Chapter 7

- 7.1 Measures of predictive accuracy
- 7.2 Information criteria and cross-validation
 - Instead of 7.2, read:
 Vehtari, A., Gelman, A., Gabry, J. (2017). Practical
 Bayesian model evaluation using leave-one-out cross-validation and WAIC. Statistics and Computing. 27(5):1413–1432. arXiv preprint.
- 7.3 Model comparison based on predictive performance
- 7.4 Model comparison using Bayes factors
- 7.5 Continuous model expansion / sensitivity analysis
- 7.5 Example (may be skipped)

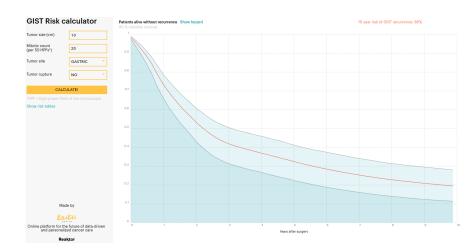
Model assessment, selection and inference after selection

- Extra material at https://avehtari.github.io/modelselection/
 - Videos, Slides, Notebooks, References
- CV-FAQ https://avehtari.github.io/modelselection/CV-FAQ.html

Predicting concrete quality



Predicting cancer recurrence



- ► True predictive performance is found out by using it to make predictions and comparing predictions to true observations
 - external validation

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 - external validation
- Expected predictive performance
 - approximates the external validation

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- Application specific utility/cost functions are important
 - eg. money, life years, quality adjusted life years, etc.

- We need to choose the utility/cost function
- ► Application specific utility/cost functions are important
 - eg. money, life years, quality adjusted life years, etc.
- ► If are interested overall in the goodness of the predictive distribution, or we don't know (yet) the application specific utility, then good information theoretically justified choice is log-score

$$\log p(y^{\text{rep}} \mid y, M),$$

- What is cross-validation
 - Leave-one-out cross-validation (elpd_loo, p_loo)
 - Uncertainty in LOO (SE)
- When is cross-validation applicable?
 - data generating mechanisms and prediction tasks
 - leave-many-out cross-validation
- Fast cross-validation
 - PSIS and diagnostics in loo package (Pareto k, n_eff, Monte Carlo SE)
 - K-fold cross-validation
- Related methods (WAIC, *IC, BF)
- Model comparison and selection (elpd_diff, se)
- Model averaging with Bayesian stacking

Stan and loo package

Computed from 4000 by 20 log-likelihood matrix

```
Estimate SE
elpd loo -29.5 \ 3.3
p_loo 2.7 1.0
```

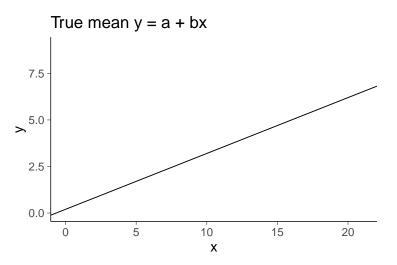
Monte Carlo SE of elpd loo is 0.1.

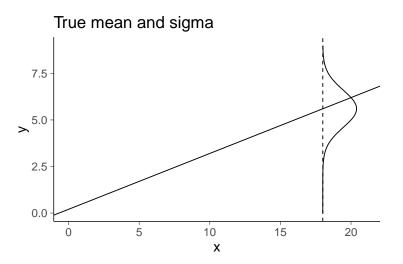
Pareto k d	liagnostic value	es:			
	_	Count	Pct.	Min.	n_eff
(-Inf, 0.5]] (good)	18	90.0%	899	
(0.5, 0.7] (ok)	2	10.0%	459	
(0.7, 1] (bad)	0	0.0%	<na></na>	
(1, Inf) (very bad)	0	0.0%	<na></na>	

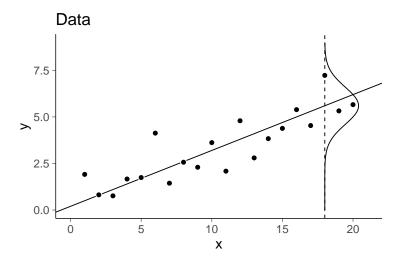
All Pareto k estimates are ok (k < 0.7). See help('pareto-k-diagnostic') for details.

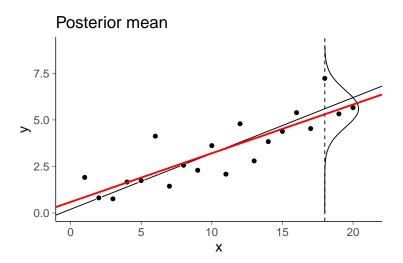
Model comparison: (negative 'elpd diff' favors 1st model, positive favors 2nd)

