P. Wasson[1*], Grace S. Chiu[2*], Alexander B. Zwart[3] and Timothy R. Binns[4]

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Fig. 1A

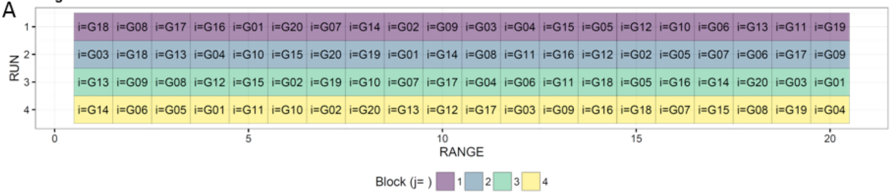
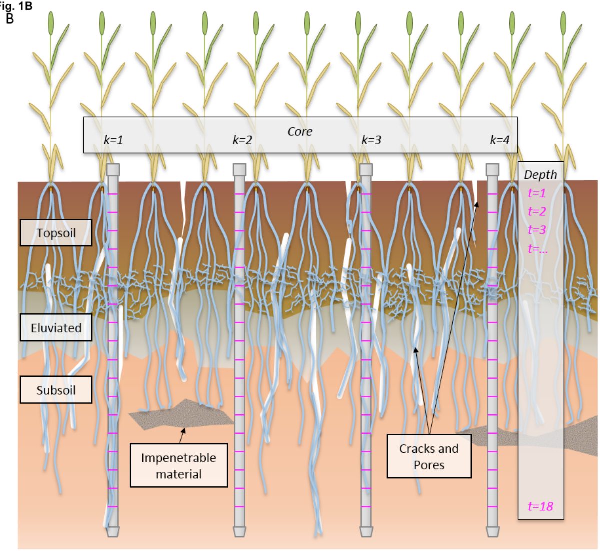
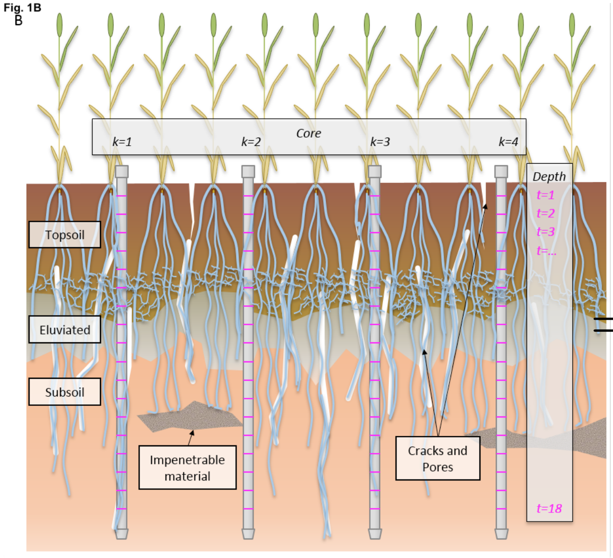


Fig. 1B


B
Core
k=1
k=2
k=3
k=4
Depth
t=1
t=2
t=3
t=...
t=18
Topsoil
Eluviated
Subsoil
Impenetrable material
Cracks and Pores



$\Longrightarrow$ y_{ijkt} !!

My co-authors

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My co-authors

Alec-Zwart_Bio.pdf

bioinformatics.org.au/ws14/wp-content/uploads/ws14/sites/5/2014/05/Alec-Zwart_Bio.pdf

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Dr Alec Zwart
CSIRO, Canberra

Biography:
Dr Zwart holds three degrees from the University of Waikato in New Zealand: BSc Honours in Computing and Mathematical Sciences, PhD in Industrial Magnetohydrodynamics and Master of Science in Statistics.

After completing his PhD in 1998, he joined New Zealand's National Institute for Water and Atmospheric Research as a mathematical modeller. He then completed his Master of Science in Statistics in 2002 and worked as a tutor, lecturer and part time statistical consultant.

Alec joined CSIRO in Canberra in 2006 as a Biometrician. He has particular interests in agricultural and horticultural statistics, particularly the robust design of agricultural/horticultural experiments and field trials and the analysis of datasets arising from such experiments.

