SOC542 Statistical Methods in Sociology II

Missing Data & Model Checking and Robustness

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Updates

- Project proposals due tomorrow at 5pm, send PDF via email
- Homework 2 grades and feedback this week

Plan

- Missing data
- Model checking
- Model robustness

Missing data

What is missing data?

- Missing data occurs when we do not have an record of any data for one or more variables for an observation.
- This can occur for a variety of reasons including
  - Skip patterns
  - Survey non-response
  - Survey error
  - Data entry errors
- The severity of the problem depends on why the data are missing and the amount of data missing

Missing data

Missing completely at random (MCAR)

- **Missing Completely at Random (MCAR)**
  - Probability x_i is missing is constant across all observations
- Discarding missing cases does not result in any bias

Missing data

Missing at random (MAR)

- **Missing at Random (MAR)**
  - Probability x_i is missing depends on observed variables.
- Discarding missing cases does not result in any bias if predictors of missingness are adjusted for.

Missing data

Missing not at random

- Missingness that depends on the missing value is considered **Missing not at Random (MNAR)**
  - e.g. Higher income respondents less likely to report income

Missing data

Simulating missingness

- We can use simulations to better understand the effects to different kinds of missingness
- Consider the following population model

$$y = 10 + 2x - 2z$$

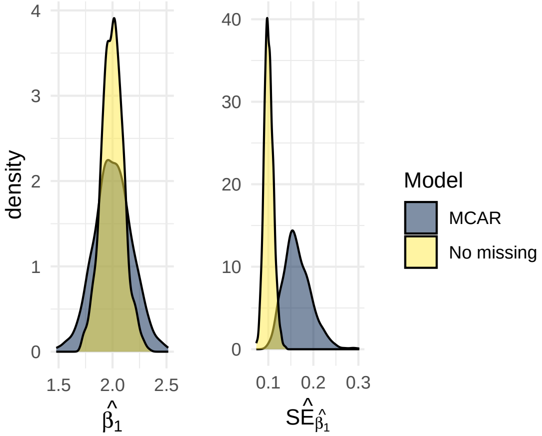
- The following regression model is estimated

$$\hat{y}_i = \hat{\beta}_0 + \hat{\beta}_1 x_i + \hat{\beta}_2 z_i + \hat{u}_i$$

- We can simulate each kind of missingess in x and analyze how it affects $\hat{\beta}_1$ and its standard error.

