

Lecture 12: Normal Means & Multiple Testing

Merlise Clyde

October 11



Normal Means Model

Suppose we have normal data with

$$Y_i \mid \mu_i, \sigma^2 \stackrel{iid}{\sim} (\mu_i, \sigma^2)$$



Normal Means Model

Suppose we have normal data with

$$Y_i \mid \mu_i, \sigma^2 \stackrel{iid}{\sim} (\mu_i, \sigma^2)$$

- Means Model $\mu_i \stackrel{iid}{\sim} g$, "random effects" distribution



Normal Means Model

Suppose we have normal data with

$$Y_i \mid \mu_i, \sigma^2 \stackrel{iid}{\sim} (\mu_i, \sigma^2)$$

- Means Model $\mu_i \stackrel{iid}{\sim} g$, "random effects" distribution

Multiple Testing

- $H_{0i} : \mu_i = 0$ versus $H_{1i} : \mu_i \neq 0$



Normal Means Model

Suppose we have normal data with

$$Y_i \mid \mu_i, \sigma^2 \stackrel{iid}{\sim} (\mu_i, \sigma^2)$$

- Means Model $\mu_i \stackrel{iid}{\sim} g$, "random effects" distribution

Multiple Testing

- $H_{0i} : \mu_i = 0$ versus $H_{1i} : \mu_i \neq 0$
- n hypotheses that may potentially be closely related, e.g. H_{01} no difference in expression gene i between cases and controls, for n genes



Strategy Ia

- p-value, p_i , or testing H_{0i} versus H_{1i} for each i



Strategy Ia

- p-value, p_i , or testing H_{0i} versus H_{1i} for each i
- $p_i < \alpha$ implies reject H_{0i} in favor of H_{1i} , e.g. $\alpha = 0.05$



Strategy Ia

- p-value, p_i , or testing H_{0i} versus H_{1i} for each i
- $p_i < \alpha$ implies reject H_{0i} in favor of H_{1i} , e.g. $\alpha = 0.05$

Limitations?



Strategy Ia

- p-value, p_i , or testing H_{0i} versus H_{1i} for each i
- $p_i < \alpha$ implies reject H_{0i} in favor of H_{1i} , e.g. $\alpha = 0.05$

Limitations?

- overall lots of type I errors potentially in testing over and over again



Strategy Ia

- p-value, p_i , or testing H_{0i} versus H_{1i} for each i
- $p_i < \alpha$ implies reject H_{0i} in favor of H_{1i} , e.g. $\alpha = 0.05$

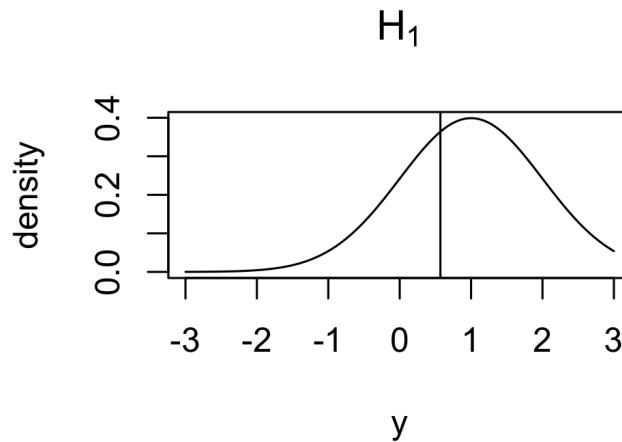
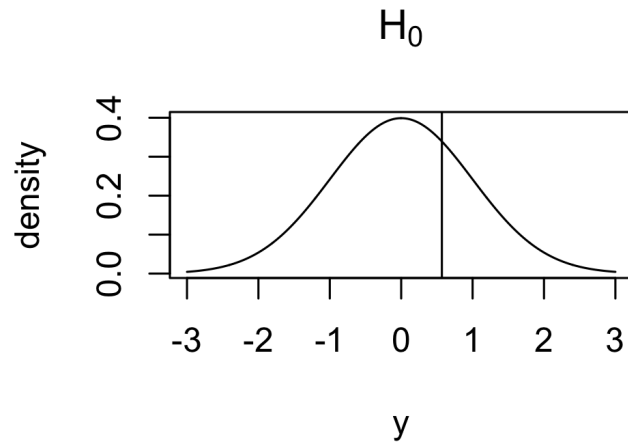
Limitations?