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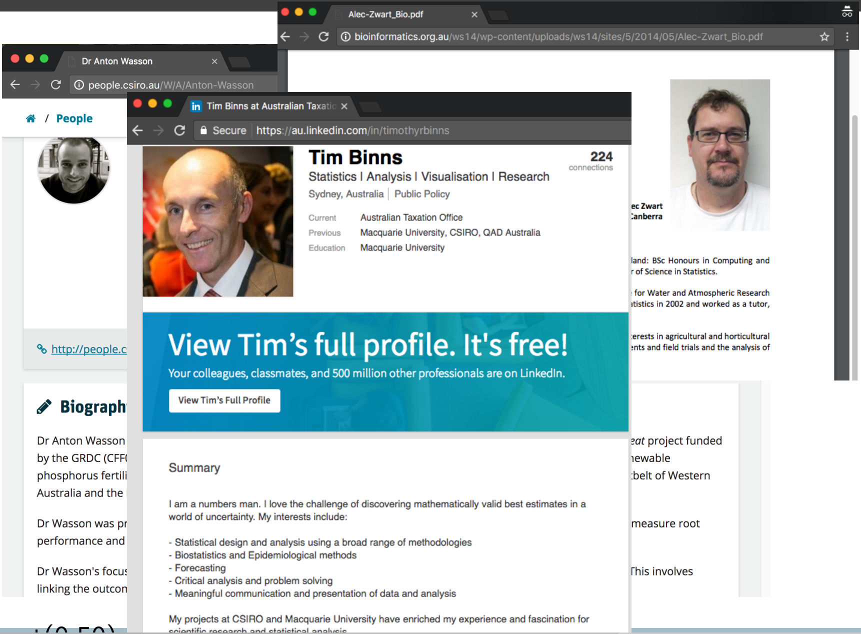

3. Inference: Pre-Chiu vs. Chiu

Pre-Chiu

Pre-Chiu

- collapse t: $w_{ij?} = f(y_{ij?1}, y_{ij?2}, ..., y_{ij?T})$, e.g., $f = \max$
- linear mixed model for $w_{ij?}$

Pre-Chiu

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  - low h^2 (≈ 0.1, I think)

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Chiu

- Don't collapse anything!!!

Pre-Chiu

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Chiu

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- y_{ijkt} longitudinal WRT t
  - 1D spatial Poisson process!
    - but obviously overdispersed $\Longrightarrow$

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    - random intensity curves $\theta_{ij}(t)$

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Chiu

- Don't collapse anything!!!
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    - but obviously overdispersed $\Longrightarrow$
    - random intensity curves $\theta_{ij}(t)$
    - Spatial dependence not yet formally modelled.

Chiu — cont'd

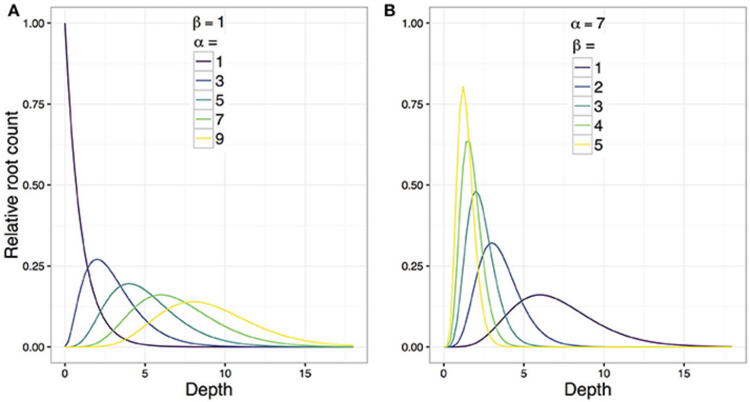

Fig. 4: Gamma probability density $\gamma_{\alpha,\beta}(t) \propto \theta_{\alpha,\beta}(t)$

Chiu — cont'd

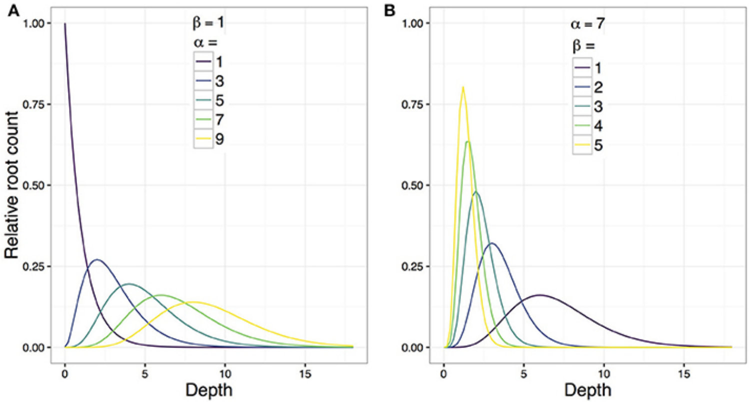

Fig. 4: Gamma probability density $\gamma_{\alpha,\beta}(t) \propto \theta_{\alpha,\beta}(t)$