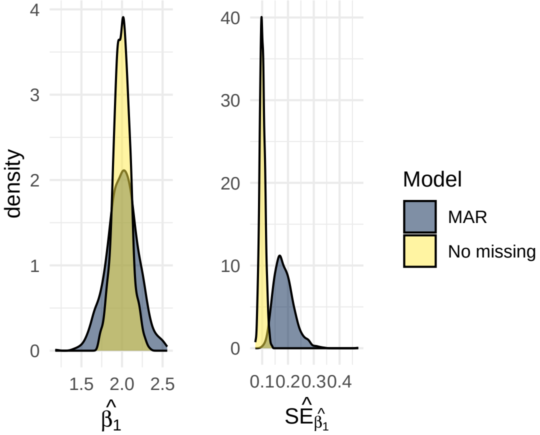
Missing data

MCAR, $p(Missing) = 0.6$



Missing data

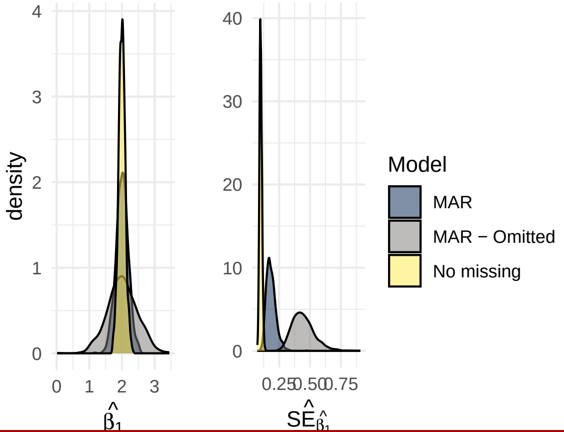
MAR, $p(Missing) = 0.8$ if $z > 0$



Missing data

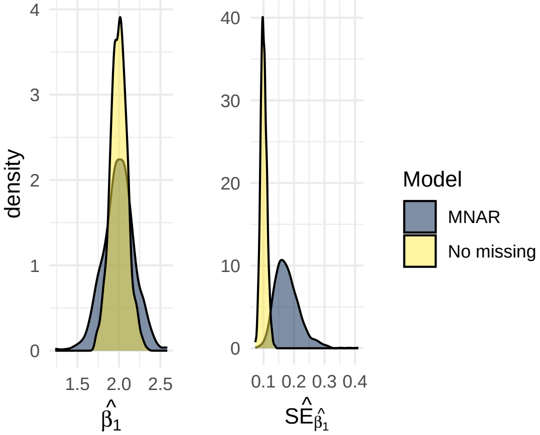
MAR, *z* omitted

```
## <ScaleContinuousPosition>
##  Range:
##  Limits:    0 --    1
```



Missing data

MNAR, $p(Missing) = 0.8$ **if** $x > -0.5$



Missing data

Missingness in practice

- It is often difficult to determine why data are missing
  - Knowledge of domain and data generation process helpful
- MCAR is a very strong assumption. MAR is more reasonable, but it is difficult to determine whether missingness is a function of an omitted variable
  - Including more predictors in a model helps to reduce such concerns
- MNAR is more problematic and may limit inferential potential

Missing data

Addressing missingness

- Three approaches
  1. Delete missing cases
  2. *Simple* imputation
  3. *Multiple* imputation

Missing data

Deleting missing data

- **Complete-case analysis / listwise deletion**
  - Delete all rows where y, x, or z are missing
- Implications
  - If not MCAR, results could be biased
  - Sample size can reduce substantially

Missing data

Deleting missing data

- **Available-case analysis / pairwise deletion**
  - Make comparisons where data are available
- In the previous example, one might use the following model to get an estimate of the effect of z on y

$$\hat{y} = \hat{\beta}_0 + \hat{\beta}_1 z_i + \hat{u}_i$$

- The x not entered into the equation to avoid dropping observations missing x.
  - One might also estimate the model including x and compare the results.
- Implications
  - Bias can occur if systematic differences between missing and non-missing cases.

Missing data

Simple imputation: Guessing the mean

- Instead of removing data, we can try to “guess” the missing values.
- A good guess is the mean of the observed data, **mean imputation**.
- Implications
  - But this can distort the distribution and underestimate the variance.

Missing data

Simple imputation

```
X <- rnorm(N)
print(mean(X))
```

```
## [1] 0.07612504
```

```
print(sd(X))
```

```
## [1] 0.9802858
```

```
X.m <- ifelse(rbinom(N, 1, 1-0.2), X, NA)
X.g <- ifelse(!is.na(X.m), X, mean(X.m[!is.na(X.m)]))
print(mean(X.g))
```

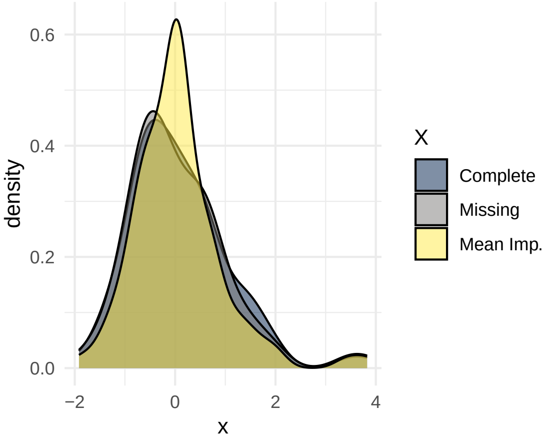
```
## [1] 0.05550062
```

```
print(sd(X.g))
```

```
## [1] 0.888347
```

Missing data

Simple imputation



Missing data

Simple imputation: Random imputation

- We can address some of the limitations of mean imputation by using the full distribution of the observed variable. This is known as **random imputation**
- However, the imputed values will not necessarily reflect the underlying association between variables and we do not make use of other information.