$$\begin{array}{ccc} \text{elpd_diff} & \text{se} \\ -0.2 & 0.1 \end{array}$$

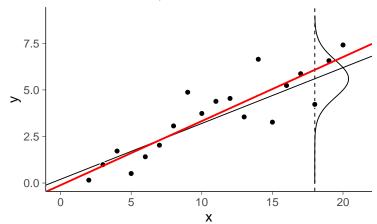


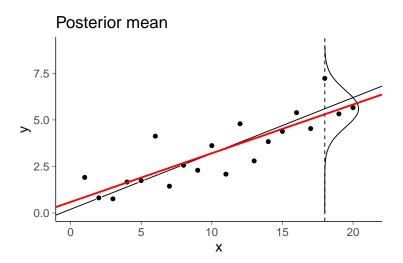


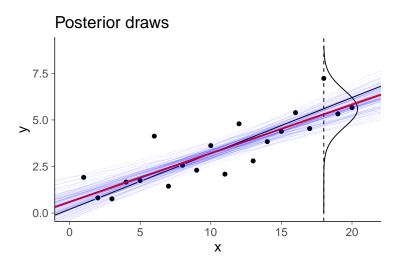


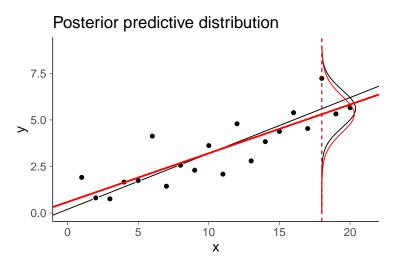


Posterior mean, alternative data realisation

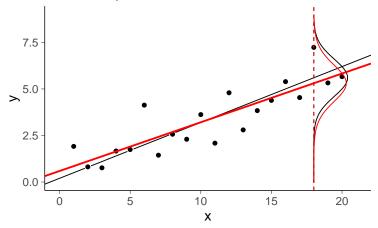




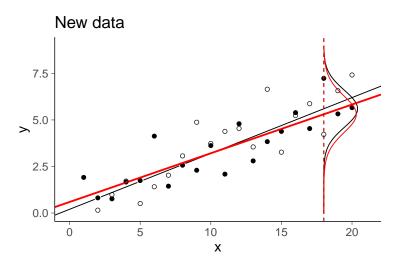


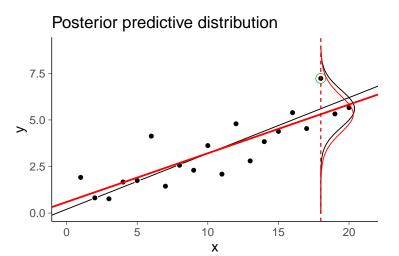


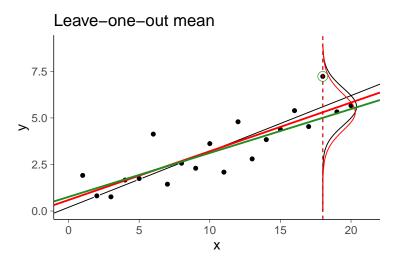
Posterior predictive distribution

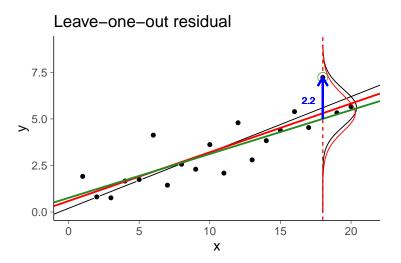


$$p(\tilde{y} \mid \tilde{x} = 18, x, y) = \int p(\tilde{y} \mid \tilde{x} = 18, \theta) p(\theta \mid x, y) d\theta$$

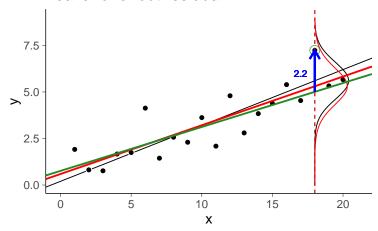






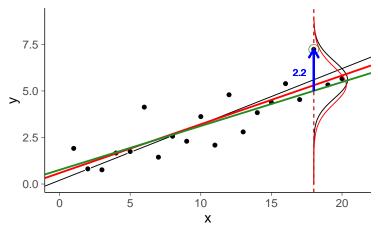


Leave-one-out residual



$$y_{18} - E[p(\tilde{y} \mid \tilde{x} = 18, x_{-18}, y_{-18})]$$

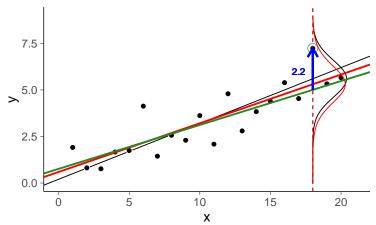
Leave-one-out residual



$$y_{18} - E[p(\tilde{y} \mid \tilde{x} = 18, x_{-18}, y_{-18})]$$

Can be use to compute, e.g., RMSE, R², 90% error

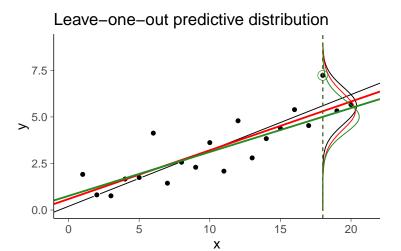
Leave-one-out residual



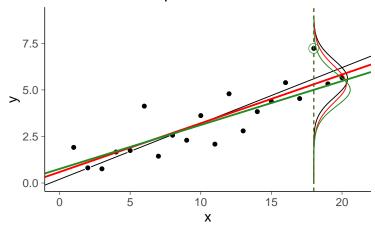
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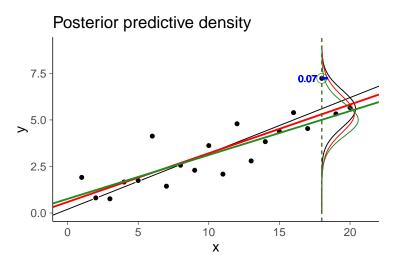
See LOO-R² at avehtari.github.io/bayes_R2/bayes_R2.html



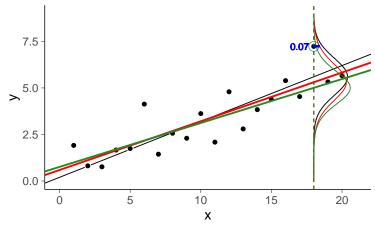
Leave-one-out predictive distribution



$$p(\tilde{y} \mid \tilde{x} = 18, x_{-18}, y_{-18}) = \int p(\tilde{y} \mid \tilde{x} = 18, \theta) p(\theta \mid x_{-18}, y_{-18}) d\theta$$

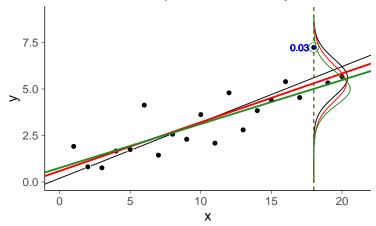


Posterior predictive density



$$p(\tilde{y} = y_{18} \mid \tilde{x} = 18, x, y) \approx 0.07$$

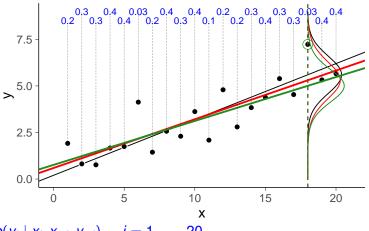
Leave-one-out predictive density



$$p(\tilde{y} = y_{18} \mid \tilde{x} = 18, x, y) \approx 0.07$$

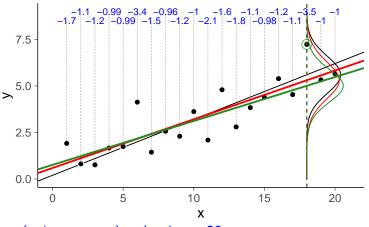
 $p(\tilde{y} = y_{18} \mid \tilde{x} = 18, x_{-18}, y_{-18}) \approx 0.03$

