Biological background

GPU-parallel Gibbs sampling of a hierarchical model of hybrid vigor in RNA-seq experiments

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Outline

- Biological background
 - Hybrid vigor
- 2 The model
- The Gibbs sampler
 - Gibbs steps
 - Estimated heterosis probabilities
 - GPU parallelism
- The software

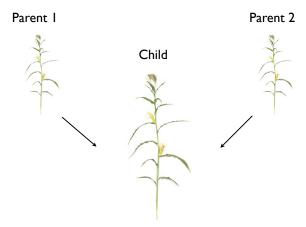
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Biological background

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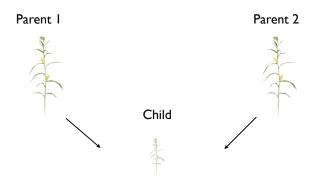
High-parent heterosis: child's trait surpasses both parents



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Low-parent heterosis: child's trait is weaker than in each parent

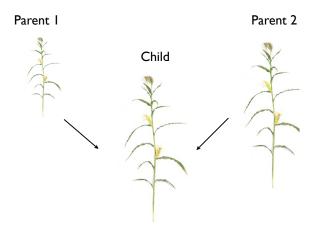


The software

Mid-parent heterosis: child's trait is different than average of parents

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High-parent heterosis in gene expression

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	Parent I			Child		Parent 2	
Gene I	100	225	0	70	279	300	106
Gene 2	0	ı	ı	50	501	2	7
Gene 3	3	4	2	700	900	0	0
Gene 4	893	400	760	5	5	1000	513
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Gene 34897	10	13	6	819	761	902	912

Low-parent heterosis in gene expression

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	Parent I			Child		Parent 2	
Gene I	100	225	0	70	279	300	106
Gene 2	0	1	1	50	501	2	7
Gene 3	3	4	2	700	900	0	0
Gene 4	893	400	760	5	5	1000	513
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Mid-parent heterosis in gene expression

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$$\begin{split} \mu(\textbf{\textit{n}},\phi_{\textbf{\textit{g}}},\alpha_{\textbf{\textit{g}}},\delta_{\textbf{\textit{g}}}) &= \begin{cases} \phi_{\textbf{\textit{g}}} - \alpha_{\textbf{\textit{g}}} & \text{sample n from parent 1} \\ \phi_{\textbf{\textit{g}}} + \delta_{\textbf{\textit{g}}} & \text{sample n from child} \\ \phi_{\textbf{\textit{g}}} + \alpha_{\textbf{\textit{g}}} & \text{sample n from parent 2} \end{cases} \\ y_{\textbf{\textit{g}},\textbf{\textit{n}}} &\stackrel{\text{ind}}{\sim} \mathsf{Poisson}(\exp(c_{\textbf{\textit{n}}} + \varepsilon_{\textbf{\textit{g}},\textbf{\textit{n}}} + \mu(\textbf{\textit{n}},\phi_{\textbf{\textit{g}}},\alpha_{\textbf{\textit{g}}},\delta_{\textbf{\textit{g}}}))) \\ c_{\textbf{\textit{n}}} &\stackrel{\text{ind}}{\sim} \mathsf{N}(0,\sigma_{\textbf{\textit{c}}}^2) \\ \sigma_{\textbf{\textit{c}}} \sim \mathsf{U}(0,\sigma_{\textbf{\textit{c}}0}) \\ \varepsilon_{\textbf{\textit{g}},\textbf{\textit{n}}} &\stackrel{\text{ind}}{\sim} \mathsf{N}(0,\eta_{\textbf{\textit{g}}}^2) \\ \eta_{\textbf{\textit{g}}}^2 &\stackrel{\text{ind}}{\sim} \mathsf{Inv-Gamma} \left(\mathsf{shape} = \frac{d}{2} \;,\; \mathsf{rate} = \frac{d \cdot \tau^2}{2} \right) \\ d \sim \mathsf{U}(0,d_0) \\ \tau^2 \sim \mathsf{Gamma}(\mathsf{shape} = a_\tau,\mathsf{rate} = b_\tau) \end{split}$$

 $\theta_s \sim N(0, \gamma_s^2)$ $\sigma_s \sim U(0, \sigma_{so})$ $\pi_s \sim \text{Beta}(a_s, b_s)$

The model

Biological background

$$\mu(n,\phi_g,\alpha_g,\delta_g) = \begin{cases} \phi_g - \alpha_g & \text{sample } n \text{ from parent } 1 \\ \phi_g + \delta_g & \text{sample } n \text{ from child} \\ \phi_g + \alpha_g & \text{sample } n \text{ from parent } 2 \end{cases}$$

$$y_{g,n} \stackrel{\text{ind}}{\sim} \text{Poisson}(\exp(c_n + \varepsilon_{g,n} + \mu(n,\phi_g,\alpha_g,\delta_g)))$$