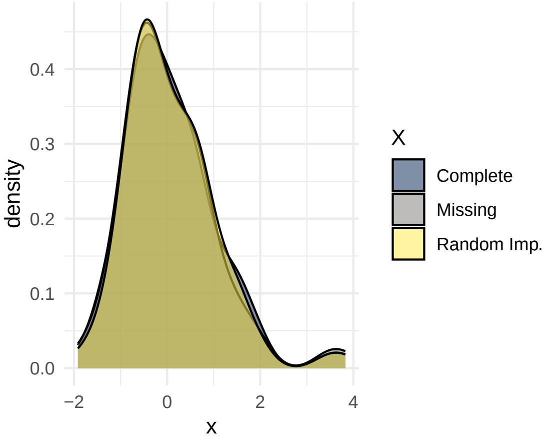
Missing data

Simple imputation: Random imputation

```
missing <- is.na(X.m)
X.g2 <- X.m
X.g2[missing] <- sample(X.m[!is.na(X.m)],
                        length(X.m[missing]),
                        replace = TRUE)
```

Missing data

Simple imputation: Random imputation



Missing data

Simple imputation: Prediction with regression

- We can improve our imputation model by making use of additional information in other variables.
  - For example, we could estimate a model to predict x using other covariates and then use these predictions in place of missing values

Missing data

Simple imputation: Prediction with regression

```r
N <- 1000
v <- rnorm(N)
w <- rnorm(N)
x <- 0.5*v + 0.5*w + rnorm(N)
y <- x - 2*w + rnorm(N)

x.m <- ifelse(rbinom(N, 1, 0.4), x, NA) # MCAR

imp.model <- lm(x.m ~ v + w)
```

Missing data

Simple imputation: Prediction with regression

```
preds <- predict(imp.model,
                 newdata = as.data.frame(cbind(v, w)))

x.imp <- x.m
for (i in 1:length(x.m)) {
    if (is.na(x.m[i])) {
        x.imp[i] <- preds[i]
    }
}
```

Missing data

Simple imputation: Prediction with regression

	Complete	Listwise	Mean	Random	Predicted
(Intercept)	-0.03	-0.04	-0.06	-0.03	-0.08
	(0.03)	(0.05)	(0.04)	(0.05)	(0.04)
x	1.04	0.99	0.89	0.34	1.02
	(0.03)	(0.04)	(0.05)	(0.04)	(0.05)
w	-2.04	-2.01	-1.69	-1.55	-2.04
	(0.03)	(0.05)	(0.05)	(0.05)	(0.05)
Num.Obs.	1000	403	1000	1000	1000
R2	0.784	0.783	0.592	0.522	0.650
R2 Adj.	0.784	0.782	0.591	0.521	0.649
RMSE	1.00	1.02	1.37	1.49	1.27

Missing data

Simple imputation

- Limitations
  - Each process becomes cumbersome if we have multiple variables with missing data and observations with more than one variable missing.
    - e.g. How do we predict x if we are missing other variables?
  - These approaches are *deterministic*, failing to take into account the uncertainty in the imputations.

Missing data

Multiple imputation

- **Multiple imputation (MI)** methods address both issues:
  - MI models use observed data to predict missing values.
  - Multiple missing variable can be imputed simultaneously.
  - Uncertainty associated with the imputation process can be incorporated into the estimates.

Missing data

Multiple imputation: Algorithms

- Multiple imputation algorithms work by using existing data to predict missing values across the entire dataset
- Generally, these algorithms use iterative procedures, predicting a subset of the missing values at a time
- These algorithms converge when the distributions of the predicted datasets look like the distributions in the original data
- Often these algorithms use Bayesian techniques such as MCMC sampling[1]

[1] See the mi command in Stata for example.

Missing data

Multiple imputation: MI in R

- There are several different MI packages available in R
- Two commonly used packages are
  - `mice` (Multivariate Imputation via Chained Equations)
  - `Amelia`
    - Particularly useful for panel data

Missing data

Multiple imputation: Pooling

- MI algorithms generate M imputed datasets.
  - In each case, we can compute an estimate, $\hat{\beta}_{1m}$ and a standard error $\hat{SE}_m$.
- The overall estimate is an average over the M datasets, known as a **pooled** estimate:[2]

$$\hat{\beta} = \frac{1}{M}\sum_{m=1}^{M}\hat{\beta}_{1m}$$

[2] See GHV p. 326 for the formula for the standard error of the pooled estimate.

