Model Checking and Comparison

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Model checking and comparison

- We have discussed the first two major steps of a Bayesian analysis:
 - Constructing a Bayesian model specifying likelihood and priors
 - Calculating the posterior either analytically or computationally
- Now we need to consider the question if the model is a good fit or which model is the best fit.
- Three related issues to consider:
 - Robustness: Is any of the model assumptions having an undue impact on the results?
 - Assessment: Does the model provide adequate fit to the data?
 - Selection: Which model (or models) should we choose for final presentation?



Sensitivity analysis

- A Bayesian data analysis is conditional on the validity of the entire structure of the model
 - Correctly specified likelihood
 - Reasonableness of the prior
- Key question: If I change the likelihood or the prior, will it change my posterior inference or conclusion?
 - No: The model is robust with respect to this assumption .
 - Yes: Document the sensitivity, think more carefully about it, and perhaps collect more data.
- Examples of sensitivity tests:
 - likelihood sensitivity: e.g. nonnormal errors; case deletion
 - common tests for both Bayesian and frequentist
 - change in prior distribution: e.g. doubling/halving a prior s.d.; increasing/decreasing a prior mean.
 - robustness in a Bayesian analysis



Model assessment

- "All models are wrong, but some are useful" George Box
- Most (if not all) models do NOT correctly reflect ALL aspects of the data generation process.
 - The goal is not to determine if a model is right or wrong
 - The key question is whether or not the models have a good enough fitness to the data
- You may have models that differ substantially that result in similar scientific conclusions!

Model assessment

 Practically we examine model's predictive accuracy, which relies on the posterior predictive distribution:

$$p(\mathbf{y}^{rep}|\mathbf{y}) = \int p(\mathbf{y}^{rep}|oldsymbol{ heta})p(oldsymbol{ heta}|\mathbf{y})doldsymbol{ heta}$$

- \mathbf{y}^{rep} denotes replicated data (data that could have been observed under the same model and same value of $\boldsymbol{\theta}$).
- If the model fits, replicated data under the model should look like the observed data.
- Monte Carlo methods are often used to compute the measures of model assessment.

Posterior predictive p-value

- Let $T(\mathbf{y}, \theta)$ be a test quantity, or discrepancy measure, which is a scalar summary of parameters and data
- Examples of test quantities:
 - Min or max
 - Mean
 - Sum of squared residuals
- Bayesian posterior predictive p-value:

$$p_{B} = E_{\theta|\mathbf{y}}[P(T(\mathbf{y}^{rep}, \theta) > T(\mathbf{y}, \theta))]$$

$$= \int P(T(\mathbf{y}^{rep}, \theta) > T(\mathbf{y}, \theta)|\theta) p(\theta|\mathbf{y})d\theta.$$

⇒ the probability that the test quantities of replicated data are more extreme than that of observed data

Posterior predictive p-value

- Note that $P(T(\mathbf{y}^{rep}, \theta) > T(\mathbf{y}, \theta)|\theta)$ parallels a classical p-value, i.e. $P(T(\mathbf{y}^{rep}, \theta) > T(\mathbf{y}, \theta)|\theta_0)$, but Bayesian p-value integrates out θ under the model.
- The Bayesian p-values are easier to compute via Monte Carlo methods!
- ullet Draw $m{ heta}^{(g)} \sim p(m{ heta}|m{y})$ and then $m{y}^{rep(g)} \sim p(m{y}^{rep}|m{ heta}^{(g)})$, and we have

$$p_{B} = \int \underline{P(T(\mathbf{y}^{rep}, \boldsymbol{\theta}) > T(\mathbf{y}, \boldsymbol{\theta})|\boldsymbol{\theta})} p(\boldsymbol{\theta}|\mathbf{y}) d\boldsymbol{\theta}$$

$$= \int \underline{\int I_{T(\mathbf{y}^{rep}, \boldsymbol{\theta}) > T(\mathbf{y}, \boldsymbol{\theta})} p(\mathbf{y}^{rep}|\boldsymbol{\theta})} p(\boldsymbol{\theta}|\mathbf{y}) \underline{d\mathbf{y}^{rep}} d\boldsymbol{\theta}$$

$$\approx \frac{1}{G} \sum_{r=1}^{G} I_{T(\mathbf{y}^{rep}(g), \boldsymbol{\theta}(g)) > T(\mathbf{y}, \boldsymbol{\theta}(g))}$$

