

# Problem Set 3

Michael Fryer

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Collaborators: ...

## 1 Entropy & Divergence

```
# Calculate Information Entropy
calc_entropy <- function(l) return(-sum(l*log(l)))
```

Suppose biased coin lands heads 60% of the time.

a) What is the entropy of this coin?

```
# 60% heads, 40% tails
p <- c(0.6, 0.4)
entropy.p <- calc_entropy(p)
```

```
## Entropy: 0.6730117
```

b) Suppose another biased coin lands tails 30% of the time. Which coin has higher entropy? Justify and explain your answer.

```
# 70% heads, 30% tails
q <- c(0.7, 0.3)
entropy.q <- calc_entropy(q)
```

```
## Entropy: 0.6108643
```

*The coin in part a) has a higher entropy than the coin in b). This is because the variance in the probabilities in b) is larger than in a) i.e. the more unique events there are with similar probabilities of occurring, the larger the entropy will be.*

c) Suppose the first coin is the true distribution and the second coin's distribution is your approximation of the first coin. What is the KL divergence between these two distributions? Explain and justify your answer.

*KL divergence is defined as:*

$$D_{KL}(p, q) = \sum_i p_i \log \left( \frac{p_i}{q_i} \right)$$

```
kl <- sum(p*log(p/q))
```

```
## KL divergence: 0.02258242
```

*We observe a KL divergence of 0.022. We expect this value to be small as p and q are relatively "close" together and the KL divergence is the average difference in log probabilities between the two models. This value would be much larger if instead q = {0.9, 0.1}.*

## 2 Collider Bias and Information Criteria

Return to the textbook example in §6.3.1, which explores the relationship between age, marriage and happiness. This example makes use of the simulation model `sim_happiness()`, which is part of the `rethinking` package:

```
d <- sim_happiness(seed=1515 , N_years=1000)
d.adults <- d[d$age > 17,] # only adults
d.adults$A <- (d.adults$age - 18) / (65 - 18)
d.adults$mid <- d.adults$married + 1
```

Compare the two models, `m6.9` and `m6.10`, using both PSIS and WAIC scores using `compare()`.

*Fit m6.9 and m6.10.*

```
# Model m6.9
m6.9 <- quap(
  alist(
    happiness ~ dnorm(mu, sigma),
    mu <- a[mid] + bA*A,
    a[mid] ~ dnorm(0, 1),
    bA ~ dnorm(0, 2),
    sigma ~ dexp(1)
  ),
  data=d.adults
)

# Model m6.10
m6.10 <- quap(
  alist(
    happiness ~ dnorm(mu, sigma),
    mu <- a + bA*A,
    a ~ dnorm(0, 1),
    bA ~ dnorm(0, 2),
    sigma ~ dexp(1)
  ),
  data=d.adults
)
```

*Score the models.*

```
psis.compare <- compare(m6.9, m6.10, func=PSIS)

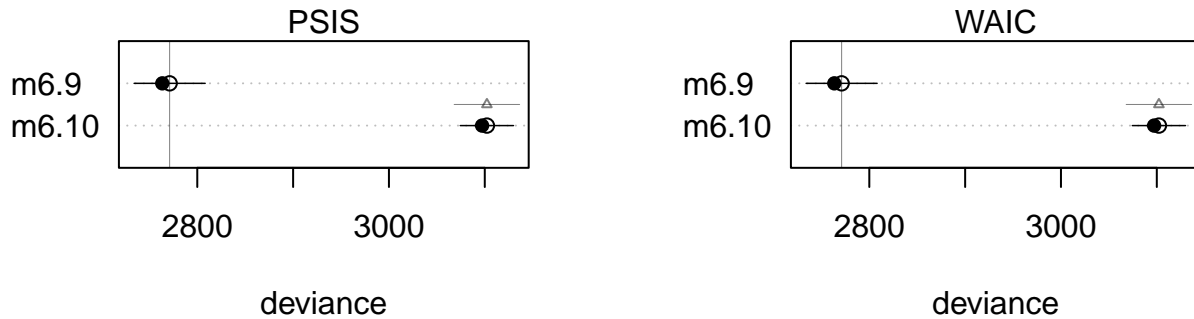
waic.compare <- compare(m6.9, m6.10, func=WAIC)
```

*Chart the models.*

##	PSIS	SE	dPSIS	dSE	pPSIS	weight
## m6.9	2771.139	37.10321	0.0000	NA	3.823583	1.000000e+00
## m6.10	3102.217	27.77867	331.0777	34.17721	2.512896	1.280557e-72

##	WAIC	SE	dWAIC	dSE	pWAIC	weight
## m6.9	2771.107	37.08184	0.0000	NA	3.807557	1.000000e+00
## m6.10	3102.197	27.76361	331.0901	34.17543	2.503099	1.272606e-72



a) Which model is expected to make better predictions according to these two information criteria? Explain your answer.