Leave-one-out predictive densities



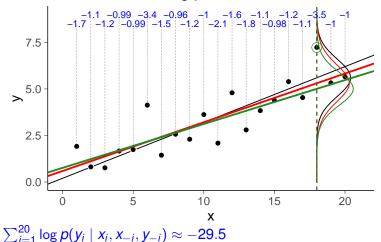
$$p(y_i \mid x_i, x_{-i}, y_{-i}), \quad i = 1, \dots, 20$$

Leave–one–out log predictive densities

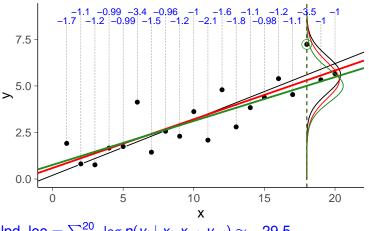


 $\log p(y_i\mid x_i,x_{-i},y_{-i}),\quad i=1,\ldots,20$

Leave–one–out log predictive densities

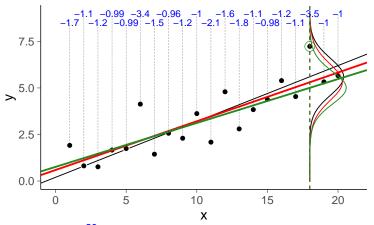


Leave–one–out log predictive densities

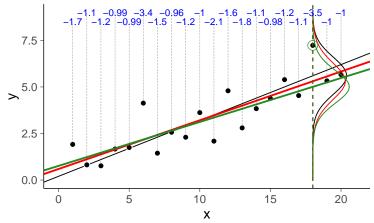


elpd_loo = $\sum_{i=1}^{20} \log p(y_i \mid x_i, x_{-i}, y_{-i}) \approx -29.5$

Leave-one-out log predictive densities

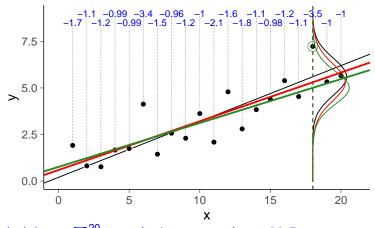


elpd_loo = $\sum_{i=1}^{20} \log p(y_i \mid x_i, x_{-i}, y_{-i}) \approx -29.5$ an estimate of log posterior pred. density for new data



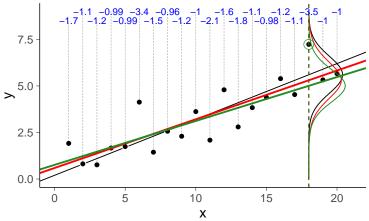
elpd_loo =
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$$lpd = \sum_{i=1}^{20} log p(y_i | x_i, x, y) \approx -26.8$$



elpd_loo =
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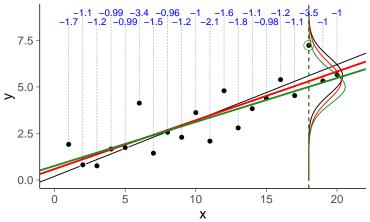
lpd = $\sum_{i=1}^{20} \log p(y_i \mid x_i, x, y) \approx -26.8$
p loo = lpd - elpd loo ≈ 2.7



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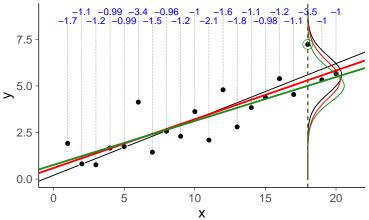
asymptotically approaches p in case of regular faithful model



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asymptotically approaches p in case of regular faithful model

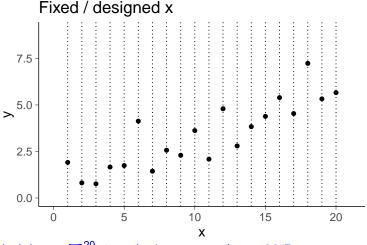
see Vehtari, Gelman & Gabry (2017a) and Vehtari & Ojanen (2012) for more



elpd_loo =
$$\sum_{i=1}^{20} \log p(y_i \mid x_i, x_{-i}, y_{-i}) \approx -29.5$$

SE = sd(log $p(y_i \mid x_i, x_{-i}, y_{-i})) \cdot \sqrt{20} \approx 3.3$

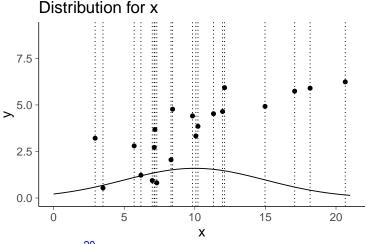
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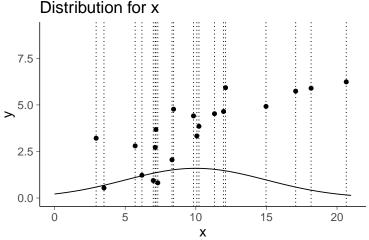
LOO is ok for fixed / designed x. SE is uncertainty about $y \mid x$.



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LOO is ok for random x. SE is uncertainty about $y \mid x$ and x.



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LOO is ok for random x. SE is uncertainty about $y \mid x$ and x. Covariate shift can be handled with importance weighting or modelling

100 package

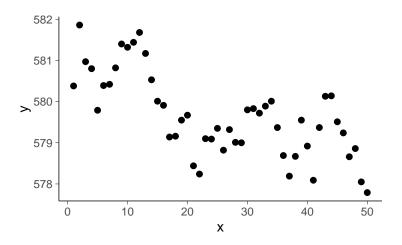
Computed from 4000 by 20 log-likelihood matrix

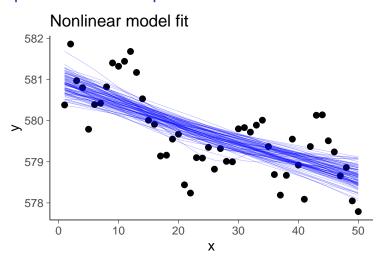
Monte Carlo SE of elpd_loo is 0.1.