Missing data

Multiple imputation with MICE

```
library(mice)
x <- x.m
data <- cbind(y, v, w, x)

M <- mice(data, m=10, method = "pmm",
          seed=08901,
          printFlag = FALSE)
```

Missing data

Multiple imputation with MICE

```r
# Impute using m=1
simple.imp <- complete(M,1)
mi.s <- lm(y ~ x + w, data = simple.imp)

# Pool over all M
fits <- with(M, lm(y ~ x + w))
mi.M <- pool(fits)
```

Missing data

Multiple imputation with MICE

	Complete	Predicted	MI m	MI M
(Intercept)	-0.03	-0.08	-0.02	-0.04
	(0.03)	(0.04)	(0.03)	(0.05)
x	1.04	1.02	0.97	0.98
	(0.03)	(0.05)	(0.03)	(0.03)
w	-2.04	-2.04	-2.01	-2.00
	(0.03)	(0.05)	(0.04)	(0.04)
Num.Obs.	1000	1000	1000	1000
Num.Imp.				10
R2	0.784	0.650	0.775	0.771
R2 Adj.	0.784	0.649	0.775	0.770
RMSE	1.00	1.27	1.02	

Missing data

Overview

- Data can be missing for several different reasons
- Important to try to diagnose reason for missingness
- Listwise deletion and simple imputation sometimes reasonable but can introduce bias, but multiple imputation preferred when several variables are missing
- Recommended to report multiple estimates to assess sensitivity to how missingness is handled

Model checking

Diagnostics

- We have already covered several different diagnostics for checking how well models fit the data
  - Residuals and standard error of the residuals
  - Predicted values
  - R^2 and adjusted R^2
  - Standard errors on coefficients and p-values
  - F-statistic

Model checking

Outliers

- Outliers are extreme data points that deviate from the distribution of other values
  - Scatterplots of raw data and residual can be helpful for identifying these
- An outlier has **leverage** if the addition of the observation results in a change in the slope of the regression line
- Such cases are considered *influential* if they result in substantial changes to the regression results
  - e.g. Differences in statistical sigificance, sign, magnitude