*In both cross-validation approximators, a lower score is better. With that metric in mind, both WAIC and PSIS expect m6.9 to be a better prediction model. However, it should be noted that both the standard error (SE) and prediction penalty (pPSIS and pWAIC) are higher in m6.9. This means that while m6.9 is a better predictor according to WAIC and PSIS, it has more uncertainty, SE.*

b) On the basis of the causal model, how should you interpret the parameter estimates from the model preferred by PSIS and WAIC?

*As WAIC and PSIS are cross-validation approximators, they estimate of how well a model does at **predictions**, one cannot, and should not, use them to inform any decisions about **causations**. That is, WAIC and PSIS scores have no bearing on if the model is the "correct" causal model. In fact, m6.9 is **not** the correct causal model, m6.10 is.*

### 3 Tulips and Interactions

Tulips need both water and light to bloom. But do water and light work independently, or do they interact? The tulips dataset in the rethinking package contains experimental data on tulip blooms under different conditions.

```
data(tulips)
d <- tulips
str(d)
```

```
## 'data.frame': 27 obs. of 4 variables:
## $ bed : Factor w/ 3 levels "a","b","c": 1 1 1 1 1 1 1 1 1 2 ...
## $ water : int 1 1 1 2 2 2 3 3 3 1 ...
## $ shade : int 1 2 3 1 2 3 1 2 3 1 ...
## $ blooms: num 0 0 111 183.5 59.2 ...
```

The dataset contains:

- **bed**: Bed identifier (grouping variable)
- **water**: Amount of water (1 = low, 2 = medium, 3 = high)
- **shade**: Amount of shade (1 = low, 2 = medium, 3 = high)
- **blooms**: Number of blooms produced

Before fitting any models, standardize the predictor variables and the outcome:

*Below, I do not standardize the predictor variables and the outcome. Instead, I scale the outcome to [0,1] and center the predictor variables such that the values are -1,0,1. This accomplishes a similar goal as standardizing but makes it easier to reason about.*

```
# Scale blooms to [0, 1]
d$B <- (d$blooms - min(d$blooms))
d$B <- d$B / max(d$B)
```

```
# Center water and shade st. the values are {-1,0,1}
d$W <- d$water - mean(d$water)
d$S <- d$shade - mean(d$shade)
```

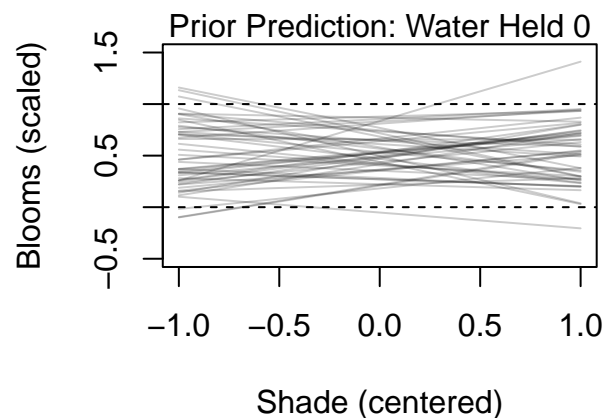
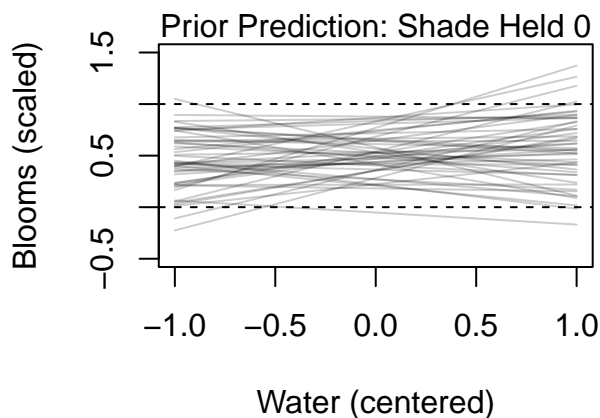
a) Fit a model (m3.1) that predicts blooms using water and shade as independent predictors (no interaction). That is, assume the effect of water on blooms is the same regardless of shade level, and vice versa.

Use prior predictive simulation to justify your priors. Write 2-3 sentences explaining your choice of priors.

**Hint:** With standardized variables, you should use relatively weak priors. A slope of 2.0 would be implausibly large for most ecological relationships.