Pareto k diagnostic values:

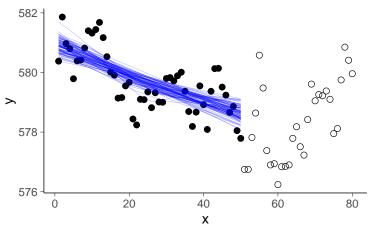
		Count	Pct.	Min.	n_eff
(-Inf, 0.5]	(good)	18	90.0%	899	
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(0.7, 1]	(bad)		0.0%	<NA $>$	
(1, Inf)	(very bad)	0	0.0%	<NA $>$	

All Pareto k estimates are ok (k < 0.7). See help('pareto-k-diagnostic') for details.

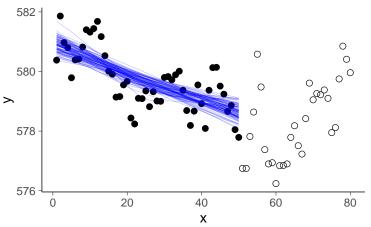




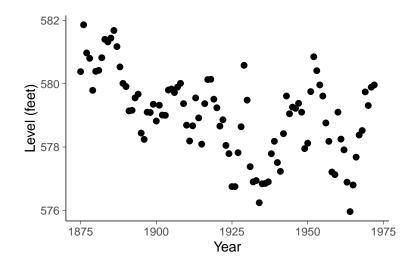




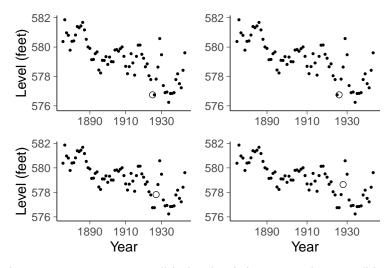




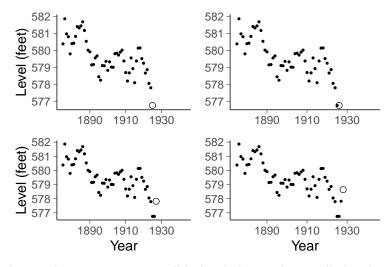
Extrapolation is more difficult



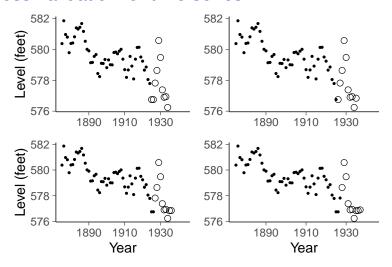
Can LOO or other cross-validation be used with time series?



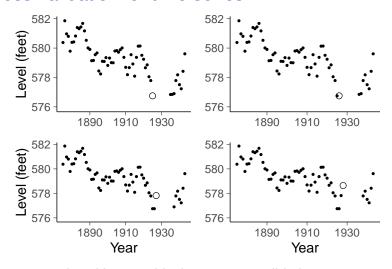
Leave-one-out cross-validation is ok for assessing conditional model



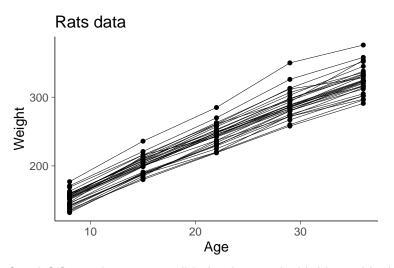
Leave-future-out cross-validation is better for predicting future



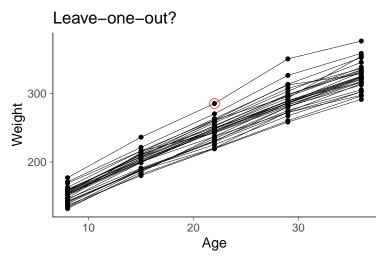
m-step-ahead cross-validation is better for predicting further future

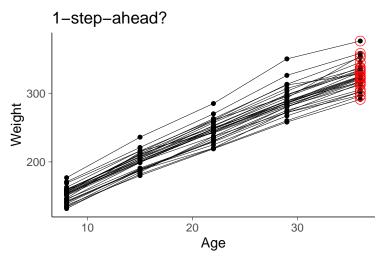


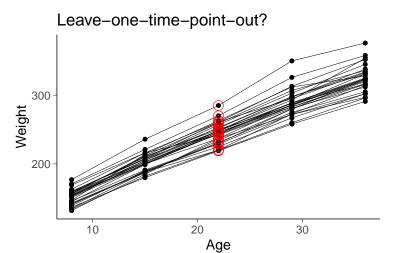
m-step-ahead leave-a-block-out cross-validation

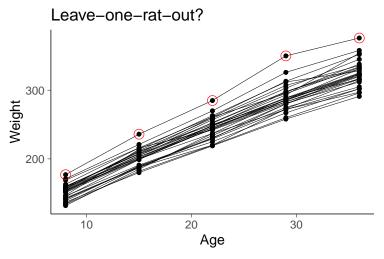


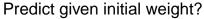
Can LOO or other cross-validation be used with hierarchical data?

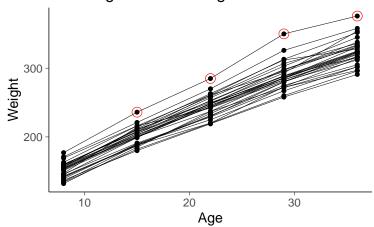












Summary of data generating mechanisms and prediction tasks

- You have to make some assumptions on data generating mechanism
- Use the knowledge of the prediction task if available
- Cross-validation can be used to analyse different parts, even if there is no clear prediction task

Fast cross-validation

- Pareto smoothed importance sampling LOO (PSIS-LOO)
- K-fold cross-validation

• We want to compute

$$p(y_i \mid x_{-i}, y_{-i}) = \int p(y_i \mid x_i, \theta) p(\theta \mid x_{-i}, y_{-i}) d\theta$$

• We want to compute $p(y_i \mid x_{-i}, y_{-i}) = \int p(y_i \mid x_i, \theta) p(\theta \mid x_{-i}, y_{-i}) d\theta$

- Proposal distribution is full posterior $\theta^{(s)} \sim p(\theta \mid x, y)$
- Target distribution is LOO-posterior $p(\theta \mid x_{-i}, y_{-i})$

We want to compute

$$p(y_i \mid x_{-i}, y_{-i}) = \int p(y_i \mid x_i, \theta) p(\theta \mid x_{-i}, y_{-i}) d\theta$$