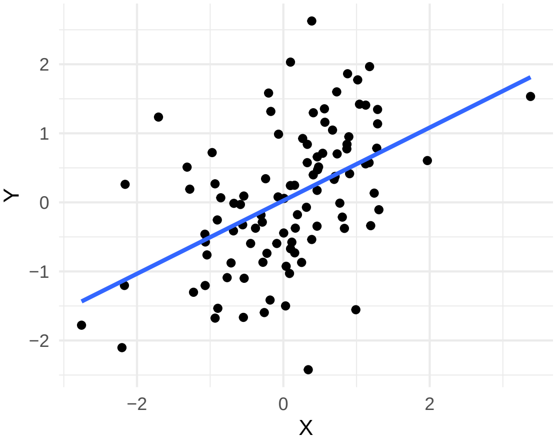
Model checking

Outliers

```r
N <- 100
X <- rnorm(N)
Y <- 0.5*X + rnorm(N)
```

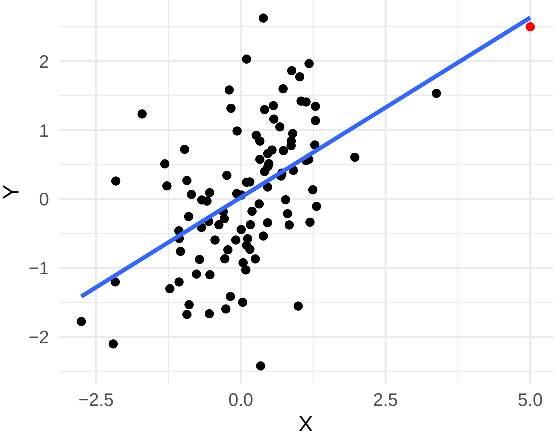
Model checking

Outliers



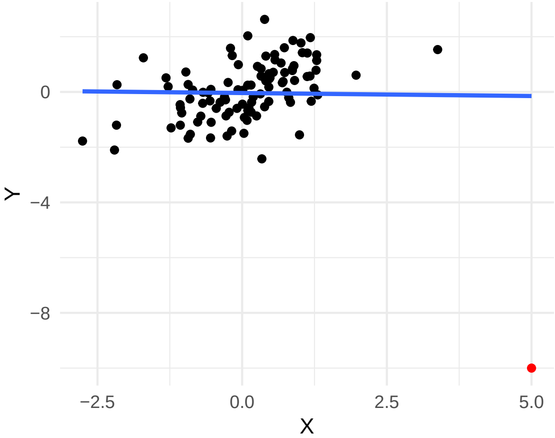
Model checking

Outliers: Outlier with low leverage



Model checking

Outliers: Outlier with high leverage



Model checking

Outliers

- Sometimes outliers may be due to data coding or quality issues, but they are often valid observations
- Summary statistics and plots can help identify outliers
- It is often defensible to drop outlier cases, but this should be clearly reported in the manuscript
  - Recommended to also conduct sensitivity checks to see how results change

Model checking

Prediction and explanation

- In sociology, we typically estimate explanatory models where the primary goal is to estimate one or more $\hat{\beta}$'s and prediction is typically used to explore relationships between variables.
- Predictive modeling focuses on **generalization error**, or how well a model predicts new data.
- This can be a useful heuristic for comparing and selecting different models, particularly when we do not have strong theory to guide model specification.[3]

[3] See Watts, Duncan J. 2014. "Common Sense and Sociological Explanations." American Journal of Sociology 120 (2): 313–51. https://doi.org/10.1086/678271 for further elaboration of this idea and Mullainathan, Sendhil, and Jann Spiess. 2017. "Machine Learning: An Applied Econometric Approach." Journal of Economic Perspectives 31 (2): 87–106. https://doi.org/10.1257/jep.31.2.87 for some discussion of the limitations of predictive modeling.

Model checking

Underfitting

- A model is **underfit** if it does not sufficiently explain the variance in the outcome.
- Consider the following population model:

$$y = \beta_0 + \beta_1 x + \beta_2 x^2 + u$$

- The following model underfits because it does not account for the quadratic relationship:

$$\hat{y} = \hat{\beta}_0 + \hat{\beta}_1 x + u$$

- In short, we fail to observe the *signal* in the data.

Model checking

Overfitting

- A model is **overfit** if it also explains *noise* in addition to the signal in the data.
- Using the previous population, consider we estimate the following model:

$$\hat{y} = \hat{\beta}_0 + \hat{\beta}_1 x + \hat{\beta}_2 x^2 + \hat{\beta}_3 z + \hat{\beta}_4 z^2 + u$$

- The additional parameters $\hat{\beta}_3$ and $\hat{\beta}_4$ do not correspond to any of the population parameters, but may still explain some of the random variance in the outcome.

Model checking

Underfitting, overfitting, and generalization error

- Models suffering from under and overfitting will fail to generalize.
  - Underfit models do not sufficiently explain variation in the outcome in the sample or population.
  - Overfit models explain patterns in the sample that do not generalize to the population.

Model checking

Cross-validation

- **Cross-validation** is an approach used in machine-learning to assess the extent to which a predictive model can generalize to unseen data.
- The technique allows us to measure generalization error:
  1. Estimate an model using a sample X.
  2. Use the fitted model to predict the outcome for a new dataset X'.
  3. Compare the predictive accuracy (e.g. mean squared error) across the two datasets:
     - Model generalizes well if $MSE(\hat{y} = f(X)) \approx MSE(\hat{y} = f(X'))$ and both are low
     - Model overfits if $MSE(\hat{y} = f(X)) << MSE(\hat{y} = f(X'))$
     - Model underfit if both MSE scores are high

Model checking

Cross-validation

- Different kinds of cross-validation procedures are often used to evaluate generalization error:
  - **k-fold cross-validation**: data are split into k subsets. Models are estimated using $k-1$ subsets and predictions made for held-out set. Prediction error is averaged over k held-out sets.
  - **Leave-one-out cross-validation**: same procedure where each subset is a single datapoint. Requires estimation of N models.