$$\phi_g \stackrel{\text{ind}}{\sim} \text{N}(\theta_\phi,\sigma_\phi^2)$$

$$\theta_\phi \sim \text{N}(0,\gamma_\phi^2)$$

$$\sigma_\phi \sim \text{U}(0,\sigma_{\phi0})$$

$$\alpha_g \stackrel{\text{ind}}{\sim} (1 - I(\alpha_g)) \cdot \pi_\alpha + I(\alpha_g) \cdot (1 - \pi_\alpha) \cdot \text{N}(\alpha_g \mid \theta_\alpha,\sigma_\alpha^2)$$

$$\theta_\alpha \sim \text{N}(0,\gamma_\alpha^2)$$

$$\sigma_\alpha \sim \text{U}(0,\sigma_{\alpha0})$$

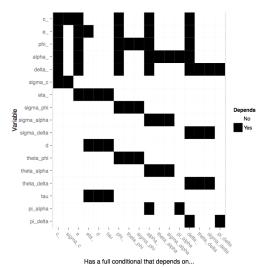
$$\pi_\alpha \sim \text{Beta}(a_\alpha,b_\alpha)$$

 $\delta_{g} \stackrel{\text{ind}}{\sim} (1 - I(\delta_{g})) \cdot \pi_{\delta} + I(\delta_{g}) \cdot (1 - \pi_{\delta}) \cdot \mathsf{N}(\delta_{g} \mid \theta_{\delta}, \sigma_{\delta}^{2})$

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Partition parameters by conditional independence.



Use these partitions as Gibbs steps.

$$y_{g,n} \stackrel{\text{ind}}{\sim} \mathsf{Poisson}(\mathsf{exp}(c_n + \varepsilon_{g,n} + \mu(n, \phi_g, \alpha_g, \delta_g)))$$

- From the appropriate full conditional distributions, sample the following:
- $\mathbf{0}$ c_1, \ldots, c_N

- \bullet τ , π_{α} , π_{δ}
- \bullet d, θ_{ϕ} , θ_{α} , θ_{δ}
- \bullet σ_c , σ_ϕ , σ_α , σ_δ , η_1^2 , ..., η_c^2
- \bullet $\varepsilon_{1,1}, \ \varepsilon_{1,2}, \ \ldots, \ \varepsilon_{1,N}, \ \varepsilon_{2,N}, \ \ldots, \ \varepsilon_{G,N}$
- $\mathbf{0}$ ϕ_1, \ldots, ϕ_G
- $\alpha_1, \ldots, \alpha_G$
- $\delta_1, \ldots, \delta_G$
 - and then repeat.

Estimated heterosis probabilities

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$$\mu(\textit{n}, \phi_{\textit{g}}, \alpha_{\textit{g}}, \delta_{\textit{g}}) = \begin{cases} \phi_{\textit{g}} - \alpha_{\textit{g}} & \text{sample } \textit{n} \text{ from parent } 1 \\ \phi_{\textit{g}} + \delta_{\textit{g}} & \text{sample } \textit{n} \text{ from child} \\ \phi_{\textit{g}} + \alpha_{\textit{g}} & \text{sample } \textit{n} \text{ from parent } 2 \end{cases}$$

$$y_{g,n} \stackrel{\text{ind}}{\sim} \text{Poisson}(\exp(c_n + \varepsilon_{g,n} + \mu(n, \phi_g, \alpha_g, \delta_g)))$$

Consider one chain with M iterations.

$$P(\text{high-parent heterosis in gene } g) \approx \frac{1}{M} \sum_{i=1}^{M} I(\delta_g^{(i)} > |\alpha_g^{(i)}|)$$

$$P(ext{low-parent heterosis in gene } g \) pprox rac{1}{M} \sum_{i=1}^{M} I(\delta_g^{(i)} < -|lpha_g^{(i)}|)$$

$$P(\text{mid-parent heterosis in gene } g) \approx \frac{1}{M} \sum_{i=1}^{M} I(\delta_g^{(i)} \neq 0)$$

Tons of opportunity for GPU parallelism across genes!

$$y_{g,n} \stackrel{\text{ind}}{\sim} \text{Poisson}(\exp(c_n + \varepsilon_{g,n} + \mu(n, \phi_g, \alpha_g, \delta_g)))$$

- Sample in parallel:
 - ϕ_{ε} 's

- α_g's
- δ_{g} 's
- $\varepsilon_{g,n}$'s
- η_g's

Example: ϕ_{σ} 's

$$y_{g,n} \stackrel{\text{ind}}{\sim} \text{Poisson}(\exp(c_n + \varepsilon_{g,n} + \mu(n, \phi_g, \alpha_g, \delta_g)))$$

$$\phi_g \stackrel{\text{ind}}{\sim} \text{N}(\theta_{\phi}, \sigma_{\phi}^2)$$

$$\theta_{\phi} \sim \text{N}(0, \gamma_{\phi}^2)$$

$$\sigma_{\phi} \sim \text{U}(0, \sigma_{\phi 0})$$

The Gibbs sampler

ullet Using parallel random walk Metropolis steps, sample the ϕ_g 's from their full conditional distributions,

$$p(\phi_g \mid \cdots) \propto \exp\left(\sum_{n=1}^{N} \left[y_{g,n} \cdot \mu(n, \phi_g, \alpha_g, \delta_g)\right] - \exp(c_n + \varepsilon_{g,n} + \mu(n, \phi_g, \alpha_g, \delta_g))\right] - \frac{(\phi_g - \theta_\phi)^2}{2\sigma_\phi^2}$$