- $\alpha \leftrightarrow$ root system's bulk
- $\beta \leftrightarrow$ root system's downward exploration/penetration
- (α, β) bivariate

Chiu — cont'd

$$y_{ijkt} \sim \text{Poisson}(\theta_{ij}(t)),$$
$$\theta_{ij}(t) = \psi_{ij} \bullet \gamma_{\alpha_i \beta_i}(t) \bullet e^{\phi_{ijt}}$$
$$\psi_{ij} = e^{\psi_0 + \kappa_j} e^{\tau_i}$$

Chiu — cont'd

$$
\begin{aligned}
y_{ijkt} &\sim \text{Poisson}(\theta_{ij}(t)), \\
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\psi_{ij} &= e^{\psi_0 + \kappa_j} e^{\tau_i}
\end{aligned}
$$

Note: Smooth $\gamma(t)$ but jagged $\theta(t)$ due to ϕ_t

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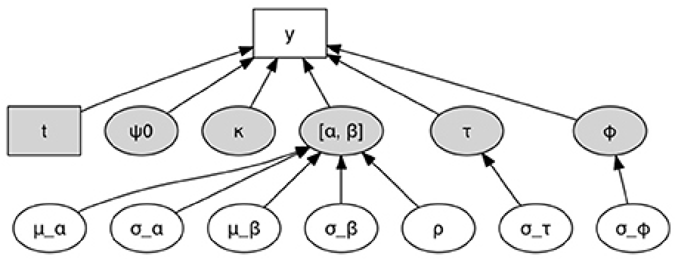


Chiu — cont'd

Binns' internship:

- Zwart and Binns learned Bayesian inference (from me)
- prelim model implementation: Gelman et al.'s *Stan*

After Binns:

- final models in paper: Chiu & Zwart

4. Key insights

First, the punchline. . .

First, the punchline. . .

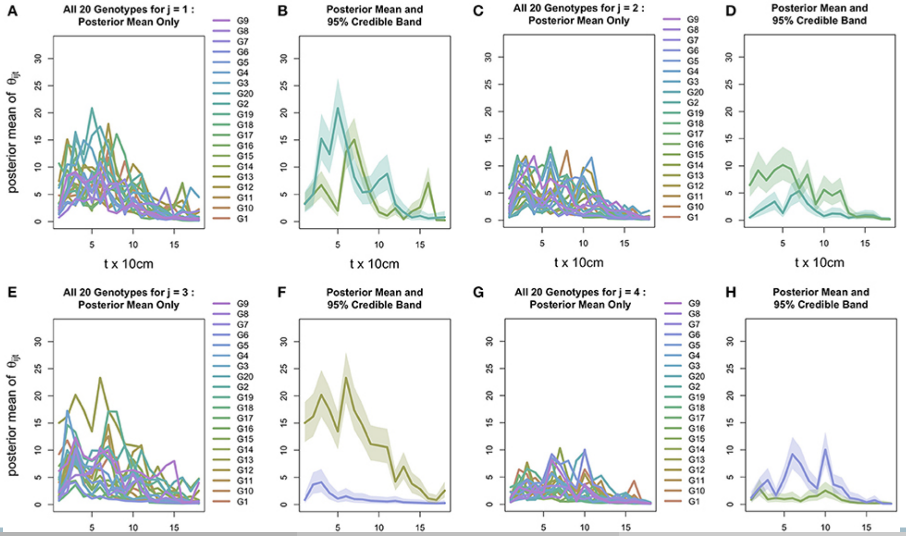
"Our integrative approach can allow selective pre-breeding programs for root distribution and may facilitate the identification of genetic markers from field data."

On to the details. . .

Heritability is high!

