

midterm

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```
library(dagitty)
library(rethinking)
library(dplyr)
library(splines)
library(ggplot2)
```

Question 1

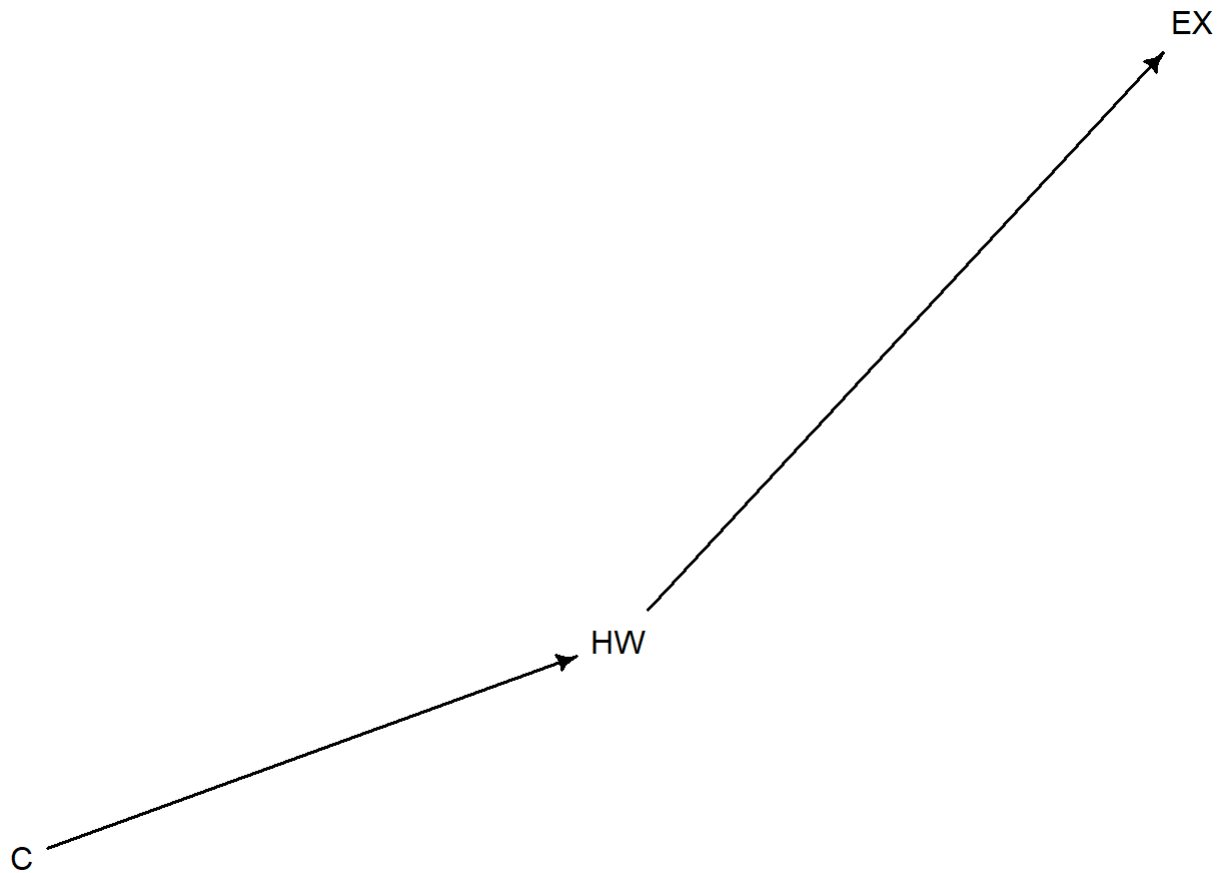
1 Conscientiousness; Exam time; Homework scores

As conscientiousness (C) is a relatively stable personality trait, we can assume no causal paths enter C. Given that C predicts GPA, we can posit a path from C to homework score (HW), probably due to more time spent on the course overall. Higher homework scores indicate understanding of the material, which would lead to faster exam times (EX). Thus we can hypothesize a causal path from HW to EX.

This gives us the DAG:

```
dag1 <- dagitty( "dag{
C -> HW -> EX }" )

drawdag(dag1)
```



```
impliedConditionalIndependencies(dag1)
```

```
## C _||_ EX | HW
```

2

For the first DAG; Assuming all variables are standardized

$HW \sim N(\mu, \sigma)$

$\mu = a + b_1 * C$

$EX \sim N(\mu, \sigma)$

$\mu = a + b_2 * HW$

3 & 4