- overall lots of type I errors potentially in testing over and over again
- α is the probability of making a type I error in an individual test, but not the probability of the family-wise type 1 error, e.g. the probability of making at least one type 1 error in the n tests)



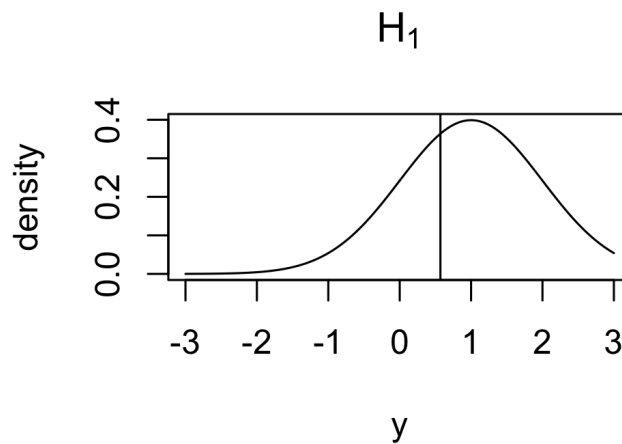
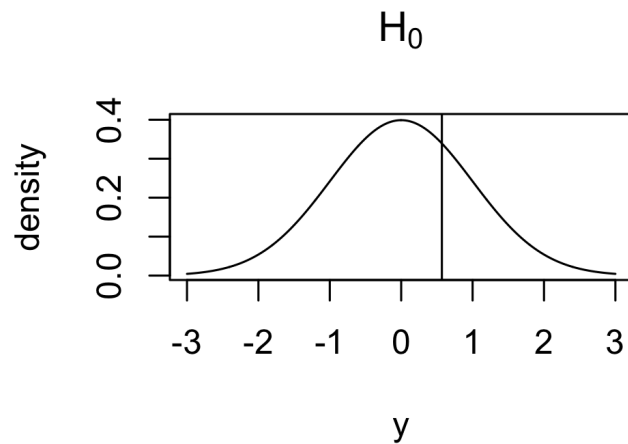
Power

- very low power (high type II error rate) because we have a single observation per hypothesis



Power

- very low power (high type II error rate) because we have a single observation per hypothesis