- Proposal distribution is full posterior $\theta^{(s)} \sim p(\theta \mid x, y)$
- Target distribution is LOO-posterior $p(\theta \mid x_{-i}, y_{-i})$
- Importance ratio

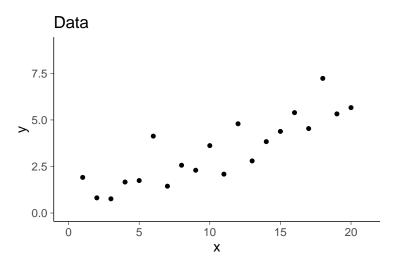
$$w_i^{(s)} = \frac{p(\theta^{(s)} \mid x_{-i}, y_{-i})}{p(\theta^{(s)} \mid x, y)} \propto \frac{1}{p(y_i \mid \theta^{(s)})}$$

We want to compute

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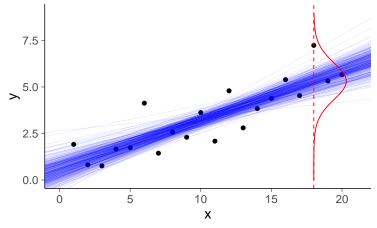
$$w_i^{(s)} = \frac{p(\theta^{(s)} \mid x_{-i}, y_{-i})}{p(\theta^{(s)} \mid x, y)} \propto \frac{1}{p(y_i \mid \theta^{(s)})}$$
$$\tilde{w}_i^{(s)} = \frac{w_i^{(s)}}{\sum_{s'=1}^{S} w_i^{(s')}}$$



Posterior draws 7.5 > 5.0 2.5 0.0 10 15 20 5 Χ

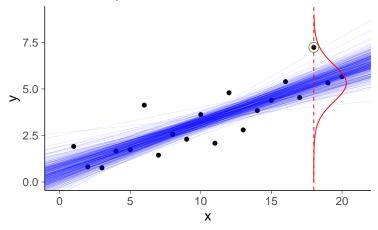
$$\theta^{(s)} \sim p(\theta \mid x, y)$$

Posterior predictive distribution



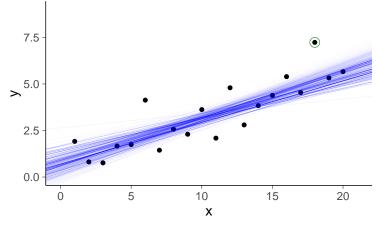
$$\theta^{(s)} \sim p(\theta \mid x, y), \quad p(\tilde{y} \mid \tilde{x}, x, y) \approx \frac{1}{S} \sum_{s=1}^{S} p(\tilde{y} \mid \tilde{x}, \theta^{(s)})$$

Posterior predictive distribution



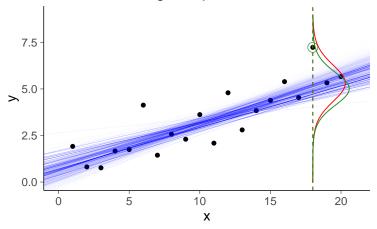
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PSIS-LOO weighted draws



$$\theta^{(s)} \sim p(\theta \mid x, y), \quad w_i^{(s)} = p(\theta^{(s)} \mid x_{-i}, y_{-i}) / p(\theta^{(s)} \mid x, y)$$

PSIS-LOO weighted predictive distribution



$$\theta^{(s)} \sim p(\theta \mid x, y), \quad w_i^{(s)} = p(\theta^{(s)} \mid x_{-i}, y_{-i}) / p(\theta^{(s)} \mid x, y)$$
$$p(y_i \mid x_i, x_{-i}, y_{-i}) \approx \sum_{s=1}^{s} [\tilde{w}_i^{(s)} p(y_i \mid x_i, \theta^{(s)})]$$

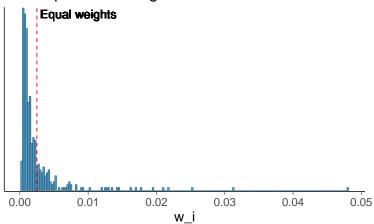
We want to compute

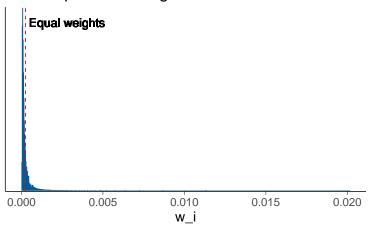
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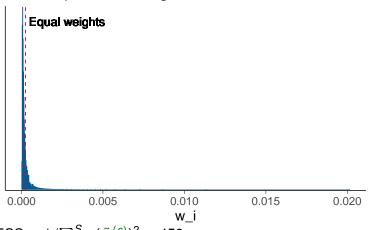
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- Target distribution is LOO-posterior $p(\theta \mid x_{-i}, y_{-i})$
- Importance ratio

$$w_i^{(s)} = \frac{p(\theta^{(s)} \mid x_{-i}, y_{-i})}{p(\theta^{(s)} \mid x, y)} \propto \frac{1}{p(y_i \mid \theta^{(s)})}$$
$$\tilde{w}_i^{(s)} = \frac{w_i^{(s)}}{\sum_{s'=1}^S w_i^{(s')}}$$

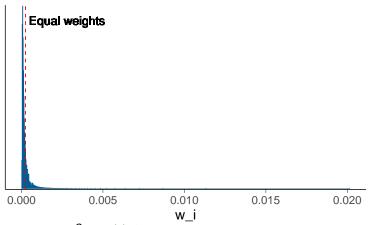
- The variability of importance weights matter
 - Pareto-k diagnostic
 - Pareto smoothed importance sampling LOO (PSIS-LOO)







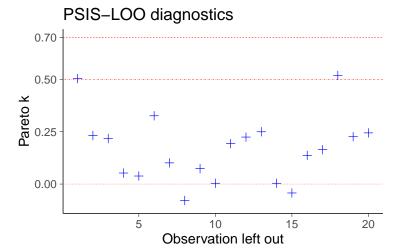
ESS
$$\approx 1/\sum_{s=1}^{S} (\tilde{w}^{(s)})^2 \approx 459$$



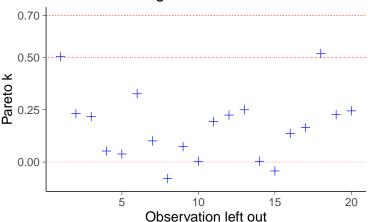
ESS
$$\approx 1/\sum_{s=1}^{S} (\tilde{\textit{w}}^{(s)})^2 \approx 459$$

Pareto $\hat{k} \approx 0.52$

- Pareto \hat{k} estimates the tail shape which determines the convergence rate of PSIS. Less than 0.7 is ok.