```
d1 <- read.csv("HuongIER.csv")
d1$C <- standardize(d1$Conscientiousness)
d1$HW <- standardize(d1$Homework)
d1$EX <- standardize(d1$Duration)
```

```

m1 <- quap(alist(
  # HW <- C
  HW ~ dnorm(mu_HW, sigma_HW),
  mu_HW <- a_HW + b1*C,
  a_HW ~ dnorm(0, 0.2),
  b1 ~ dnorm(0, 0.5),
  sigma_HW ~ dexp(1),

  # EX <- HW
  EX ~ dnorm(mu_EX, sigma_EX),
  mu_EX <- a_EX + b2*HW,
  a_EX ~ dnorm(0, 0.2),
  b2 ~ dnorm(0, 0.5),
  sigma_EX ~ dexp(1)

),data=d1)

```

```
precis(m1)
```

##		mean	sd	5.5%	94.5%
##	a_HW	6.905000e-06	0.04881911	-0.07801547	0.07802928
##	b1	9.469843e-01	0.05094026	0.86557192	1.02839668
##	sigma_HW	2.847768e-01	0.03540160	0.22819819	0.34135537
##	a_EX	-2.176478e-05	0.08850541	-0.14147051	0.14142698
##	b2	-7.890414e-01	0.09860633	-0.94663337	-0.63144945
##	sigma_EX	5.583043e-01	0.06910002	0.44786909	0.66873943

The coefficients support the hypothesis, with a large positive association between C and HW ($b_1=0.95$, 89% CI: 0.87 to 1.03), and large negative association between HW and EX ($b_2=-0.79$, 89% CI: -0.95 to -0.63). We can also test the conditional independency implied by the DAG

- CI = credibility interval of the posterior

```

m2 <- quap(alist(
  # EX ~ C + HW
  EX ~ dnorm(mu, sigma),
  mu <- a + bC*C + bHW*HW,
  a ~ dnorm(0, 0.2),
  c(bC, bHW) ~ dnorm(0, 0.5),
  sigma ~ dexp(1)
),data=d1)

```

```
precis(m2)
```

```
##           mean      sd      5.5%      94.5%
## a      -3.895769e-07 0.08886643 -0.1420261  0.1420253
## bC     -1.609330e-01 0.25281895 -0.5649865  0.2431205
## bHW     -6.407442e-01 0.25328282 -1.0455391 -0.2359494
## sigma  5.611404e-01 0.06976911  0.4496359  0.6726449
```

The zero-order correlation matrix:

```
d1 %>% select(C, HW, EX) %>% cor()
```

```
##           C           HW           EX
## C      1.0000000  0.9568923 -0.7805966
## HW     0.9568923  1.0000000 -0.8207747
## EX    -0.7805966 -0.8207747  1.0000000
```

It seems the strong negative correlation between C and EX is explained by HW, as evidenced by the uncertainty of the posterior distribution of the bC slope in the multiple regression.

Thus, the proposed DAG is supported by the data.

Question 1

```
rm(list=ls())
d2 <- read.csv("HuongYerkes.csv")
str(d2)
```

```
## 'data.frame':   40 obs. of  3 variables:
## $ Subject   : int  1 2 3 4 5 6 7 8 9 10 ...
## $ Motivation: int  0 0 0 0 0 0 0 0 0 0 ...
## $ Score     : int  80 64 71 88 69 70 64 69 76 76 ...
```

```
d2$M <- standardize(d2$Motivation)
d2$S <- standardize(d2$Score)
d2$M_sq <- d2$M^2
```

We will test and compare a linear model, a quadratic model, and a spline while using regularizing (narrow) priors to reduce risk of overfitting

Linear model:

$$S \sim N(\mu, \sigma)$$

$$\mu = a + b * M$$

Quadratic model:

$$S \sim N(\mu, \sigma)$$

$$\mu = a + b_1 M + b_2 M^2$$

B-Spline:

$S \sim N(\mu, \sigma)$

$\mu = a + \sum_{k=1}^K w(k) * b(k,i)$

Q2 & Q3

Model syntax