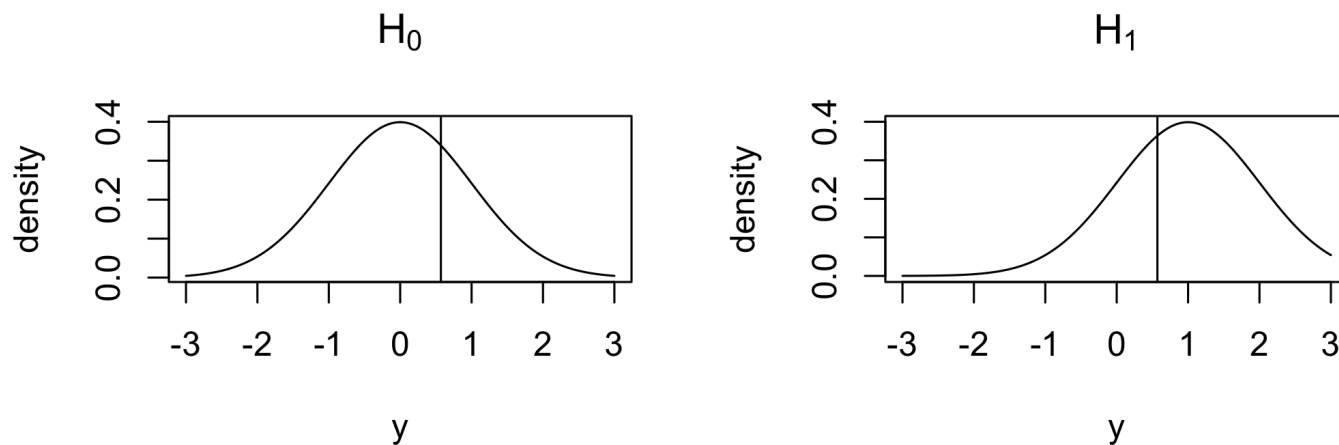


- low power unless we have good separation between the two distributions (large difference relative to noise)



Power

- very low power (high type II error rate) because we have a single observation per hypothesis



- low power unless we have good separation between the two distributions (large difference relative to noise)
- low power may actually lead to very few type I errors even in multiple testing but often still lots of type I and type II errors



Strategy 1b

Adjust the level of each test to reflect how many tests you are conducting

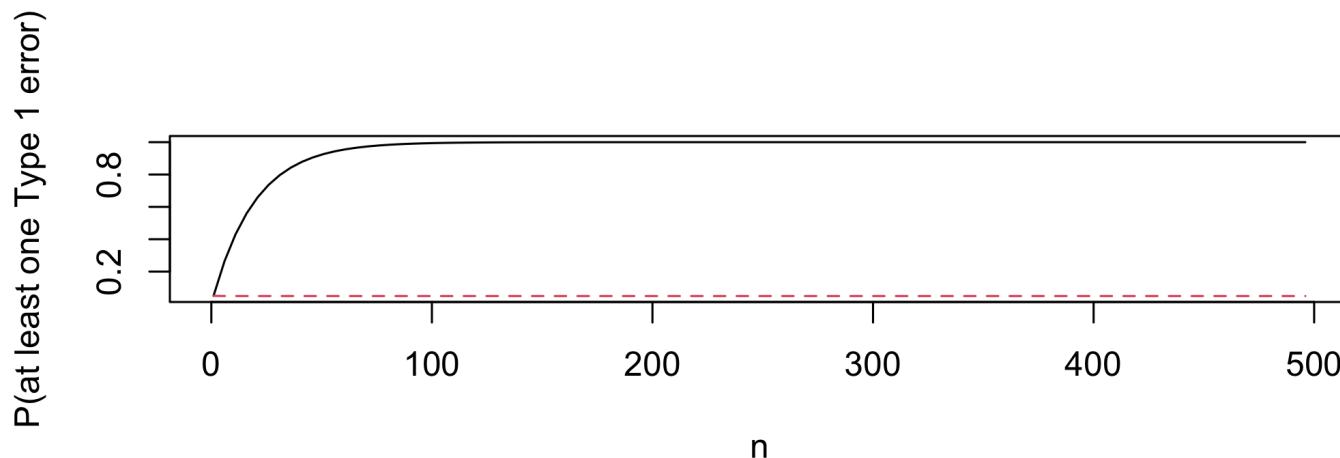


Strategy 1b

Adjust the level of each test to reflect how many tests you are conducting

- Probability of at least one Type I error if tests are independent

$$1 - \Pr(0 \text{ Type I errors in } n \text{ tests}) = 1 - (1 - \alpha)^n$$



- to control the increase in Type I errors with n we may need to decrease the α threshold with n



Classical Strategy

- control the family-wise error rate. Assuming independence across tests (reality ?) replace α with α/n



Classical Strategy

- control the family-wise error rate. Assuming independence across tests (reality ?) replace α with α/n

Bonferroni correction: keeps overall family wise error at α



Classical Strategy

- control the family-wise error rate. Assuming independence across tests (reality ?) replace α with α/n

