Information related to Exam 1.

1 Information

- When: Tu Oct 11, 230-430PM (note later end time as compared to class time).

- Where: The exam is in person for all students, except for those students registered via UWW or those who have indicated at the start of the course that they need to be online for specific reasons.

- In-person location: Morill MOR1N349 (note different class room to accommodate later end time!). I will email students who take it online separately with details.

- Material:

  - All modules so far, 1-8
  - HWs 1,2,3. Extra credit HW questions are included except for HW2-2b (properties of Bayes estimators, this question HW2-2b is excluded from the material for this exam).
  - Additional note: when provided with a model specification and corresponding formula and output from a `brm` fit, you are expected to be able to read the information from the summary of the fit. An example is included slide 15, module 8, and below, from hw3 exercise 3.

Format of exam/what types of Qs to expect:

- Exam is closed book but I will add the pdf of a normal density in the exam itself, that you can refer to if needed, as follows:

  - When $y|\mu, \sigma^2 \sim N(\mu, \sigma^2)$, then $p(y|\mu, \sigma^2) = \frac{1}{\sqrt{2\pi}\sigma} \exp\left(\frac{-1}{2\sigma^2}(\mu - y_i)^2\right)$.

- There is no model fitting/use of R/Stan in this exam.

- In the exam, you will be presented with information about a data set, a research question or questions associated with those data, the specification one or more models (including at least one hierarchical regression model), and printed outputs from selected model(s). Based on the information provided, you may be asked a variety of questions, including but not limited to questions related to

  - interpretation of model parameters,
  - how to construct point point estimates and CIs for outcomes of interest using posterior samples from a model fit (you would not able to do the calculation but instead, you would write out in equations how you would go about calculating the outcomes of interest),
  - interpretation of MCMC diagnostics.

```
summary(fit)
```

```
##  Family: gaussian
##   Links: mu = identity; sigma = identity
## Formula: y ~ (1 | ethnicgroup)
##    Data: dat (Number of observations: 2400)
##   Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup draws = 4000
##
## Group-Level Effects:
## ~ethnicgroup (Number of levels: 40)
##               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)     1.10      0.15     0.84     1.43 1.01      704     1192
##
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept    20.06      0.20    19.67    20.47 1.01      454      787
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma     2.01      0.03     1.96     2.07 1.00     4329     2893
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

The point estimates (means or medians) are given below, as well as the 95% CIs:\

Parameter	Posterior mean	95% CI
μ_α; Intercept	20.1	(19.7, 20.5)
σ_α; sd(Intercept)	1.10	(0.84, 1.43)
σ_y; sigma	2.01	(1.96, 2.07)