Posterior predictive p-value

- An extreme Bayesian p-value suggest discrepancy between the fitted model and the observed data.
- Different test quantities can target different aspects of the model
 - Sum of squared residuals: overall model fitness
 - Min/Max: tail behavior
- Caution: Bayesian p-value SHOULD NOT be compared across models – not for model choice!

Marginal checks via cross validation

- So far, we have focused on replicated data from the joint posterior predictive distribution.
- An alternative is to evaluate the marginal prediction for each i separately.
- Use cross-validation marginal predictive distributions:

$$p_i = P(y_i^{rep} \le y_i | \mathbf{y}_{(-i)})$$

where $\mathbf{y}_{(-i)}$ denotes the vector of all the data except the i^{th} value.

- Useful for identifying outliers or checking model calibration
- Marginal predictive p-values close to 0 or 1 suggest overdispersion.
- Other Marginal checks ...

Cross-validation Residuals

• "Leave-one out" (LOO) residual:

$$r_i = y_i - E(y_i|\mathbf{y}_{(i)}).$$

• Again, Monte Carlo methods can be used for easy computation. Draws $\theta^{(g)} \sim p(\theta|\mathbf{y})$, and we have

$$E(y_i|\mathbf{y}_{(i)}) = E_{\theta}[E(y_i|\mathbf{y}_{(i)}, \theta)]$$

$$= \int E(y_i|\theta)p(\theta|\mathbf{y}_{(i)})d\theta$$

$$\approx \int E(y_i|\theta)p(\theta|\mathbf{y})d\theta$$

$$\approx \frac{1}{G}\sum_{g=1}^{G}E(y_i|\theta^{(g)}).$$

- Approximation should be adequate unless the dataset is small and y_i is an extreme outlier
- Same $\theta^{(g)}$'s may be used for each $i=1,\ldots,n$.

Conditional predictive ordinate

Conditional predictive ordinate (CPO):

$$p(y_i|\mathbf{y}_{(i)}) = \int p(y_i|\theta)p(\theta|\mathbf{y}_{(i)})d\theta$$

$$\approx \int p(y_i|\theta)p(\theta|\mathbf{y})d\theta$$

• Similarly, the CPO can be computed via Monte Carlo approximation:

$$p(y_i|\mathbf{y}_{(i)}) \approx \frac{1}{G}\sum_{g=1}^G p(y_i|\boldsymbol{\theta}^{(g)}).$$

- Low CPOs indicate poor fit by the model.
- log(CPO), the log pseudo marginal likelihood (LPML) is often used in practice for computational convenience.

Bayesian Model Selection

Suppose we want to choose between the models

$$M_1:$$
 $Y = \beta_0 + \epsilon, \ \epsilon \sim N(0, \sigma^2)$
 $M_2:$ $Y = \beta_0 + X\beta + \epsilon, \ \epsilon \sim N(0, \sigma^2)$

- Two general ways for model selection in Bayesian framework:
 - Based on predictive performance
 - Bayes factor

Predictive Model Selection

- Evaluating the accuracy of predictions offers a general approach to model comparison.
- Two problems:
 - Measures of predictive accuracy
 - Methods for estimating predictive accuracy

