The heterosis problem: a comparison of Eric's method with edgeR, baySeq, and ShrinkBayes

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The heterosis problem: a comparison of Eric's method with edgeR, baySeq, and ShrinkBayes

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Mock heterosis data

			Parei	nt (1))		Pare	nt (2))		Hybr	id (3)		Truth
HPH (Feature 1	3	4	2	1	0	0	1	0	700	900	825	860)	1
HPH (Feature 2	0	1	1	0	2	7	5	18	50	501	400	90		1
	Feature 3	100	225	0	15	300	106	200	400	70	279	100	123		0
LPH (Feature 4	893	400	760	901	1000	513	760	580	5	5	6	7		1
	Feature 25000	10	13	6	4	902	912	999	825	819	761	800	465	-	0

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Simulation workflow

- Simulate 30 datasets:
 - 10 datasets with 4 samples (libraries, columns, etc.) per group
 - ▶ 10 with 8 per group
 - ▶ 10 with 16 per group
- For each simulated dataset, test for heterosis with
 - empirical Bayes with STAN (Eric's method)
 - edgeR
 - baySeq
 - ▶ ShrinkBayes
- Compare methods with ROC curves
- Check FDR control

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Apply edgeR to real data to get simulation parameters

Normalization factors



Main effects and dispersions

Parent (1)	Parent (2)	Hybrid (3)	Dispersion
$\mu_{1,1}$	$\mu_{1,2}$	$\mu_{1,3}$	ψ_1
$\mu_{2,1}$	$\mu_{2,2}$	$\mu_{2,3}$	ψ_2
$\mu_{27888,1}$	$\mu_{27888,2}$	$\mu_{27888,3}$	ψ_{27888}

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Generating the data

▶ Does feature *f* truly have heterosis?

$$\operatorname{truth}_f = I(\mu_{f,3} > \max(\mu_{f,1}, \mu_{f,2}) \text{ or } \mu_{f,3} < \min(\mu_{f,1}, \mu_{f,2}))$$

► For a dataset with 4 libraries per group,

$$y_{f,i} \stackrel{\text{iid}}{\sim} NB \left(\exp \left(c_i + \mu_{f,t(i)} \right), \ \psi_f \right)$$

- \blacktriangleright t(i) is the group of library i.
- ▶ Resimulate to increase the number of libraries per group.
- Remove extremely low-count features.
- ► Take a random subset of 25000 features from the remaining ones.

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Mock example data with 4 samples per treatment group

		Parent (1)				Pare	nt (2))	ı	Hybrid (3)			Truth	
HPH (Feature 1	3	4	2	1	0	0	1	0	700	900	825	860	1
HPH (Feature 2	0	1	1	0	2	7	5	18	50	501	400	90	1
	Feature 3	100	225	0	15	300	106	200	400	70	279	100	123	0
LPH (Feature 4	893	400	760	901	1000	513	760	580	5	5	6	7	1
	Feature 25000	10	13	6	4	902	912	999	825	819	761	800	465	0

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Fit a loglinear model to estimate main effects $\mu_{f,t}$

- Feature f = 1, ..., 25000
- ▶ Treatment group t = 1 (parent), 2 (parent), 3 (hybrid)
- Likelihood ratio tests to get p-values $p_{f,1}$, $p_{f,2}$

$$H_{0,1}: \mu_{f,3} = \mu_{f,1}$$
 $H_{a,1}: \mu_{f,3} \neq \mu_{f,1}$
 $H_{0,2}: \mu_{f,3} = \mu_{f,2}$ $H_{a,2}: \mu_{f,3} \neq \mu_{f,2}$

