Predictive diagnostics reveal that $m_{\text{current}}$ is not good enough; what now?

(model) $A$: So model expansion: embed $m_{\text{current}}$ in a richer model class, of which it's a special case, with the "direction" of "richer" determined by what the predictive diagnostics showed you is wrong with $m_{\text{current}}$.

\[
A_{\text{richer}} \quad \text{and} \quad m_{\text{current}}
\]

Here, deficiency of $m_{\text{current}}$:
\[
\{ (\mu, \sigma^2) \mid \mathbf{x} \sim \mathcal{N}(\mu, \sigma^2) \} \quad \text{weakly} \quad \rightarrow \quad \{ (\bar{\mu}, 1/\sigma^2) \mid \mathbf{x} \sim \mathcal{N}(\mu, \sigma^2) \}
\]

$r_{\text{richer}}$ should have heavier tails than $m_{\text{current}}$: $G$.
A: we need a new, more general, concept.

Bayes' theorem has no conjugate prior, now.

\[ (E, \varnothing, \{\{(x_i, y_i)\} \mid i \in N \}) \to \mathbb{P}(\theta) \]

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\(\theta = (\beta_0, \beta_1, \ldots, \beta_k, \sigma) \sim \mathcal{N}(k) \quad (k > n)\)

\(\beta_j = 0 \iff \text{feature } j \text{ does not help predict } y\quad (j = 1, \ldots, k)\)

\[
p(\theta | y) = c 
\]

\[
p(\theta) \cdot p(y | \theta)
\]

only at most \(k, < n\) of the \(\beta_j\) are nonzero in study

\[
(\theta = \{\theta_1, \ldots, \theta_k\})
\]

\[
k = 10,000\quad k = 32,000
\]

Icelandic genome study