Model checking

Cross-validation: `loo`

- The `rstanarm` package includes a function `loo`, which computes an approximation of leave-one-out cross-validation, avoiding the need to fit N models.
- Models can be compared using the *expected log pointwise predictive density* (ELPD), a quantity that captures the predictive accuracy of the model (McElreath 7.2-4, GHV 11.8).
- The function can also be used to compute a k-fold CV score and information theoretic measures of model fit.[4]

[4] See the documentation and vignette for further details on implementation.

Model checking

Cross-validation: LOO-CV

```
x <- rnorm(N)
z <- rnorm(N)
y <- 0.1*x + 2*(x^2) + rnorm(N)
df <- as.data.frame(y,x,z)

m <- stan_glm(y ~ x + I(x^2),  data = df,
                family = "gaussian", chains =1 , refresh = 0)
m.u <- stan_glm(y ~ x,  data = df,
                family = "gaussian", chains =1 , refresh = 0)
m.o <- stan_glm(y ~ x + I(x^2) + z + I(z^2),  data = df,
                family = "gaussian", chains =1 , refresh = 0)
```

Model checking

Cross-validation: LOO-CV

The loo function provides an approximation of the LOO-CV for an estimated model

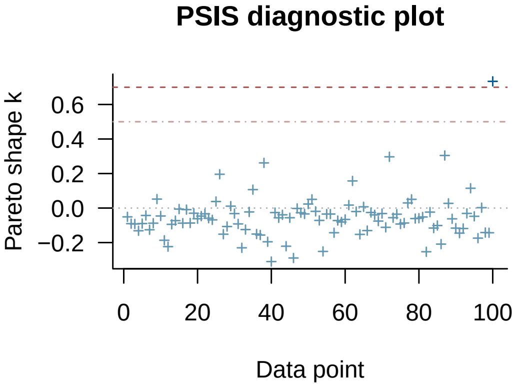
```
print(loo(m))
```

```
##
## Computed from 1000 by 100 log-likelihood matrix
##
##          Estimate   SE
## elpd_loo   -150.1  6.7
## p_loo         3.1  0.5
## looic       300.2 13.5
## ------
## Monte Carlo SE of elpd_loo is 0.1.
##
## All Pareto k estimates are good (k < 0.5).
## See help('pareto-k-diagnostic') for details.
```

Model checking

Cross-validation: LOO-CV

Individual points are scored using Pareto-Smoothed Importance Sampling (PSIS). High *pareto k* values ($k > .7$) indicate observations with high leverage.



Model checking

Cross-validation: LOO-CV

- loo_compare can be used to compare different models. The results rank the models from best to worst.

```
loo_compare(loo(m), loo(m.u), loo(m.o))
```

```
##      elpd_diff se_diff
## m       0.0       0.0
## m.o    -2.1       0.8
## m.u -107.1      17.8
```

Model checking

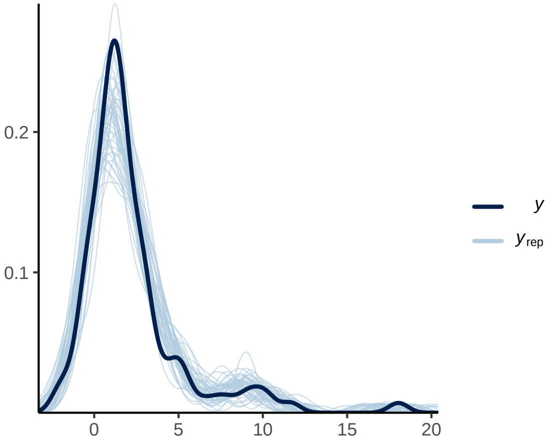
Posterior predictive checks

- We can also evaluate Bayesian models by examining the posterior predictive distribution.
- Recall that Bayesian models are *generative*:
  - We can use the posterior distribution to make predictions, creating new, hypothetical datasets.
- These predictions can be used to evaluate how well the models fit the data, including key statistics.