Tons of opportunity for GPU parallelism across genes!

$$y_{g,n} \stackrel{\text{ind}}{\sim} \text{Poisson}(\exp(c_n + \varepsilon_{g,n} + \mu(n, \phi_g, \alpha_g, \delta_g)))$$

- Use parallel reductions to calculate sufficient statistics for:
 - C_n's

- τ. d
- θ_{ϕ} , θ_{α} , θ_{δ}
- σ_{ϕ} , σ_{α} , σ_{δ} , σ_{ϵ}
- π_{α} , π_{δ}

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Pairwise summation: an example reduction

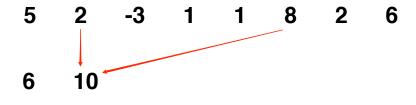
• Let's take the pairwise sum of the vector,

$$(5, 2, -3, 1, 1, 8, 2, 6)$$

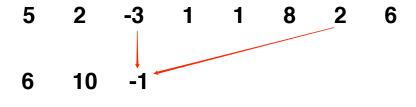
using 1 block of 4 threads.



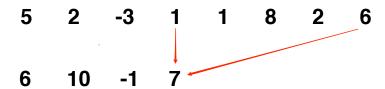
Thread 0



Thread 1



Thread 2



Thread 3

5 2

-3

8

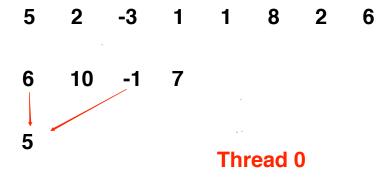
2

6

6 10

-1 7

Synchronize threads



6 10 -1 7 5 17

Thread 1

10

17

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Synchronize Threads

5 2 -3 1 1 8 2 6

6 10 -1 7



Thread 0

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$$\begin{split} y_{g,n} & \overset{\text{ind}}{\sim} \operatorname{Poisson}(\exp(c_n + \varepsilon_{g,n} + \mu(n,\phi_g,\alpha_g,\delta_g))) \\ & \varepsilon_{g,n} \overset{\text{ind}}{\sim} \mathsf{N}(0,\eta_g^2) \\ & \eta_g^2 \overset{\text{ind}}{\sim} \operatorname{Inv-Gamma}\left(\operatorname{shape} = \frac{d}{2} \;,\; \operatorname{rate} = \frac{d \cdot \tau^2}{2}\right) \\ & d \sim \mathsf{U}(0,d_0) \\ & \tau^2 \sim \operatorname{Gamma}(\operatorname{shape} = a_\tau,\operatorname{rate} = b_\tau) \\ & p(\tau^2 \mid \cdots) \\ & = \operatorname{Gamma}\left(\operatorname{shape} = a_\tau + \frac{Gd}{2} \;,\; \operatorname{rate} = b_\tau + \frac{d}{2}\sum_{g=1}^G \frac{1}{\eta_g^2}\right) \end{split}$$

Using a parallel reduction (NVIDIA's CUDA C/C++ Thrust library), calculate the sufficient statistic:

$$\sum_{g=1}^{G} \frac{1}{\eta_g^2}$$

Use an efficient rejection sampler to sample τ^2 .

Example: d

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$$\begin{split} y_{g,n} &\stackrel{\text{ind}}{\sim} \mathsf{Poisson}(\exp(c_n + \varepsilon_{g,n} + \mu(n,\phi_g,\alpha_g,\delta_g))) \\ \varepsilon_{g,n} &\stackrel{\text{ind}}{\sim} \mathsf{N}(0,\eta_g^2) \\ \eta_g^2 &\stackrel{\text{ind}}{\sim} \mathsf{Inv\text{-}Gamma}\left(\mathsf{shape} = \frac{d}{2} \;,\; \mathsf{rate} = \frac{d \cdot \tau^2}{2}\right) \\ d \sim \mathsf{U}(0,d_0) \\ \tau^2 \sim \mathsf{Gamma}(\mathsf{shape} = a_\tau,\mathsf{rate} = b_\tau) \\ p(d \mid \cdots) \propto \Gamma(d/2)^{-G} \left(\frac{d \cdot \tau^2}{2}\right)^{\mathsf{Gd}/2} \left(\prod_{g=1}^G \eta_g^2\right)^{-(d/2+1)} \exp\left(-\frac{d \cdot \tau^2}{2}\sum_{g=1}^G \frac{1}{\eta_g^2}\right) I(0 < d < d_0) \end{split}$$

 Using parallel reductions (NVIDIA's CUDA C/C++ Thrust library), calculate the sufficient statistics:

$$\prod_{g=1}^G \eta_g^2 \qquad \qquad \sum_{g=1}^G \frac{1}{\eta_g^2}$$

• Use a random-walk metropolis step to sample d.

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The software

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• In progress...

The Gibbs sampler

 Slides and video will be available at http://will-landau.com/research.html.

Sources

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