```
lm <- quap(alist(
  S ~ dnorm(mu, sigma),
  mu <- a + b*M,
  a ~ dnorm(0, 0.2),
  b ~ dnorm(0, 0.2),
  sigma ~ dexp(1)
),data=d2)

qm <- quap(alist(
  S ~ dnorm(mu, sigma),
  mu <- a + b*M + b_2*M_sq,
  a ~ dnorm(0, 0.2),
  c(b, b_2) ~ dnorm(0, 0.2),
  sigma ~ dexp(1)
),data=d2)

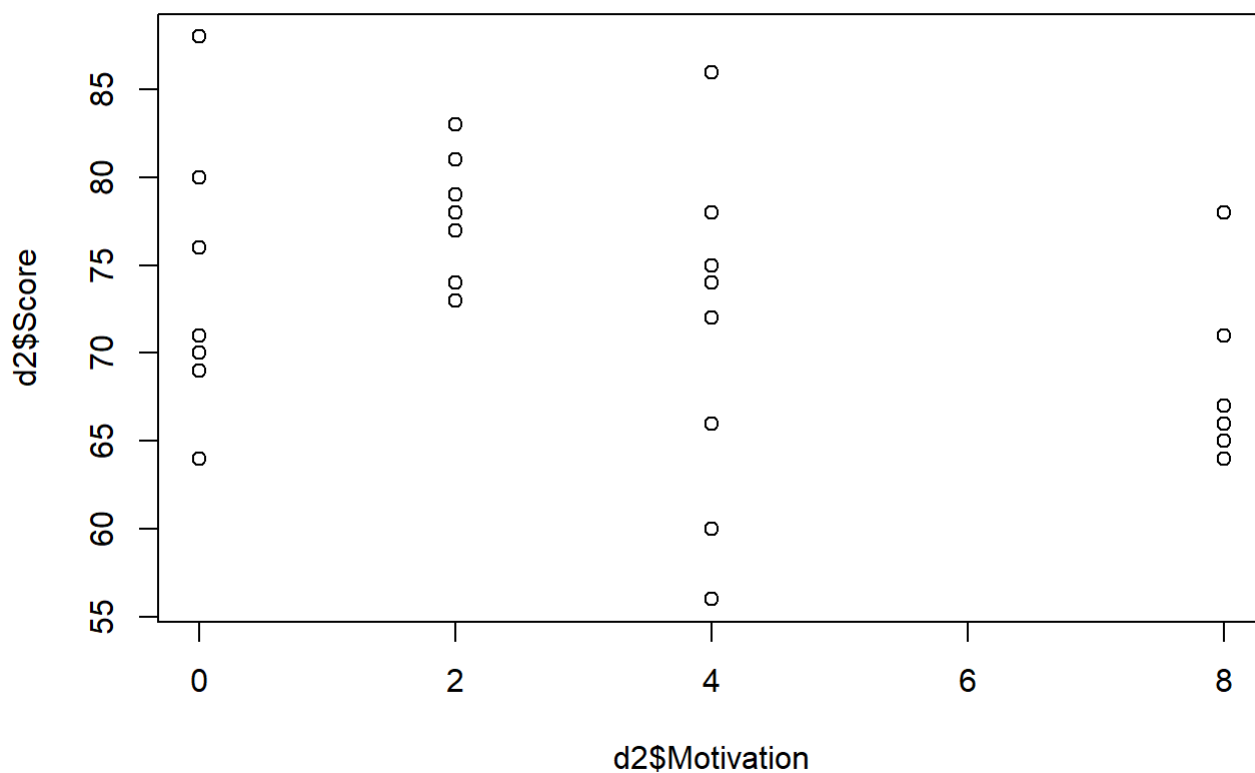
num_knots <- 5
knot_list <- quantile(d2$M, probs=seq(0, 1, length.out=5))

B <- bs(d2$M,
  knots = knot_list[-c(1, num_knots)],
  degree=3, intercept=T)

sm <- quap(
  alist(
    S ~ dnorm(mu, sigma),
    mu <- a + B %*% w,
    a ~ dnorm(0, 0.2),
    w ~ dnorm(0, 5), #influences wigglyness
    sigma ~ dexp(1)
  ),data=list(S=d2$S, B=B),
  start=list(w=rep(0, ncol(B)))
)
```

Plot data and inspect results