Final p-value:

$$p_{f, \text{edgeR}} = \begin{cases} p_{f,1}/2 & \widehat{\mu}_{f,3} < \widehat{\mu}_{f,1} \leq \widehat{\mu}_{f,2} \text{ or } \widehat{\mu}_{f,3} > \widehat{\mu}_{f,1} \geq \widehat{\mu}_{f,2} \\ p_{f,2}/2 & \widehat{\mu}_{f,3} < \widehat{\mu}_{f,2} \leq \widehat{\mu}_{f,1} \text{ or } \widehat{\mu}_{f,3} > \widehat{\mu}_{f,2} \geq \widehat{\mu}_{f,1} \\ 1 & \widehat{\mu}_{f,1} \leq \widehat{\mu}_{f,3} \leq \widehat{\mu}_{f,2} \text{ or } \widehat{\mu}_{f,2} \leq \widehat{\mu}_{f,3} \leq \widehat{\mu}_{f,1} \end{cases}$$

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edgeR

- ▶ Built on inla (integrated nested Laplace approximation).
- empirical Bayes with a zero-inflated NB likelihood and normal priors.
- ▶ I reparameterize

$$\begin{split} \phi_f &= \frac{\mu_{f,1} + \mu_{f,2}}{2} \qquad \text{(parental mean)} \\ \alpha_f &= \frac{\mu_{f,2} - \mu_{f,1}}{2} \qquad \text{(half parental difference)} \\ \delta_f &= \mu_{f,3} - \frac{\mu_{f,1} + \mu_{f,2}}{2} \qquad \text{(hybrid effect)} \end{split}$$

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 $\alpha_f = \text{ half parental difference}$ $\delta_f = \text{ hybrid effect}$

Use contrasts to calculate final posterior probabilities of heterosis:

$$p_{f,\mathtt{ShrinkBayes}} = \begin{cases} 0 & \left| \widehat{\delta}_f \right| < \left| \widehat{\alpha}_f \right|, \, \mathtt{o.w.:} \\ P(\delta_f + \alpha_f > 0 \mid \mathtt{data}) & \widehat{\delta}_f > -\widehat{\alpha}_f \\ P(\delta_f - \alpha_f > 0 \mid \mathtt{data}) & \widehat{\delta}_f > \widehat{\alpha}_f \\ P(\delta_f - \alpha_f < 0 \mid \mathtt{data}) & \widehat{\delta}_f < \widehat{\alpha}_f \\ P(\delta_f + \alpha_f < 0 \mid \mathtt{data}) & \widehat{\delta}_f < -\widehat{\alpha}_f \end{cases}$$

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- ▶ Estimate main effects $\mu_{f,t}$ using edgeR.
- Calculate the posterior probability that each feature satisfies:

Model	Constraint
M_1	All $\mu_{f,t}$'s equal
M_2	$\mu_{f,1} = \mu_{f,2}$
M_3	$\mu_{f,1} = \mu_{f,3}$
M_4	$\mu_{f,2} = \mu_{f,3}$
M_5	All $\mu_{f,t}$'s distinct

► Final posterior probabilities of heterosis:

$$p_{f, \text{baySeq}} = \begin{cases} 0 & \widehat{\mu}_{f, 1} \leq \widehat{\mu}_{f, 3} \leq \widehat{\mu}_{f, 2} \text{ or} \\ & \widehat{\mu}_{f, 2} \leq \widehat{\mu}_{f, 3} \leq \widehat{\mu}_{f, 1} \end{cases}$$

$$P(M_2 \mid \text{data}) + P(M_5 \mid \text{data}) & \text{otherwise}$$

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Calculating false positive rate (FPR) and true positive rate (TPR)

- ROC = Receiver Operating Characteristic
- N_{true} heterosis features, N_{false} null features.
- Results of testing each feature for heterosis
 - For edgeR, the ranks are p-values.
 - For the other methods, take p(no heterosis | data) for each feature.

rank	0.802	0.935	0.539	0.001		0.500	0.603
truth	0	0	1	1		1	0

Sort by rank.

rank	0.000	0.001	0.005	0.006	 0.901	1.000
truth	1	1	0	1	 0	0

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▶ In practice, we would declare the lowest-rank features to have heterosis.

rank	0.000	0.001	0.005	0.006	 0.901	1.000
truth	1	1	0	1	 0	0

With 2 heterosis genes and 1 null gene, say,

$$FPR = \frac{1}{N_{false}}$$
 $TPR = \frac{2}{N_{true}}$

 Repeat for multiple cutoffs to get multiple (FPR, TPR) pairs.