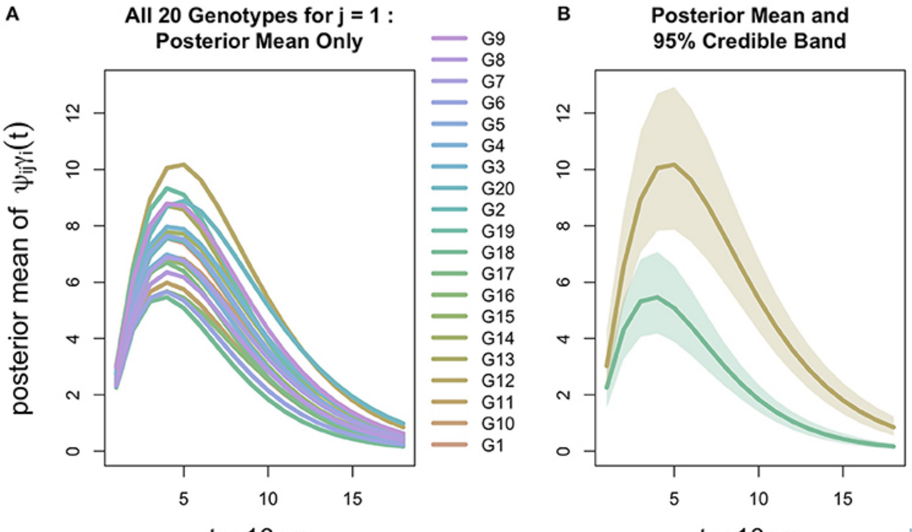
Heritability is high!

Posterior mean intensity curves $\theta_{ij}(t)$ (Fig. 6):



Heritability is high!

Posterior mean idealized intensity curves $\psi_{ij}\gamma_i(t)$ (Fig. 5):



Heritability is high!

More formally:

$$\sigma^2_{\log\theta(t)} = \sigma^2_{\text{genes}}(t) + \sigma^2_\phi$$

$$\sigma^2_{\text{genes}}(t) = \sigma^2_\tau + (\log t)^2(e^{\sigma^2_\alpha} - 1)e^{2\mu_\alpha+\sigma^2_\alpha} + t^2(e^{\sigma^2_\beta} - 1)e^{2\mu_\beta+\sigma^2_\beta} - (t\log t)(e^{\rho\sigma_\alpha\sigma_\beta} - 1)e^{\mu_\alpha+\mu_\beta+(\sigma^2_\alpha+\sigma^2_\beta)/2}$$

$$h^2_h(t) = \frac{\sigma^2_{\text{genes}}(t)}{\sigma^2_{\text{genes}}(t) + \sigma^2_\phi} =$$ depth-specific heritability of intensity function

h^2_h = heritability of overall architecture

= harmonic mean of $h^2_h(t)$

Heritability is high!

More formally:

$$\sigma^2_{\log\theta(t)} = \sigma^2_{\text{genes}}(t) + \sigma^2_\phi$$

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$$h^2_h(t) = \frac{\sigma^2_{\text{genes}}(t)}{\sigma^2_{\text{genes}}(t) + \sigma^2_\phi} = \text{depth-specific heritability of intensity function}$$

$$h^2_h = \text{heritability of overall architecture}$$

$$= \text{harmonic mean of } h^2_h(t)$$

Multiresolution definition

Heritability is high!

$h^2_{\alpha(-\beta)}$ = heritability of root bulk's location (and size) on log scale, ignoring its relation with penetration rate

$$= \text{harmonic mean of } \left\{ \frac{(\log t)^2(e^{\sigma_\alpha^2}-1)e^{2\mu_\alpha+\sigma_\alpha^2}}{(\log t)^2(e^{\sigma_\alpha^2}-1)e^{2\mu_\alpha+\sigma_\alpha^2}+\sigma_\phi^2} \text{ for } t>1 \right\}$$

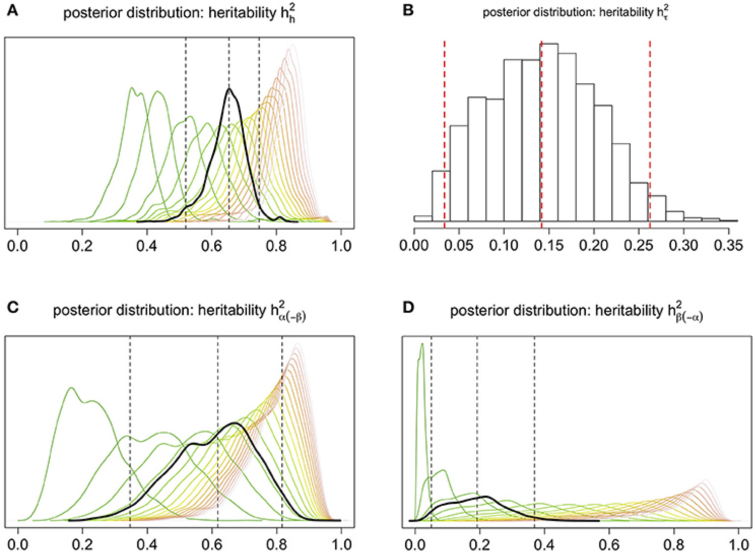
$h^2_{\beta(-\alpha)}$ = heritability of root's decline rate of penetration on log scale, ignoring its relation with bulk location