```
plot(x=d2$Motivation, y=d2$Score)
```



```
precis(lm)
```

##		mean	sd	5.5%	94.5%
##	a	-1.107761e-05	0.1165024	-0.1862044	0.18618227
##	b	-2.593468e-01	0.1191597	-0.4497870	-0.06890649
##	sigma	9.065033e-01	0.1011006	0.7449250	1.06808160

Conditional on the linear model and data, 89% of the posterior probability infers a regression slope coefficient between -0.45 and -0.07.

Plot posterior predictions of the linear model against the data

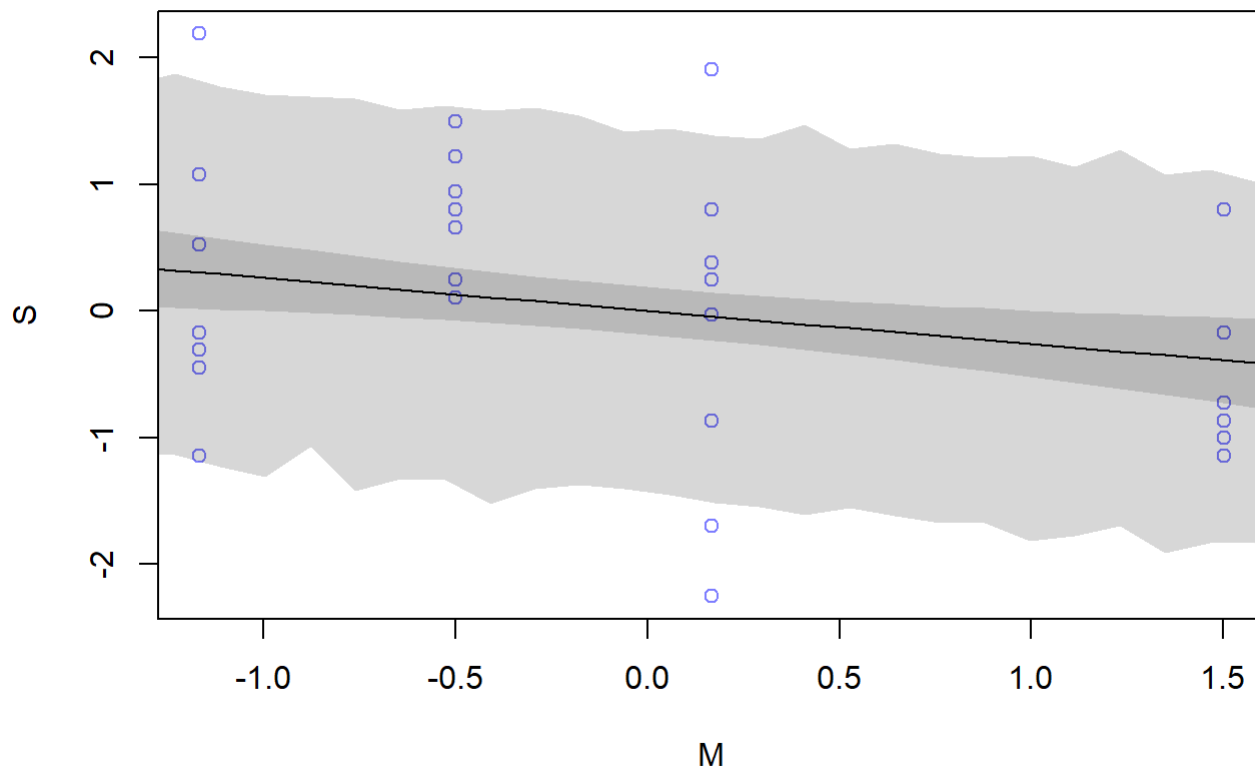
```

# extract samples from the posterior probability distribution
lm_post <- extract.samples(lm, n=10000)
# link function to generate a distribution of mu values for each value of M
mu.link <- function(M) lm_post$a + lm_post$b*M
# new horizontal axis to plot posterior predictions
m.seq <- seq(from=-1.7, to=1.7, length.out=30)
# apply link function to new horizontal axis of M values
mu <- sapply(m.seq, mu.link)
# distribution of posterior mu values of S for 30 values of M

# summarize the posterior predictions with mean and 89% percentile intervals
mu.mean <- apply(mu, 2, mean)
mu.PI <- apply(mu, 2, PI, prob=0.89)