Bonferroni correction: keeps overall family wise error at α

- if we have 10,000 tests $\alpha_{\text{Bon}} = 0.05/10000$ very small



Classical Strategy

- control the family-wise error rate. Assuming independence across tests (reality ?) replace α with α/n

Bonferroni correction: keeps overall family wise error at α

- if we have 10,000 tests $\alpha_{\text{Bon}} = 0.05/10000$ very small
- in the extremely low power setting, probably very few tests exceed the new threshold (conservative)



False Discovery Rate (FDR)

- FDR threshold α_{FDR}



False Discovery Rate (FDR)

- FDR threshold α_{FDR}
- if $p_i < \alpha_{\text{FDR}}$, call this a "discovery"



False Discovery Rate (FDR)

- FDR threshold α_{FDR}
- if $p_i < \alpha_{\text{FDR}}$, call this a "discovery"
- collect all of our discoveries, say 100 out of 10,000 genes



False Discovery Rate (FDR)

- FDR threshold α_{FDR}
- if $p_i < \alpha_{\text{FDR}}$, call this a "discovery"
- collect all of our discoveries, say 100 out of 10,000 genes
- we want that the proportion of discoveries that are false (i.e H_0 was actually true) to be small



False Discovery Rate (FDR)

- FDR threshold α_{FDR}
- if $p_i < \alpha_{\text{FDR}}$, call this is a "discovery"
- collect all of our discoveries, say 100 out of 10,000 genes
- we want that the proportion of discoveries that are false (i.e H_0 was actually true) to be small
- control the proportion of false discoveries at level α instead of individual p-values



False Discovery Rate (FDR)

- FDR threshold α_{FDR}
- if $p_i < \alpha_{\text{FDR}}$, call this is a "discovery"
- collect all of our discoveries, say 100 out of 10,000 genes
- we want that the proportion of discoveries that are false (i.e H_0 was actually true) to be small
- control the proportion of false discoveries at level α instead of individual p-values
- Benjamini & Hochberg (BH) (1995 JRSS-B) propose a simple choice for α_{FDR} based on n and assuming n independent tests



False Discovery Rate (FDR)

- FDR threshold α_{FDR}
- if $p_i < \alpha_{\text{FDR}}$, call this is a "discovery"
- collect all of our discoveries, say 100 out of 10,000 genes
- we want that the proportion of discoveries that are false (i.e H_0 was actually true) to be small
- control the proportion of false discoveries at level α instead of individual p-values
- Benjamini & Hochberg (BH) (1995 JRSS-B) propose a simple choice for α_{FDR} based on n and assuming n independent tests
- Issue: we will still have lower power in this low data scenario!



False Discovery Rate (FDR)

- FDR threshold α_{FDR}
- if $p_i < \alpha_{\text{FDR}}$, call this is a "discovery"
- collect all of our discoveries, say 100 out of 10,000 genes
- we want that the proportion of discoveries that are false (i.e H_0 was actually true) to be small
- control the proportion of false discoveries at level α instead of individual p-values
- Benjamini & Hochberg (BH) (1995 JRSS-B) propose a simple choice for α_{FDR} based on n and assuming n independent tests
- Issue: we will still have lower power in this low data scenario!
- Borrow strength!



Strategy II: Hierarchical Model

$$Y_i \mid \mu_i, \sigma^2 \stackrel{iid}{\sim} (\mu_i, \sigma^2)$$
$$\mu_i \stackrel{iid}{\sim} g$$



Strategy II: Hierarchical Model

$$Y_i \mid \mu_i, \sigma^2 \stackrel{iid}{\sim} (\mu_i, \sigma^2)$$
$$\mu_i \stackrel{iid}{\sim} g$$