$$= \text{harmonic mean of } \left\{ \frac{t^2(e^{\sigma_\beta^2}-1)e^{2\mu_\beta+\sigma_\beta^2}}{t^2(e^{\sigma_\beta^2}-1)e^{2\mu_\beta+\sigma_\beta^2}+\sigma_\phi^2} \right\}$$

$$h^2_\tau = \frac{\sigma_\tau^2}{\sigma_\tau^2+\sigma_\phi^2}$$ = heritability of intensity function's intercept on log scale

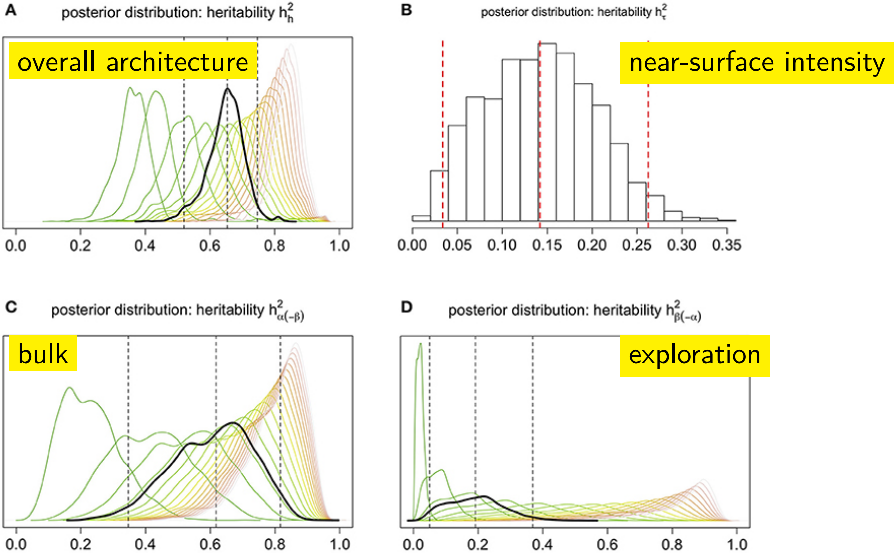
Heritability is high!

Posteriors of heritability metrics (Fig. 7):



Heritability is high!

Posteriors of heritability metrics (Fig. 7):



High heritability of bulking

High heritability of bulking

> *"[It s]uggests that a breeding program could successfully alter the depth at which a root system proliferates."*

Low τ-heritability

Low τ-heritability

"Sampling position [in the field] is likely to have a strong influence on the surface root counts."

Bulking up vs. Exploring

Bulking up vs. Exploring

$0.9 \approx \text{median } P(\ \text{cor}(\alpha_i, \beta_i) > 0 \mid \text{data})$

Bulking up vs. Exploring

$0.9 \approx$ median $P(\text{ cor}(\alpha_i, \beta_i) > 0 \mid \text{data})$

- Tendency to explore downwards negates tendency to bulk up away from surface.

Bulking up vs. Exploring

$0.9 \approx \text{median } P(\text{ cor}(\alpha_i, \beta_i) > 0 \mid \text{data})$

- Tendency to explore downwards negates tendency to bulk up away from surface.
- "*[P]lants have evolved randomness and instability in their root system development (Forde, 2009). . . which may facilitate exploration. . . of the soil for cracks and pores. [O]ur model implies that more branching near the surface gives better access to the subsoil.*"

In closing

Australian National University

In closing

"If a paper uses a t test to solve an environmental research problem that no one else has been able to solve, we will publish it."

— Peter Guttorp in an *Environmetrics* Editorial Board Meeting as Co-Editor-in-Chief

References

Search for `Grace S Chiu` on Google Scholar or Research Gate.