*Since we are scaling and centering our data instead of standardizing it, our priors will not all be mean 0. We will predict our outcome prior will have  $\mu = 0.5$  as we scaled our blooms to  $[0, 1]$  and the predictor prior will have  $\mu = 0$  as we centered that data. For our standard deviations, we will use  $\sigma = 0.25$  for our outcome prior. This is because  $\pm 2\sigma$  would put blooms at impossible values for our small world i.e.  $> 0$  or  $< 1$ . For the same reasons, we will use  $\sigma = 0.25$  for our predictor variables.*

```
N <- 50
a <- rnorm(N, 0.5, 0.25)
bS <- rnorm(N, 0, 0.25)
bW <- rnorm(N, 0, 0.25)
```



```
m3.1 <- quap(
  alist(
    B ~ dnorm(mu, sigma),
    mu <- a + bW*W + bS*S,
    a ~ dnorm(0.5, 0.25),
    bW ~ dnorm(0, 0.25),
    bS ~ dnorm(0, 0.25),
    sigma ~ dexp(1)
  ),
  data=d
)
```

b) Now fit a model (m3.2) that includes an interaction between water and shade. This allows the effect of water on blooms to depend on the level of shade (and vice versa).

**Hint:** In the model formula, you can specify the interaction as  $W * S$ , which is shorthand for  $W + S + W * S$ . Or you can write out all three terms explicitly.

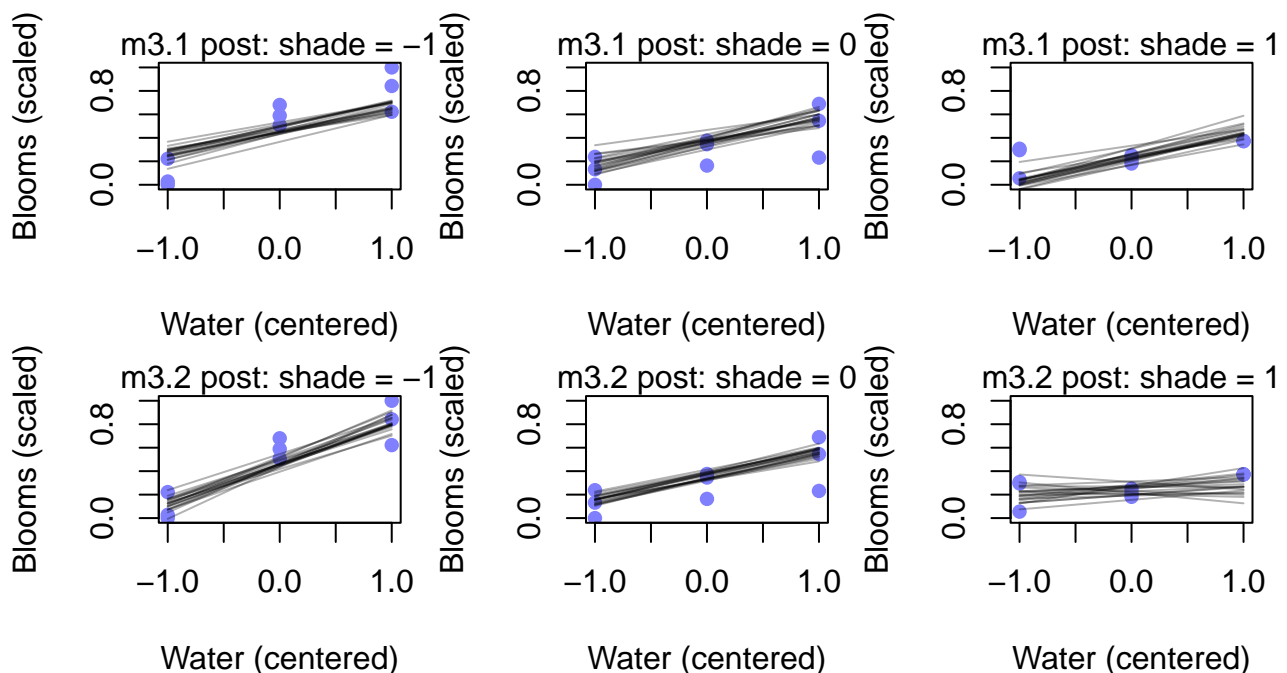
```
m3.2 <- quap(
  alist(
```

```

B ~ dnorm(mu, sigma),
mu <- a + bW*W + bS*S + bWS*W*S,
a ~ dnorm(0.5, 0.25),
bW ~ dnorm(0, 0.25),
bS ~ dnorm(0, 0.25),
bWS ~ dnorm(0, 0.25),
sigma ~ dexp(1)
),
data=d
)

```

Plot the posterior predictions for both models (m3.1 and m3.2) side by side. For each model, create a plot showing how predicted blooms change with water at different levels of shade (e.g., plot three lines for shade = -1, 0, 1).



c) Use both PSIS and WAIC to compare your two models. Which model is expected to make better predictions? Is the difference substantial?