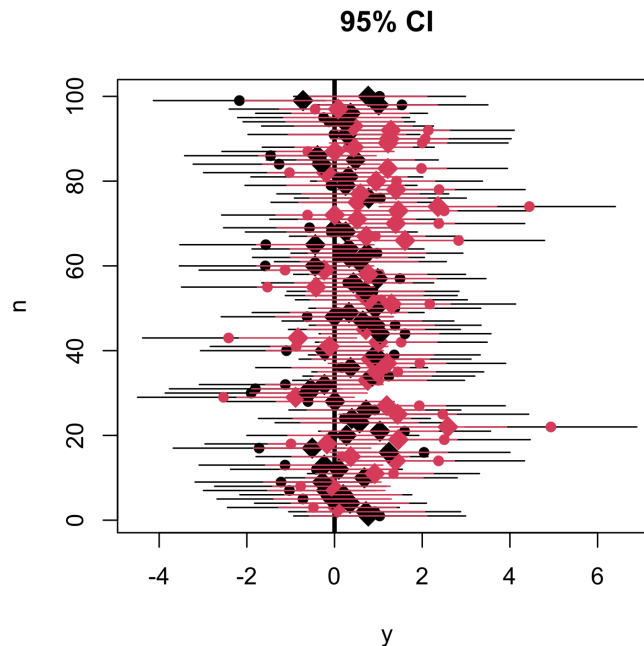
- naive approach: choose g as $N(\mu, \sigma_\mu^2)$ & estimate μ and σ_μ^2 (Empirical Bayes) $\hat{\mu} = \bar{y}$ and $s_y^2 = 1 + \hat{\sigma}_\mu^2$, so $\hat{\sigma}_\mu^2 = \max(0, 1 - s_y^2)$



Strategy II: Hierarchical Model

$$Y_i \mid \mu_i, \sigma^2 \stackrel{iid}{\sim} (\mu_i, \sigma^2)$$
$$\mu_i \stackrel{iid}{\sim} g$$

- naive approach: choose g as $N(\mu, \sigma_\mu^2)$ & estimate μ and σ_μ^2 (Empirical Bayes) $\hat{\mu} = \bar{y}$ and $s_y^2 = 1 + \hat{\sigma}_\mu^2$, so $\hat{\sigma}_\mu^2 = \max(0, 1 - s_y^2)$



Informal approach to testing

- Conclude in favor of H_{1i} if $0 \notin (\mu_{Li}, \mu_{Ui})$



Informal approach to testing

- Conclude in favor of H_{1i} if $0 \notin (\mu_{Li}, \mu_{Ui})$
- otherwise fail to reject



Informal approach to testing

- Conclude in favor of H_{1i} if $0 \notin (\mu_{Li}, \mu_{Ui})$
- otherwise fail to reject

Question: Do we expect this approach to have a huge Type I error rate exploding with n (# tests)? Why or why not?

- shrinkage and borrowing of information leads to narrower CI



Informal approach to testing

- Conclude in favor of H_{1i} if $0 \notin (\mu_{Li}, \mu_{Ui})$
- otherwise fail to reject

Question: Do we expect this approach to have a huge Type I error rate exploding with n (# tests)? Why or why not?

- shrinkage and borrowing of information leads to narrower CI
- information from the other y_i s enters into the posterior for μ_i through the estimates of μ and σ_μ^2



Informal approach to testing

- Conclude in favor of H_{1i} if $0 \notin (\mu_{Li}, \mu_{Ui})$
- otherwise fail to reject

Question: Do we expect this approach to have a huge Type I error rate exploding with n (# tests)? Why or why not?

- shrinkage and borrowing of information leads to narrower CI
- information from the other y_i s enters into the posterior for μ_i through the estimates of μ and σ_μ^2

$$\mu_i \mid y_1, \dots, y_n \sim N \left(\frac{y_i + \hat{\mu}/\hat{\sigma}_\mu^2}{1 + 1/\hat{\sigma}_\mu^2}, \frac{1}{1 + 1/\hat{\sigma}_\mu^2} \right)$$



Informal approach to testing

- Conclude in favor of H_{1i} if $0 \notin (\mu_{Li}, \mu_{Ui})$
- otherwise fail to reject

Question: Do we expect this approach to have a huge Type I error rate exploding with n (# tests)? Why or why not?