Model checking

Posterior predictive checks

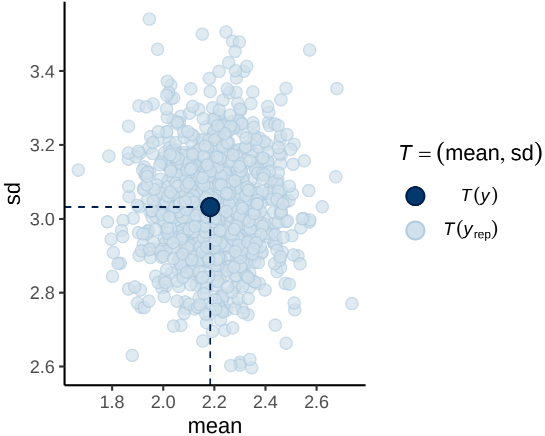
```
pp_check(m) + theme_classic()
```



Model checking

Posterior predictive checks

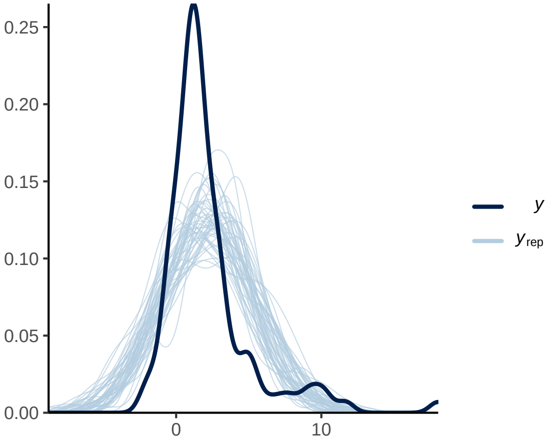
```
pp_check(m, plotfun = "stat_2d", stat = c("mean", "sd")) + theme_classi
```



Model checking

Posterior predictive checks

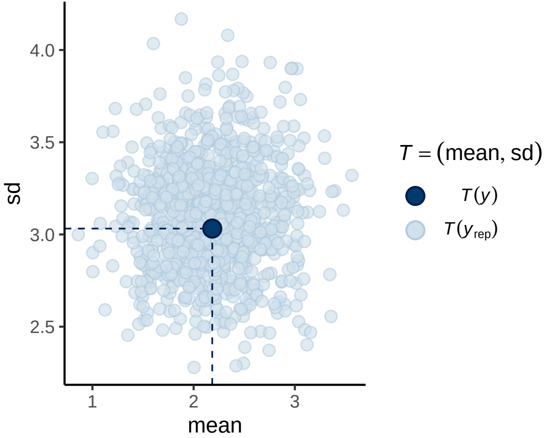
```
pp_check(m.u) + theme_classic()
```



Model checking

Posterior predictive checks

```
pp_check(m.u, plotfun = "stat_2d", stat = c("mean", "sd")) + theme_clas
```



Model checking

Additional Bayesian diagnostics

- There are several other diagnostics specific to Bayesian inference and help to determine whether the MCMC algorithms have worked.[5]
  - **R-hat values** indicate whether a model has converged.
    - Values should be 1.01 or less.
  - **Divergent transitions** indicate problems with the MCMC estimation.
    - The sampler is making large “jumps” rather than smoothly exploring the posterior distribution. You will receive a warning in the output.
  - **Trace plots** are useful for assessing MCMC chains.
    - Ideally, chains should be moving randomly, without strong autocorrelation.

[5] See the Stan documentation for discussion of these issues and how to address them.

Model checking

Multicollinearity

- Recall that multicollinearity occurs when predictors are highly correlated and results in increased variance.
- High pairwise correlations might indicate *potential* collinearity, but the issue can only be diagnosed after controlling for all relevant predictors.

Model checking

Multicollinearity: VIF

- The **Variance Inflation Factor (VIF)** can be used to diagnose highly collinear predictors.
- Consider the population model $y = \beta_0 + \beta_i x_i + \beta_j x_j + ... + \beta_k x_k + u$
- A score is calculated for each *independent variable* using the following approach:
  - For x_i in $x_{i=1}, ..., x_k$, regress $x_i = \alpha_0 + \alpha_1 x_j + ... + \alpha_2 x_k + u$
  - Use R^2 from the model to calculate $VIF(\hat{\beta}_i) = \frac{1}{1 - R_i^2}$
- VIF scores greater than $\approx 5 - 10$ indicate that a predict is highly collinear with one or more of the other predictors.

