

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

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# Outline

- 1 Biological background
  - Hybrid vigor
- 2 The model
- 3 The Gibbs sampler
  - Gibbs steps
  - Estimated heterosis probabilities
- 4 Acceleration with GPUs
  - An aside on GPUs
  - GPU parallelism in the model
  - Parallel reductions
- 5 The software

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

Parent 1



Parent 2



Child



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

Parent 1



Parent 2



Child



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

Parent 1



Parent 2



Child



# High-parent heterosis in gene expression

	Parent 1			Child		Parent 2	
Gene 1	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
...	...	...	...	...	...	...	...
Gene 34897	10	13	6	819	761	902	912

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# The model

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

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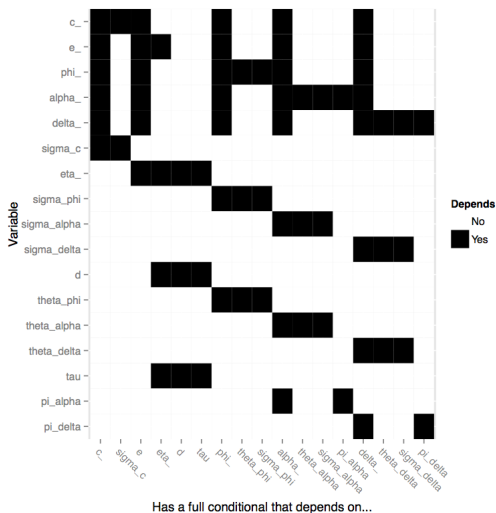
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# Partition parameters by conditional independence.





# Use these partitions as Gibbs steps.

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①  $c_1, \dots, c_N$

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- 5  $\varepsilon_{1,1}, \varepsilon_{1,2}, \dots, \varepsilon_{1,N}, \varepsilon_{2,N}, \dots, \varepsilon_{G,N}$

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- 6  $\phi_1, \dots, \phi_G$

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- 6  $\phi_1, \dots, \phi_G$
- 7  $\alpha_1, \dots, \alpha_G$

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- 4  $\sigma_c, \sigma_\phi, \sigma_\alpha, \sigma_\delta, \eta_1^2, \dots, \eta_G^2$
- 5  $\varepsilon_{1,1}, \varepsilon_{1,2}, \dots, \varepsilon_{1,N}, \varepsilon_{2,N}, \dots, \varepsilon_{G,N}$
- 6  $\phi_1, \dots, \phi_G$
- 7  $\alpha_1, \dots, \alpha_G$
- 8  $\delta_1, \dots, \delta_G$

- and then repeat.



# Estimated heterosis probabilities

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# Outline

- 1 Biological background
  - Hybrid vigor
- 2 The model
- 3 The Gibbs sampler
  - Gibbs steps
  - Estimated heterosis probabilities
- 4 Acceleration with GPUs**
  - An aside on GPUs
  - GPU parallelism in the model
  - Parallel reductions
- 5 The software

# The single instruction, multiple data (SIMD) paradigm

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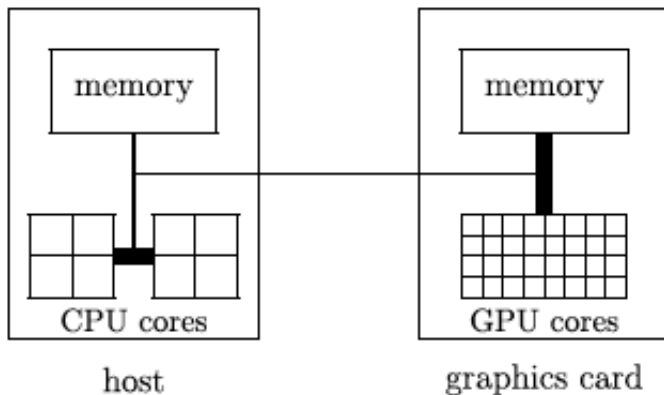
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- We can similarly *parallelize* a lot more than just loops.