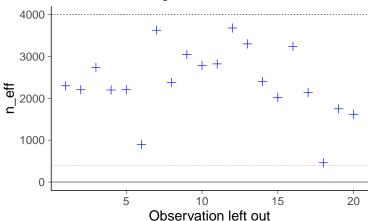
PSIS-LOO diagnostics



Pareto k diagnostic values:

		Count	Pct.	Min .	n_eff
(-Inf, 0.5]	(good)	18	90.0%	899	
(0.5, 0.7]	(ok)	2	10.0%	459	
(0.7, 1]	(bad)	0	0.0%	<NA $>$	
(1, Inf)	(very bad)	0	0.0%	<NA $>$	

PSIS-LOO diagnostics



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100 package

Computed from 4000 by 20 log-likelihood matrix

Monte Carlo SE of elpd_loo is 0.1.

Pareto k diagnostic values:

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All Pareto k estimates are ok (k < 0.7). See help('pareto-k-diagnostic') for details.

see more in Vehtari, Gelman & Gabry (2017b)

Pareto smoothed importance sampling (PSIS)

- Replace the largest weights with ordered statistics of the fitted Pareto distribution
 - equivalent to using model to filter the noise out of the weights

See more in Vehtari, Simpson, Gelman, Yao & Gabry (2021)

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- Replace the largest weights with ordered statistics of the fitted Pareto distribution
 - equivalent to using model to filter the noise out of the weights
- Reduced variability compared to the plain IS
- Reduced bias compared to the truncated IS
- Asymptotically consistent under some mild conditions

See more in Vehtari, Simpson, Gelman, Yao & Gabry (2021)

Stan code

$$\log(w_i^{(s)}) = \log(1/p(y_i \mid x_i, \theta^{(s)})) = -\log_{\text{lik}[i]}$$

Stan code

```
\log(w_i^{(s)}) = \log(1/p(y_i \mid x_i, \theta^{(s)})) = -\log_{\text{lik}[i]}
model {
  alpha ~ normal(pmualpha, psalpha);
  beta ~ normal(pmubeta, psbeta);
  y ~ normal(mu, sigma);
generated quantities {
  vector[N] log lik;
  for (i in 1:N)
    log lik[i] = normal lpdf(v[i] | mu[i], sigma);
```

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\log(w_i^{(s)}) = \log(1/p(v_i \mid x_i, \theta^{(s)})) = -\log \text{ lik[i]}
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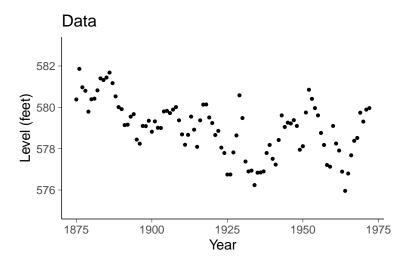
RStanARM and BRMS compute log_lik by default

- PSIS-LOO for hierarchical models
 - leave-one-group out is challenging for PSIS-LOO
 - see Merkel, Furr and Rabe-Hesketh (2018) for an approach using quadrature integration
 - Stan demo of the challenges and integrated LOO at https://avehtari.github.io/modelselection/roaches.html

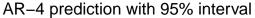
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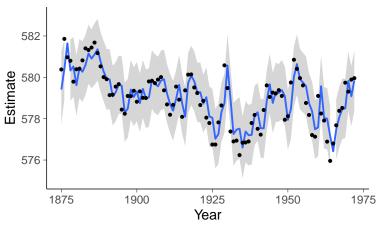
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- PSIS-LOO for time series
 - Approximate leave-future-out cross-validation (LFO-CV)
 - mc-stan.org/loo/articles/loo2-lfo.html

LFO-CV



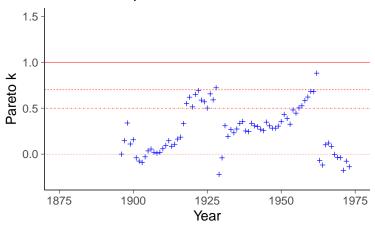
LFO-CV





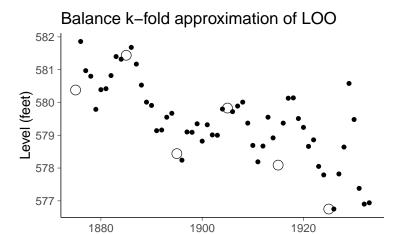
LFO-CV

PSIS-1-step-ahead with refits



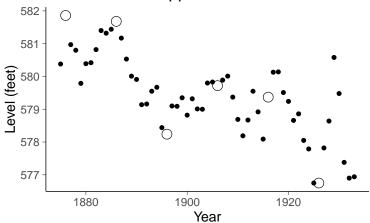
K-fold cross-validation

- K-fold cross-validation can approximate LOO
 - the same use cases as with LOO
- K-fold cross-validation can be used for hierarchical models
 - good for leave-one-group-out
- K-fold cross-validation can be used for time series
 - with leave-block-out

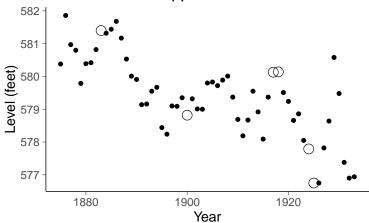


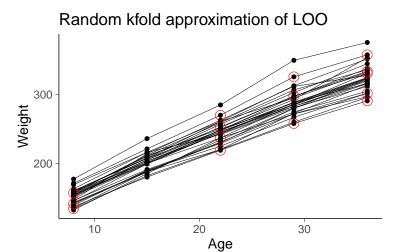
Year

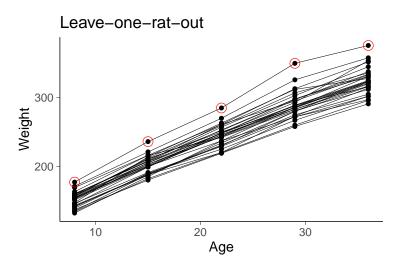
Balance k-fold approximation of LOO

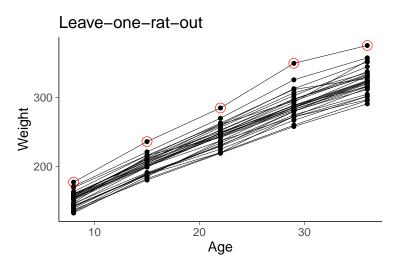


Random k-fold approximation of LOO









kfold_split_random()
kfold_split_balanced()
kfold_split_stratified()