Model checking

Multicollinearity: VIF

```
N <- 1000
x <- rnorm(N)
x2 <- rnorm(N)
x3 <- 3*x + rnorm(N)
y <- x + 2*x2 + 0.5*x3 + rnorm(N)
m <- lm(y ~ x + x2 + x3)

library(car)
vif(m) %>% round(1)
```

```
##   x  x2  x3
## 9.6 1.0 9.6
```

Model robustness

Defining robustness

- **Model robustness** refers to how *robust* the results of a given model are to alternative specifications.
  - The concern is that a result (such as $p < 0.05$) is sensitive to a particular, arbitrary specification.
- We typically try to mitigate such concerns by estimating several specifications of a model.

Model robustness

How robust are our results?

- Recent work calls for greater attention to specification issues as a way to address robustness concerns (Young and Holsteen 2017, Muñoz and Young 2018).
  - Critique: Reporting a handful of ad hoc specifications is insufficient to ensure robustness.
  - Solution: Estimate models with *every possible combination of independent variables* and assess the distribution of coefficients.
  - The goal is to explore the entire *model space* and to construct a distribution of estimates.

Model robustness

How robust are our results?

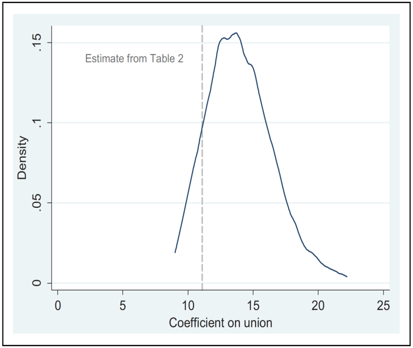


Figure 1. Modeling distribution of union wage premium.
Note: Kernel density graph of estimates from 1,024 models. Vertical line indicates the preferred estimate of an 11 percent union wage premium as reported in Table 2.

Young and Holsteen 2017.

Model robustness

How robust are our results?

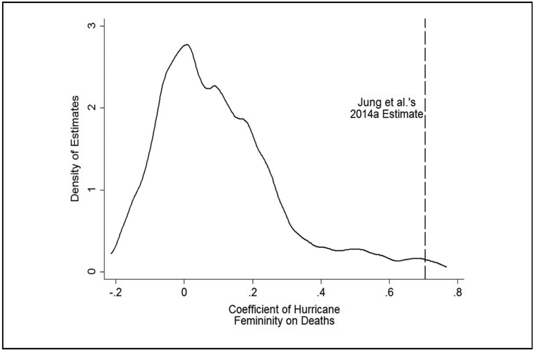


Figure 3. Model robustness results on Jung et al. (2014a) data.
Note: Kernel density graph of estimates from 1,152 models. See Table 6 for more information about the modeling distribution.

Muñoz and Young 2018.

Model robustness

Bayesian Model Averaging

- Bayesian statisticians have proposed a similar idea known as **Bayesian Model Averaging (BMA)**
  - Estimate several models and construct an average across the models, weighted by the model fit, i.e. higher weights to better models.
- There has been some debate about whether this approach is preferable to the Young-Holsteen-Muñoz technique.
  - Proponents of BMA contend that we should not weight all models equally, some are better than others.
  - Young and colleagues argue that it is problematic to weight different models if we do not know which is better a priori and that weighting requires more assumptions.[6]

[6] See Slez' 2017 comment on Young and Holsteen and the rejoinder by the latter and Bruce Western's 2018 comment on Muñoz and Young

Model robustness

Multiverse analysis

"We suggest that instead of performing only one analysis, researchers could perform a multiverse analysis, which involves performing all analyses across the whole set of alternatively processed data sets corresponding to a large set of reasonable scenarios . . . A multiverse analysis offers an idea of how much the conclusions change because of arbitrary choices in data construction and gives pointers as to which choices are most consequential in the fragility of the result."[7]

[7] Steegen et al. 2016

Conclusions

- Missing data
  - Carefully examine any patterns of missing data
  - Choose an appropriate strategy to address the problem
- Model checking
  - Use diagnostic checks to identify and address potential issues with models
- Model robustness
  - Estimate multiple specifications to ensure results are robust
  - Robustness simulations, BMA, and multiverse analyses provide systematic approaches to evaluate robustness

Next week

- Spring break!
- After spring break
  - Generalized linear models

Lab

- Missing data and imputation