# simulate Score values for each value of M, and get 89% PI
sim.scores <- sim(lm, data=list(M=m.seq))
scores.PI <- apply(sim.scores, 2, PI, prob=0.89)
# plot posterior predictions of mu, and simulated Scores again raw data
plot(S~M, data=d2, col="blue")
lines(m.seq, mu.mean)
shade(mu.PI, m.seq)
shade(scores.PI, m.seq)

```



The bulk of the posterior predictive distribution describes a negative slope. The regression slopes seem to reliably underestimate Scores for (standardized) Motivation values of -0.5. Further, 4 data points lie outside the 89% probability interval for simulated scores

Now for quadratic model

```
precis(qm)
```

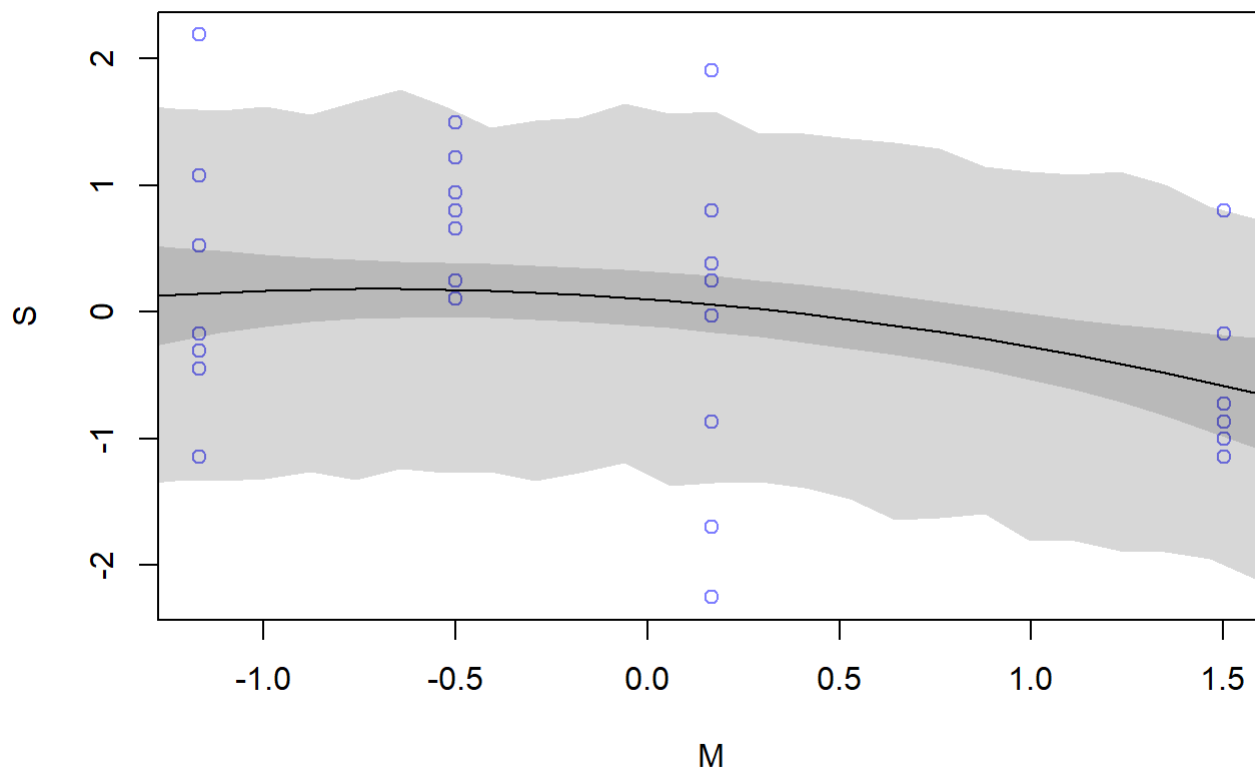
##		mean	sd	5.5%	94.5%
## a		0.1019033	0.13778356	-0.1183015	0.32210804
## b		-0.2195140	0.12073054	-0.4124647	-0.02656328
## b_2		-0.1554496	0.11524601	-0.3396350	0.02873578
## sigma		0.8830168	0.09880565	0.7251063	1.04092728

Not sure if the coefficients are interpretable. Let's just plot