WAIC has same assumptions as LOO

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- LOO makes the prediction assumption more clear, which helps if K-fold-CV is needed instead
- Multiplying by -2 doesn't give any benefit (Watanabe didn't multiply by -2)

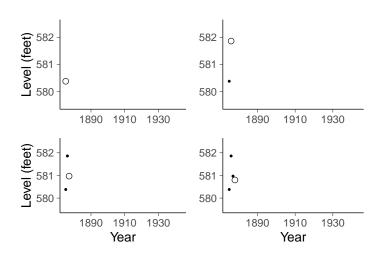
*IC

- AIC uses maximum likelihood estimate for prediction
- DIC uses posterior mean for prediction
- BIC is an approximation for marginal likelihood
- TIC, NIC, RIC, PIC, BPIC, QIC, AICc, ...

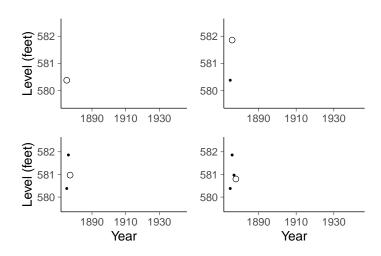
Marginal likelihood / Bayes factor

 Like leave-future-out 1-step-ahead cross-validation but starting with 0 observations

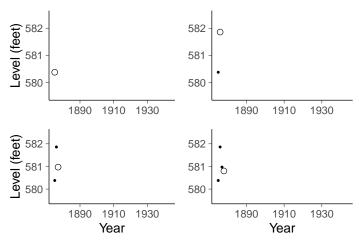
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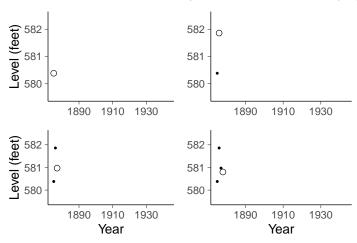
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Cross-validation for model assessment

- CV is good for model assessment when application specific utility/cost functions are used
 - e.g. 90% absolute error

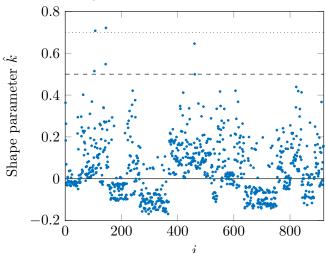
Cross-validation for model assessment

- CV is good for model assessment when application specific utility/cost functions are used
 - e.g. 90% absolute error
- Also useful in model checking in similar way as posterior predictive checking (PPC)
 - model misspecification diagnostics (e.g. Pareto-k and p_loo)
 - checking calibration of leave-one-out predictive posteriors (ppc_loo_pit in bayesplot)

see demos avehtari.github.io/modelselection/

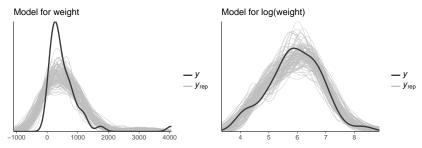
Radon example

PSIS-LOO diagnostics



see Vehtari, Gelman & Gabry (2017a)

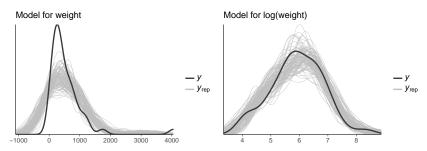
Posterior predictive checking is often sufficient



Predicting the yields of mesquite bushes.

Gelman, Hill & Vehtari (2020): Regression and Other Stories, Chapter 11.

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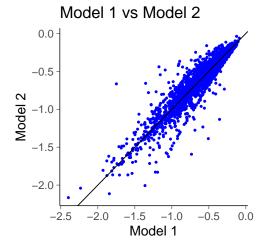
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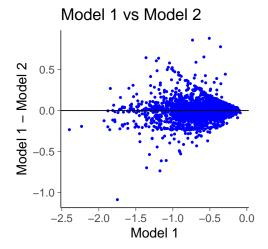
- BDA3, Chapter 6
- Gabry, Simpson, Vehtari, Betancourt, Gelman (2019). Visualization in Bayesian workflow. JRSS A, https://doi.org/10.1111/rssa.12378
- mc-stan.org/bayesplot/articles/graphical-ppcs.html

 With good priors that keep the prior on predictive space consistent, there is no need to do model selection to avoid overfitting

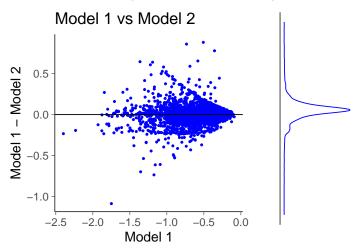
- Logistic regression for predicting probability of switching well with high arsenic level in rural Bangladesh
 - Model 1: log(arsenic) + distance
 - Model 2: log(arsenic) + distance + education level



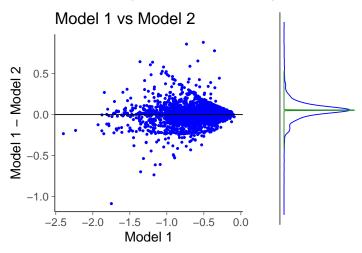
Model 1: $\widehat{\text{elpd}}_{\text{Loo}}(\mathbf{M}_a \mid y^{\text{obs}}) \approx \text{-1952}$, SE=16 Model 2: $\widehat{\text{elpd}}_{\text{Loo}}(\mathbf{M}_b \mid y^{\text{obs}}) \approx \text{-1938}$, SE=17



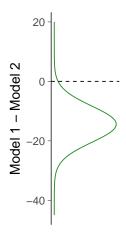
Difference: $\widehat{\text{elpd}}_{\text{Loo}}(M_a, M_b \mid y^{\text{obs}}) \approx -14.4$, SE = 6.1