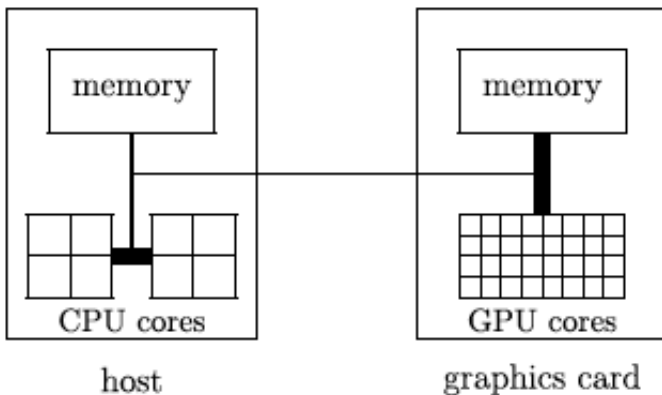
# CPU / GPU cooperation

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- The CPU (“host”) is in charge.
- The CPU sends computationally intensive instruction sets to the GPU (“device”) just like a human uses a pocket calculator.



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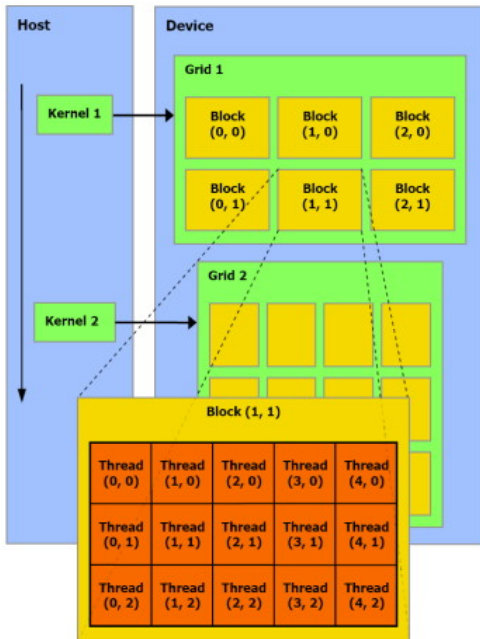
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- I could have also used 1 block with 4 threads and given the threads different pairs of numbers.





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

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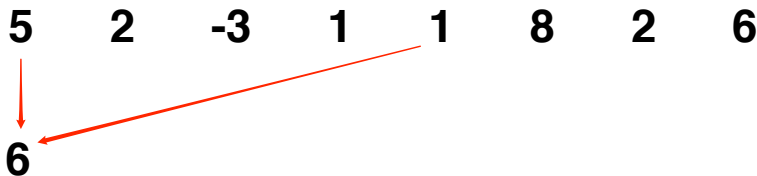
# Parallel reductions

- A **reduction** is an operation on a vector that produces a scalar.
- Repeatedly apply a binary operator to pairs of elements in the vector to get the scalar.
- Let's take the pairwise sum of the vector,

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

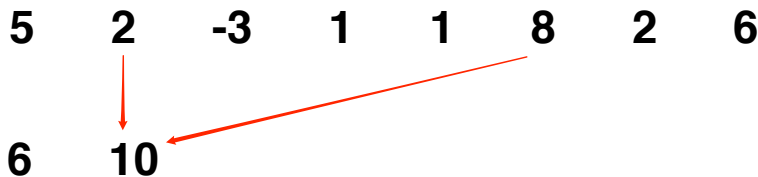
using 1 block of 4 threads.

# Pairwise summation: an example reduction



**Thread 0**

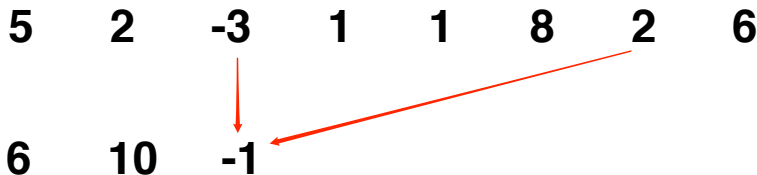
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**Thread 1**




## Pairwise summation: an example reduction



**Thread 2**

# Pairwise summation: an example reduction

5	2	-3	1	1	8	2	6
6	10	-1	7				



**Thread 3**

## Pairwise summation: an example reduction

5      2      -3      1      1      8      2      6

6      10      -1      7

---

**Synchronize threads**

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**Thread 0**

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**Synchronize Threads**

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↓      ↙  
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$$p(\tau^2 \mid \dots)$$

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- Use an efficient rejection sampler to sample  $\tau^2$ .



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

# Outline

- 1 Biological background
  - Hybrid vigor
- 2 The model
- 3 The Gibbs sampler
  - Gibbs steps
  - Estimated heterosis probabilities
- 4 Acceleration with GPUs
  - An aside on GPUs
  - GPU parallelism in the model
  - Parallel reductions
- 5 The software

# The software

- In progress...

# Sources

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