```
qm_post <- extract.samples(qm, n=10000)
pred_dat <- list(M=m.seq, M_sq=m.seq^2)
mu.link <- function(M) qm_post$a + qm_post$b*M + qm_post$b_2*M^2
mu <- sapply(m.seq, mu.link)

mu.mean <- apply(mu, 2, mean)
mu.PI <- apply(mu, 2, PI, prob=0.89)

sim.scores <- sim(qm, data=pred_dat)
scores.PI <- apply(sim.scores, 2, PI, prob=0.89)
# plot posterior predictions of mu, and simulated Scores again raw data
plot(S~M, data=d2, col=range(2))
lines(m.seq, mu.mean)
shade(mu.PI, m.seq)
shade(scores.PI, m.seq)
```

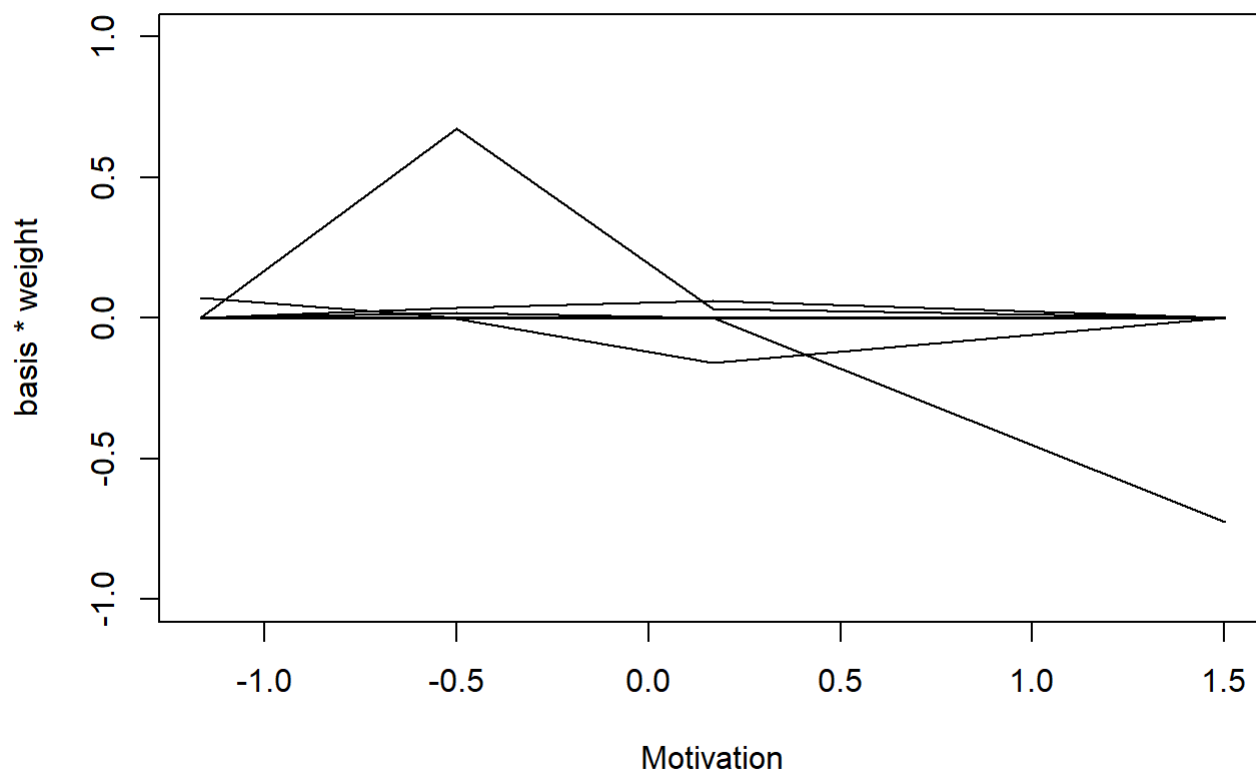
Does not look too different from the linear model. The same 4 points lie outside the 89% interval of simulated Scores.

Now for the spline model

Plot weights for basis functions

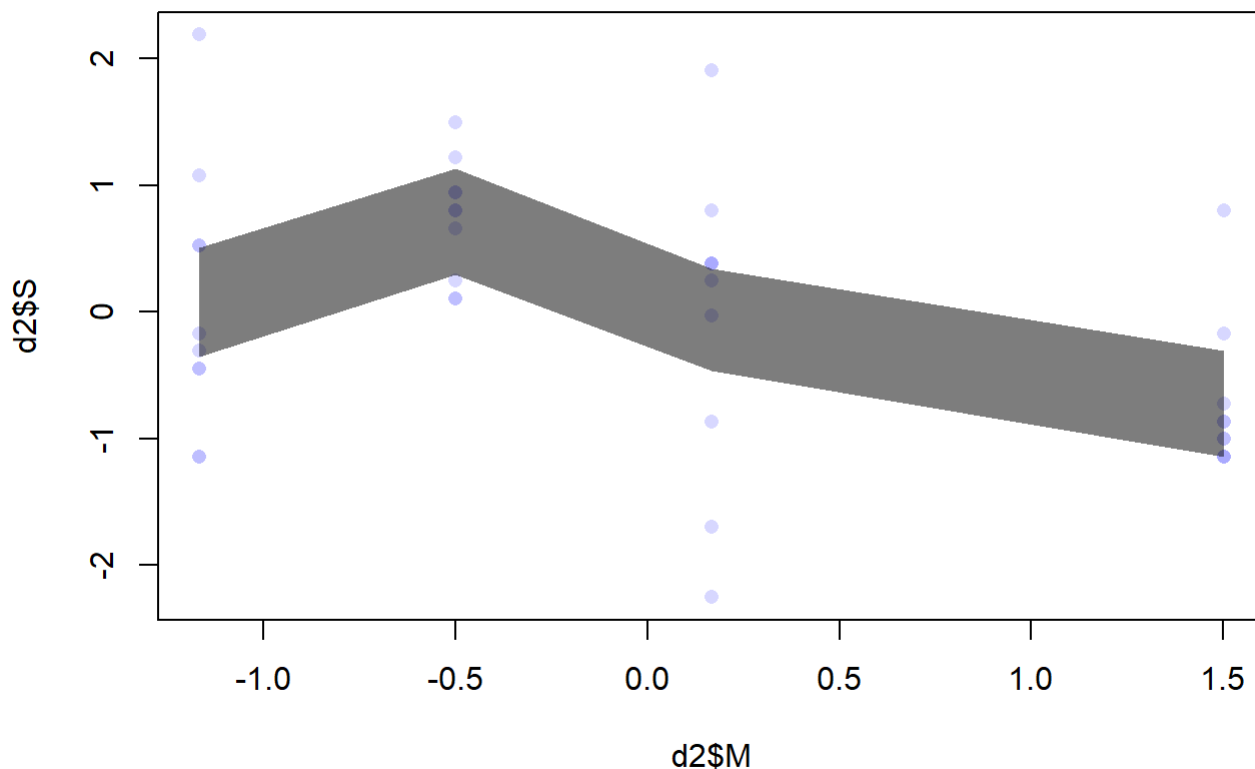
```
sm_post <- extract.samples(sm, n=10000)