Create the comparison plot using `plot(compare(m3.1, m3.2))` and interpret what you see. Write 3-4 sentences explaining:

- Which model performs better
- How large the difference is relative to the standard error
- What this tells you about whether water and shade interact in affecting tulip blooms

Score the models.

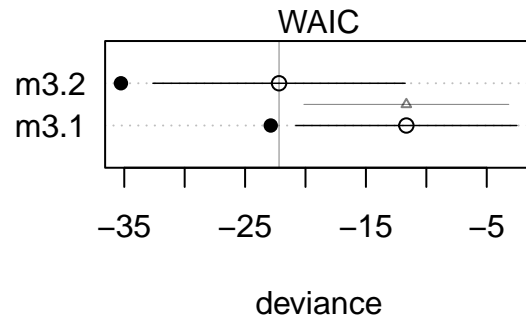
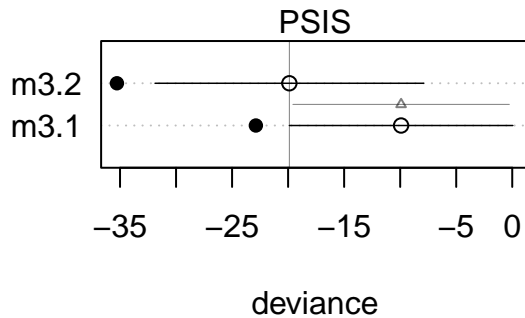
```
psis.compare <- compare(m3.1, m3.2, func=PSIS)
```

```
waic.compare <- compare(m3.1, m3.2, func=WAIC)
```

Chart the models.

##	PSIS	SE	dPSIS	dSE	pPSIS	weight
## m3.2	-19.888147	11.98897	0.000000	NA	7.693312	0.993208772
## m3.1	-9.917529	9.97304	9.970618	9.657799	6.479925	0.006791228

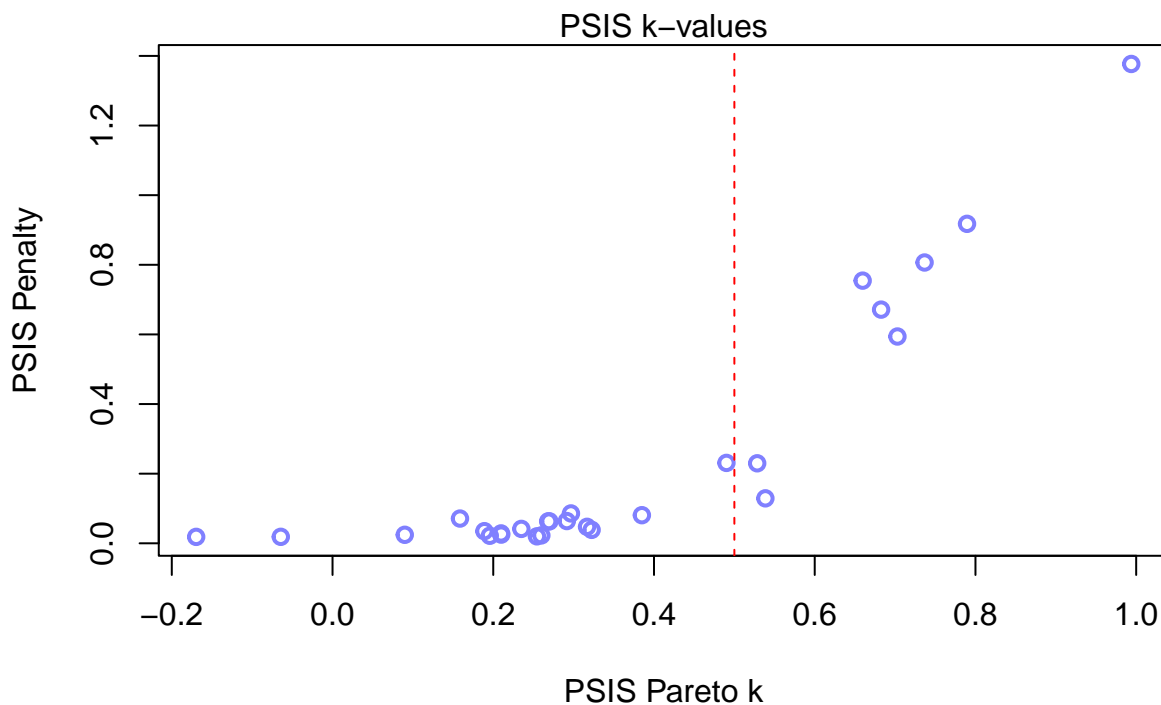
##	WAIC	SE	dWAIC	dSE	pWAIC	weight
## m3.2	-22.19026	10.438988	0.00000	NA	6.542255	0.994873897
## m3.1	-11.65372	9.145693	10.53654	8.481705	5.611829	0.005126103