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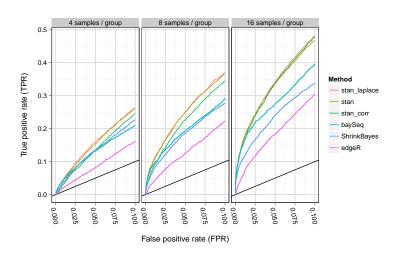
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Example ROC curves

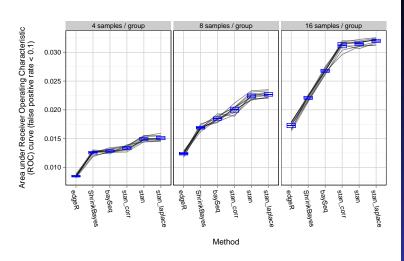


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Constructing ROC curves

Areas under ROC curves



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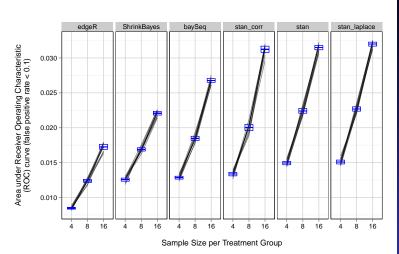
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ROC results

- Let $p_{(f)}$ (f = 1, ..., 25000) be the ordered ranks
 - For edgeR, the ranks are now q-values.
 - For the other methods, take p(no heterosis | data) for each feature.
- ▶ Let $I_{(f)} = I$ (feature of $p_{(f)}$ is not heterosis)
- ► Method 1:

$$\overline{p}_m = \frac{1}{m} \sum_{f=1}^m p_{(f)} \qquad \overline{l}_m = \frac{1}{m} \sum_{f=1}^m l_{(f)}$$

- ▶ To control FDR, we need $\overline{I}_m \leq \overline{p}_m$.
- ▶ Plot $\overline{I}_m \overline{p}_m$ vs \overline{p}_m for multiple m.
- ► Method 2:

$$\overline{p}_m = \frac{1}{100} \sum_{f=m}^{m+100} p_{(f)} \qquad \overline{I}_m = \frac{1}{100} \sum_{f=m}^{m+100} I_{(f)}$$

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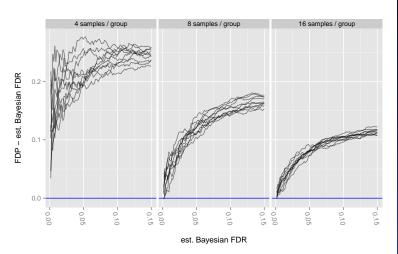
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Method 1: stan_laplace



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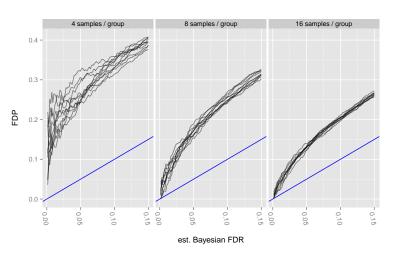
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Method 1: stan_laplace



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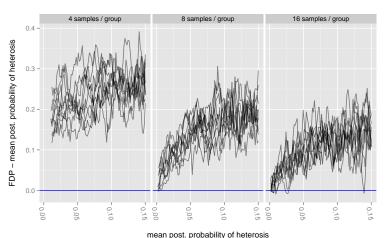
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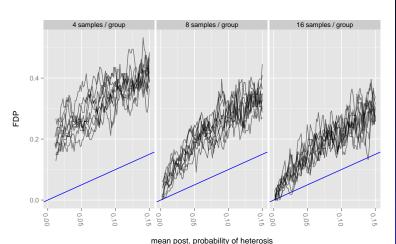
Method 2: stan_laplace



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Method 2: stan_laplace



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