- shrinkage and borrowing of information leads to narrower CI
- information from the other y_i s enters into the posterior for μ_i through the estimates of μ and σ_μ^2

$$\mu_i \mid y_1, \dots, y_n \sim N \left(\frac{y_i + \hat{\mu}/\hat{\sigma}_\mu^2}{1 + 1/\hat{\sigma}_\mu^2}, \frac{1}{1 + 1/\hat{\sigma}_\mu^2} \right)$$

- when σ_μ^2 is small credible intervals are much narrower than with MLE



Hypothetical Setting

- first $i = 1, 2, 3$ "signals" (H_{1i} is true)



Hypothetical Setting

- first $i = 1, 2, 3$ "signals" (H_{1i} is true)
- add $n - 3$ nulls (H_{0i} is true)



Hypothetical Setting

- first $i = 1, 2, 3$ "signals" (H_{1i} is true)
- add $n - 3$ nulls (H_{0i} is true)

Does throwing in more nulls lead to more Type I errors?

- what happens to $\hat{\mu}$ and $\hat{\sigma}_{\mu}^2$?
- what happens to the credible intervals?



Informal Approach B

- an issue with the $N(\mu, \sigma_\mu^2)$ for g in the hypothetical setting is that it can capture only noise and not the signals. (signals are outliers under normal model)



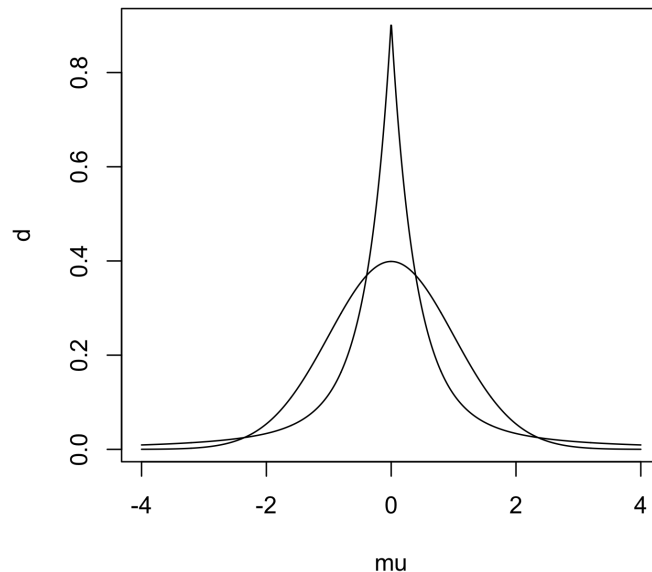
Informal Approach B

- an issue with the $N(\mu, \sigma_\mu^2)$ for g in the hypothetical setting is that it can capture only noise and not the signals. (signals are outliers under normal model)
- choose a more flexible g to capture both noise and signal!



Informal Approach B

- an issue with the $N(\mu, \sigma_\mu^2)$ for g in the hypothetical setting is that it can capture only noise and not the signals. (signals are outliers under normal model)
- choose a more flexible g to capture both noise and signal!



Local-Global Scale Mixtures of Normals

Local scale

$$\begin{aligned}\mu_i \mid \lambda_i, \tau &\sim N(0, \lambda_i \tau) \\ \lambda_i &\sim f \quad \text{local-scale} \\ \tau &\sim h \quad \text{global-scale}\end{aligned}$$



Local-Global Scale Mixtures of Normals

Local scale

$$\begin{aligned}\mu_i \mid \lambda_i, \tau &\sim N(0, \lambda_i \tau) \\ \lambda_i &\sim f \quad \text{local-scale} \\ \tau &\sim h \quad \text{global-scale}\end{aligned}$$