When comparing our two models using PSIS and WAIC we see similar results. With each method, m3.2 is expected to perform better (lower values). When comparing the difference, *dPSIS* and *dWAIC*, we observe that it is slightly larger than the standard error *SE* which tells us that these models are substantially different. What the result of this comparison tells us is that when including interaction, m3.2 we get better results on our predictions.

d) Examine the pointwise PSIS diagnostics for your preferred model. Are there any problematic observations (high Pareto *k* values)? If so, which observations are influential and why might they be outliers?

**Hint:** Use `PSIS(model, pointwise=TRUE)` and examine the *k* values.



## Max Pareto k-value: 0.994

## Values >0.5: 6 (22.2%)

When there are Pareto *k* values above 0.5, their importance weight can be unreliable. This is an indicator of a potential outlier. The highest Pareto *k* value we observe is 0.994 with 6 total observations (22.2%) being above 0.5.

e) Based on your analysis, write 2-3 sentences answering: Do water and light work independently to affect tulip blooms, or do they interact? What does this mean biologically?

*Given that the model which included the interaction has the highest score in both PSIS and WAIC, it is tempting to assume that*

*As stated above, we observe shifting slopes in **b)** for **m3.2** at varying levels of shade. This would not be able to happen if there was not interaction. Given that **m3.2** is also the best performing model, it is tempting to affirm that this implies causation. That is, that water and shade interact to cause blooms. However, we cannot make causal affirmations based on the WAIC and PSIS score. That being said, there is a possible biological explanation for such an interaction to support the causal claim. That being, that tulips need both light and water to produce blooms. This is, of course, obvious. Plants need light and nutrients to grow.*

## 4 Reflection

Look back at Problems 2 and 3. Both involve interactions, but of different kinds:

- In Problem 2, you examined collider bias, where conditioning on a variable (marriage status) creates a spurious association between age and happiness
- In Problem 3, you examined multiplicative interactions, where the effect of one variable (water) depends on the level of another (shade)

Write 3-4 sentences explaining: What is the difference between these two types of “interactions”? How are they similar and how are they different from a causal modeling perspective?

## 5 AI Declaration

AI was not used for this assignment although, I probably should have because I had a bug in my models where I had  $d \sim \exp(1)$  written instead of  $d \sim \text{dexp}(1)$  so the predictions made no sense and it took me forever to find it.

## 6 Appendix

```
# Plots a standardized predictor x
plot_prior_prediction <- function(x, ylim, xlab, ylab, title="Prior Prediction") {
  plot(NULL, xlim=range(x), ylim=ylim, xlab=xlab, ylab=ylab)
  mtext(title)
  # Graph all the lines
  for (i in 1:N) {
    curve(a[i] + b[i]*x,
          from=min(x), to=max(x),
          col=col.alpha("black", 0.2), add=TRUE
    )
  }
  # Bounds of impossibilities
  abline(h=0, lty=2)
  abline(h=1, lty=2)
}

# Plot the posterior predictions for blooms
plot_post_prediction_blooms <- function(m, m.name) {
  for (s in -1:1) {
    i <- which(d$S==s)
    plot(d$W[i], d$B[i],
         xlim=c(-1, 1), ylim=c(0, 1),
         xlab="Water (centered)", ylab="Blooms (scaled)",
         pch=16, col=rangi2
    )
    mtext(sprintf("%s post: shade = %d", m.name, s))
    post <- link(m, data=data.frame(S=s, W=-1:1))
    for (j in 1:20) lines(-1:1, post[j,], col=col.alpha("black", 0.3))
  }
}

# Plot psis k-values
psis <- PSIS(m3.1, pointwise=TRUE)
plot(psis$k, psis$penalty,
     xlab="PSIS Pareto k", ylab="PSIS Penalty",
     col=rangi2, lwd=2
)
mtext("PSIS k-values")
abline(v=0.5, col="red", lty=2)
```