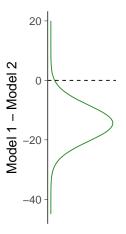
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```
> loo_compare(model1, model2)
	elpd_diff se_diff
model2 0.0 0.0
model1 -14.4 6.1
```

8 schools - Model comparison

```
\begin{array}{ccc} > \mathsf{loo\_compare}(\mathsf{pooled}\,,\,\,\mathsf{hierarchical}\,) \\ & & \mathsf{elpd\_diff} \quad \mathsf{se\_diff} \\ \mathsf{pooled} & 0.0 & 0.0 \\ \mathsf{hierarchical} & -0.3 & 0.7 \end{array}
```

No difference between pooled and hierarchical for predicting the future observations for a new school (exchangeble with the schools in the data).

Poisson vs Hurdle-Poisson example

```
\begin{array}{ccc} & & \text{elpd\_diff} & \text{se\_diff} \\ \text{Hurdle-Poisson} & 0.0 & 0.0 \\ \text{Poisson} & -215.9 & 22.1 \end{array}
```

Clear difference (which was also obvious in posterior predictive checks)

1. The models make very similar predictions

2. The models are misspecified with outliers in the data

3. The number of observations is small

- 1. The models make very similar predictions
 - if $|\widehat{\text{elpd}}_{\text{Loo}}(M_a, M_b \mid y^{\text{obs}})| < 4$, SE is not reliable, but the difference is small anyway
 - selecting a "wrong" model has small cost
 - in nested case the skewness favors the simpler model
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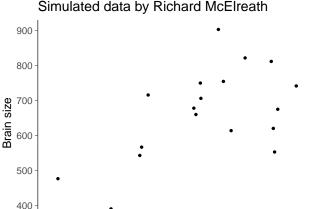
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- 3. The number of observations is small
 - in nested case the skewness favors the simpler model
 - any inference with small *n* is difficult
 - if $|\widehat{\text{elpd}}_{\text{Loo}}(\mathbf{M}_a, \mathbf{M}_b \mid y^{\text{obs}})| > 4$, model is well specified, and n > 100 then the normal approximation is good

- In nested case, often easier and more accurate to analyse posterior distribution of more complex model directly avehtari.github.io/modelselection/betablockers.html
 - instead of comparing Model 1: $y \sim \operatorname{normal}(\alpha, \sigma)$ vs Model 2: $y \sim \operatorname{normal}(\alpha + \beta x, \sigma)$ look at the posterior of β directly

- Classic example is polynomial model with increasing number of components
 - overfits also with Bayesian inference and weak priors

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50

Mass of animal

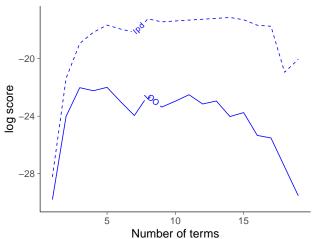
60

40

30

- Classic example is polynomial model with increasing number of components
 - overfits also with Bayesian inference and weak priors

Polynomial basis functions



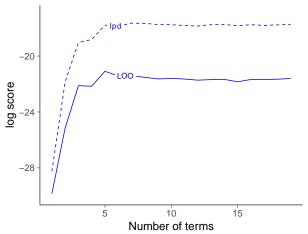
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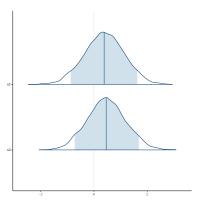
Gaussian process basis functions



Model is not needed to avoid overfitting

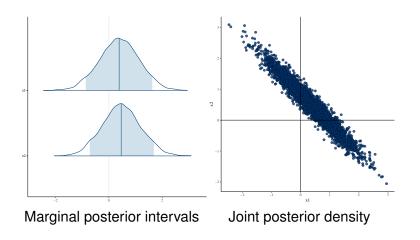
- No overfiiting when using good priors that keep the prior on the predictive space approximately constant when more components are added, e.g.
 - Gaussian procesees
 - (regularized) Horseshoe for sparsity
 - R2-D2 and R2-D2-M2 for prior on R2

Sometimes predictive model comparison can be useful



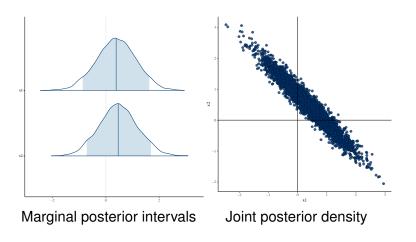
Marginal posterior intervals

Sometimes predictive model comparison can be useful



rstanarm + bayesplot

Sometimes predictive model comparison can be useful



rstanarm + bayesplot

see also Collinear demo

What if one is not clearly better than others?

- Continuous expansion including all models?
 - and then analyse the posterior distribution directly avehtari.github.io/modelselection/betablockers.html
 - sparse priors like regularized horseshoe prior instead of variable selection
 video, refs and demos at avehtari.github.io/modelselection/

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Model averaging

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- If needed integrate over the model space = model averaging

Model averaging

- Prefer continuous model expansion
- If needed integrate over the model space = model averaging
- Bayesian stacking may work better than BMA in case of misspecified models or small data
 - Yao, Vehtari, Simpson, & Gelman (2018)

Cross-validation and model selection

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 - the difference between models is clear

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 - selection process can lead to severe overfitting
- Overfitting in selection process is not unique for cross-validation

Selection induced bias and overfitting

- Selection induced bias in cross-validation
 - same data is used to assess the performance and make the selection
 - the selected model fits more to the data
 - the CV estimate for the selected model is biased
 - recognized already, e.g., by Stone (1974)

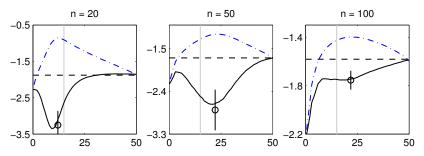
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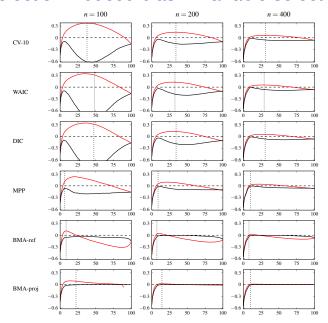
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- Bigger problem if there is a large number of models as in covariate selection

Selection induced bias in variable selection



Selection induced bias in variable selection



- It's good to think predictions of observables, because observables are the only ones we can observe
- Cross-validation can simulate predicting and observing new data
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