Measures of predictive accuracy

- The predictive performance of a model is generally assessed by scoring functions and rules.
- Scoring functions: refer to measures of predictive accuracy for point prediction, which reports a single predicted value.
 - Example: Mean squared error, $-\frac{1}{n}\sum_{i=1}^{n}(y_i^*-E(y_i^*|\theta))^2$
 - MSE is easy to interpret but less appropriate for non-normal data
- Scoring rules: refer to measures of predictive accuracy for probabilistic prediction, which captures the full uncertainty in prediction.
 - Example: Log predictive density or log-likelihood, $log(p(y^*|\theta))$
 - The log predictive density is natural for fitness evaluation as it is closed related to the Kullback-Leibler information

Evaluating using log predictive density

 Ideally, predictive performance would be evaluated using external validation data y*

$$lpd = \log(p(y^*|\mathbf{y})) = \int p(y^*|\theta)p(\theta|\mathbf{y})d\theta$$

 With future data unknown, we average over the distribution of future data => expected log predictive density

$$elpd = E(\log(p(y^*|\mathbf{y}))) = \int \log(p(y^*|\mathbf{y}))p(y^*)d\mathbf{y}^*$$

We can plug in $p(y^*)$ estimate from the data, but this will lead to too optimistic estimate of fitness.

For n data points, we evaluate predictive accuracy by taking one at
 a time ⇒ expected log pointwise predictive density

$$elppd = \sum_{i=1}^{n} E(\log(p(y_i^*|\mathbf{y})))$$

Methods for estimating predictive accuracy

- We will discuss three approaches to estimate out-of sample predictive accuracy using available data:
 - Within-sample accuracy
 - Adjusted within-sample accuracy
 - Cross-validation

Within-sample accuracy

- Naïve estimates using the log predictive accuracy for existing data
- Examples:

deviance =
$$-2 \log p(\mathbf{y}|\hat{\theta})$$

 $Ippd = \sum_{i=1}^{n} \log \int p(y_i|\theta)p(\theta|\mathbf{y})d\theta$
 $\approx \sum_{i=1}^{n} \log \left(\frac{1}{G}\sum_{g=1}^{G}p(y_i|\theta^{(g)})\right)$

where $\hat{\theta}$ could be either a frequentist or Bayesian point estimate, and $\theta^{(g)}$ are draws from the posterior $p(\theta|\mathbf{y})$.

 Overestimate the predictive accuracy due to fitting and evaluating model with the same data



Adjusted within-sample accuracy

- Adjust the naïve estimates to account for overfitting
- Usually substract a correction for the number of parameters in the model
- Examples: AIC, DIC, WAIC
- Can give reasonable answers but are only being correct at best in expectation.

Akaike Information Criteria (AIC)

The most common frequentist approach to adjust within-sample accuracy

$$AIC = -2\log p(\mathbf{y}|\hat{\theta}_{MLE}) + 2k$$
 where $\hat{\theta}_{MLE}$ is the MLE and k is the number of parameters.

- Adds a penalty for model complexity to the deviance,
- Does NOT work well for Bayesian models with hierarchical structure or informative priors, in which the effective number of parameters is difficult to determine

Effective number of parameters

Consider the one-way ANOVA model

 $Y_i | \theta_i \stackrel{ind}{\sim} N(\theta_i, 1/\tau_i)$ and $\theta_i \stackrel{iid}{\sim} N(\mu, 1/\lambda), i = 1, \dots, k$ Suppose μ, λ , and τ_i are known. How many parameters are in this model?

- If $\lambda = \infty$, all $\theta_i = \mu$ and there are 0 free parameters
- If $\lambda = 0$, the θ_i are unconstrained and there are k free parameters
- In practice, $0 < \lambda < \infty$ so the "effective number of parameters" is somewhere in between!
- The effective number of parameter reflects the true complexity of a model
- Question: How to determine it?