- density that is concentration around zero to shrink noise to zero



Local-Global Scale Mixtures of Normals

Local scale

$$\begin{aligned}\mu_i \mid \lambda_i, \tau &\sim N(0, \lambda_i \tau) \\ \lambda_i &\sim f \quad \text{local-scale} \\ \tau &\sim h \quad \text{global-scale}\end{aligned}$$

- density that is concentration around zero to shrink noise to zero
- heavy tails avoid over-shrinkage of signals (want heavier than normal)



Local-Global Scale Mixtures of Normals

Local scale

$$\begin{aligned}\mu_i \mid \lambda_i, \tau &\sim N(0, \lambda_i \tau) \\ \lambda_i &\sim f \quad \text{local-scale} \\ \tau &\sim h \quad \text{global-scale}\end{aligned}$$

- density that is concentration around zero to shrink noise to zero
- heavy tails avoid over-shrinkage of signals (want heavier than normal)
- Includes:
 - horseshoe
 - generalized double pareto
 - Dirichlet Laplace



Note

- a single Gaussian or Double Exponential prior (Bayes Lasso) have exponential tails same as likelihood (in the normal means problem)



Note

- a single Gaussian or Double Exponential prior (Bayes Lasso) have exponential tails same as likelihood (in the normal means problem)
- single parameter controls tail behaviour and concentration at zero



Note

- a single Gaussian or Double Exponential prior (Bayes Lasso) have exponential tails same as likelihood (in the normal means problem)
- single parameter controls tail behaviour and concentration at zero
- will overshrink the signal if there are many noise cases



Note

- a single Gaussian or Double Exponential prior (Bayes Lasso) have exponential tails same as likelihood (in the normal means problem)
- single parameter controls tail behaviour and concentration at zero
- will overshrink the signal if there are many noise cases
- Good shrinkage prior allows separate control of the concentration around zero and tails



Note

- a single Gaussian or Double Exponential prior (Bayes Lasso) have exponential tails same as likelihood (in the normal means problem)
- single parameter controls tail behaviour and concentration at zero
- will overshrink the signal if there are many noise cases
- Good shrinkage prior allows separate control of the concentration around zero and tails
- tails need to exhibit bounded influence



Note

- a single Gaussian or Double Exponential prior (Bayes Lasso) have exponential tails same as likelihood (in the normal means problem)
- single parameter controls tail behaviour and concentration at zero
- will overshrink the signal if there are many noise cases
- Good shrinkage prior allows separate control of the concentration around zero and tails
- tails need to exhibit bounded influence
- continuous versions/relaxations of a spike and slab prior

$$\mu_i \sim \pi_0 \delta_0 + (1 - \pi)g$$



Note

- a single Gaussian or Double Exponential prior (Bayes Lasso) have exponential tails same as likelihood (in the normal means problem)
- single parameter controls tail behaviour and concentration at zero
- will overshrink the signal if there are many noise cases
- Good shrinkage prior allows separate control of the concentration around zero and tails
- tails need to exhibit bounded influence
- continuous versions/relaxations of a spike and slab prior

$$\mu_i \sim \pi_0 \delta_0 + (1 - \pi)g$$

- allows formal Bayes multiple testing $H_{0i} : \mu = 0$



Note

- a single Gaussian or Double Exponential prior (Bayes Lasso) have exponential tails same as likelihood (in the normal means problem)
- single parameter controls tail behaviour and concentration at zero
- will overshrink the signal if there are many noise cases
- Good shrinkage prior allows separate control of the concentration around zero and tails
- tails need to exhibit bounded influence
- continuous versions/relaxations of a spike and slab prior

$$\mu_i \sim \pi_0 \delta_0 + (1 - \pi)g$$

- allows formal Bayes multiple testing $H_{0i} : \mu = 0$
- $\pi_0 = \Pr(H_{0i} \text{ is true})$ another unknown to learn from the data; provides automatic adjustment for multiple testing error!