Deviance Information Criteria

• DIC is the Bayesian analog of AIC, defined as

$$DIC = -2 \log p(\mathbf{y}|\hat{\theta}_{Bayes}) + 2p_{DIC}$$

where MLE is replaced by the posterior mean $\hat{\theta}_{Bayes}$, and k is replaced by the effective number of parameters p_{DIC}

• The effective number of parameters in the DIC is defined as

$$p_{DIC} = 2 \left(\log p(\mathbf{y}|\hat{\theta}_{Bayes}) - E_{\theta}[\log p(\mathbf{y}|\theta)] \right)$$

$$\approx 2 \left(\log p(\mathbf{y}|\hat{\theta}_{Bayes}) - \frac{1}{G} \sum_{g=1}^{G} \log p(\mathbf{y}|\theta^{(g)}) \right)$$

where $\theta^{(g)}$ are MCMC draws from the posterior $p(\theta|\mathbf{y})$.

- For the one-way ANOVA model, $p_{DIC} = \sum_{i=1}^{k} \frac{\tau_i}{\tau_i + \lambda} \Rightarrow$ Clearly $0 < p_{DIC} < k$ as desired.
- An alternative expression for p_{DIC} is

$$p_{DIC_{alt}} = 2var_{\theta}[\log p(\mathbf{y}|\theta)]$$

Watanabe-Akaike Information Criteria (WAIC)

• The WAIC is a fully Bayesian version of AIC, defined as

WAIC =
$$-2Ippd + 2p_{WAIC}$$

 $\approx -2\sum_{i=1}^{n} \log \left(\frac{1}{G}\sum_{g=1}^{G} p(y_i|\theta^{(g)})\right) + 2p_{WAIC}$

• Two estimates for the effective number of parameters:

$$p_{WAIC_1} = 2\sum_{i=1}^{n} \left\{ \log(E_{\theta}[p(y_i|\theta)]) - E_{\theta}[\log p(y_i|\theta)] \right\}$$
or,
$$p_{WAIC_2} = 2\sum_{i=1}^{n} var_{\theta}[\log p(y_i|\theta)]$$

- p_{WAIC}, is recommended as it gives results closer to LOO-CV.
- WAIC is advantageous over AIC and DIC in that it averages over the posterior distribution rather than conditioning on a point estimate.

Leave-one-out Cross Validation

Procedure:

- Partition the data into a training set and a holdout set with a single data point in the holdout
- Calculate log predictive density for the holdout data, $log(p(y_i|\mathbf{y}_{(-i)}))$
- Repeat for all data points, and obtain

$$Ippd_{loo-cv} = \sum_{i} log(p(y_i|\mathbf{y}_{(-i)}))$$

- Avoid overfitting
- Can be computationally expensive
- Does NOT work well for structured data, e.g. spatial data, time series, etc.

Model Selection using Bayes factors

• The Bayes factor for comparing two models M_1 versus M_2 is

$$BF(M_2; M_1) = \frac{p(\mathbf{y} \mid M_2)}{p(\mathbf{y} \mid M_1)} = \frac{\int p(\mathbf{y} | \theta_2, M_2) \pi(\theta_2 | M_2) d\theta_2}{\int p(\mathbf{y} | \theta_1, M_1) \pi(\theta_1 | M_1) d\theta_1}.$$

- When there are multiple models for comparison, we can estimate Bayes factors by sampling over model space:
 - To treat the model indicator M as a parameter, and sample it with other parameters using MCMC, producing a stream of samples $\{M^{(g)}\}_{g=1}^G$ from $p(M|\mathbf{y})$.
 - A simple estimate of posterior model probability is then

$$\hat{p}(M = j | \mathbf{y}) = \frac{\# \text{ of } M^{(g)} = j}{\text{total } \# \text{ of } M^{(g)}}$$

- Bayes factor between any two models can be computed as

$$\widehat{BF}_{jj'} = \frac{\widehat{p}(M=j|\mathbf{y})/\widehat{p}(M=j'|\mathbf{y})}{p(M=j)/p(M=j')}.$$

Model Selection using Bayes factors

Strengths:

- Works well when underlying model is discrete
- Works for non-nested models

Weakness:

- Problematic when underlying model is continuous
- Requires proper priors
- Sensitive to dimensionality of the problem