w <- apply(sm_post$w , 2 , mean )
plot( NULL , xlim=range(d2$M) , ylim=c(-1,1) ,
      xlab="Motivation" , ylab="basis * weight" )
for ( i in 1:ncol(B) ) lines( d2$M , w[i]*B[,i] )
```



Plot spline

```
mu <- link(sm)
mu_PI <- apply(mu,2,PI,0.89)
plot(d2$M , d2$S , col=col.alpha(rangi2,0.3) , pch=16 )
shade(mu_PI, d2$M, col=col.alpha("black",0.5) )
```



Compare the predictive accuracy between models

Predictive accuracy is assessed by the average log-probability of a model to estimate relative divergence from the “true” data generating model. The average log-probability is estimated by summing the models log-probability of each observation.

To compute this for a Bayesian model, we calculate the log pointwise predictive density (lppd):

First, we compute log=probabilities for each observation:

1. Draw 10,000 samples for each parameter from the posterior probability distribution.
2. Use those 10,000 parameter samples to estimate 10,000 (standardized) Score values for each 40 observed value of (standardized) Motivation using the model specification relating Motivation to Score (linear, quadratic, spline).
3. Return log-probabilities of each simulated observation (conditional on the model)
4. Prepare data for plotting

```
logprob_lm <- sim(lm, ll=T, n=1e4)
logprob_lm_plot <- data.frame(
  observation = as.factor(seq(1:40)),
  means = apply(logprob_lm, 2, mean),
  sd = apply(logprob_lm, 2, sd)
)
```

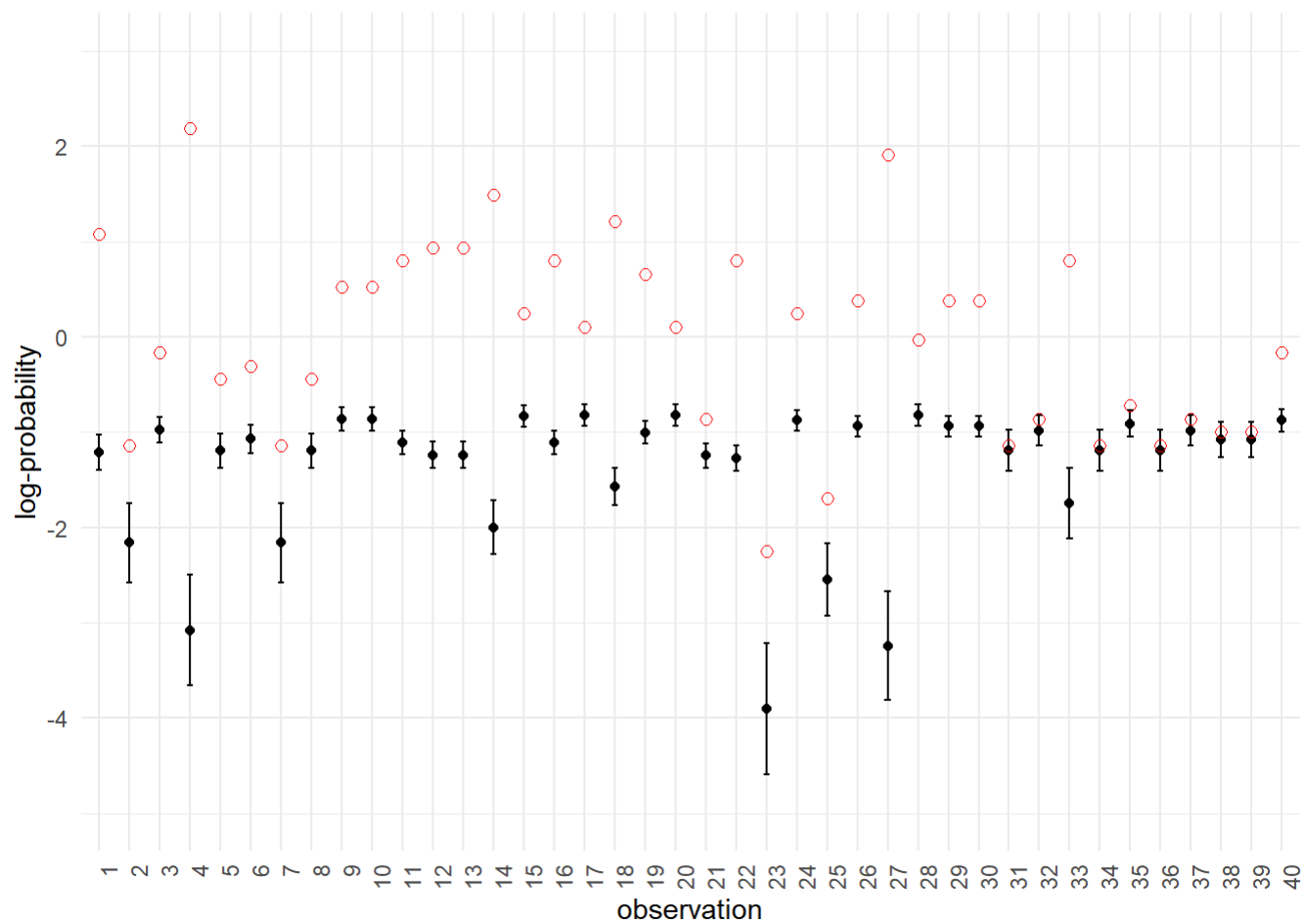
```
logprob_qm <- sim(qm, ll=T, n=1e4)
logprob_qm_plot <- data.frame(
  observation = as.factor(seq(1:40)),
  means = apply(logprob_qm, 2, mean),
  sd = apply(logprob_qm, 2, sd)
)
```

```
logprob_sm <- sim(sm, ll=T, n=1e4)
logprob_sm_plot <- data.frame(
  observation = as.factor(seq(1:40)),
  means = apply(logprob_sm, 2, mean),
  sd = apply(logprob_sm, 2, sd)
)
```

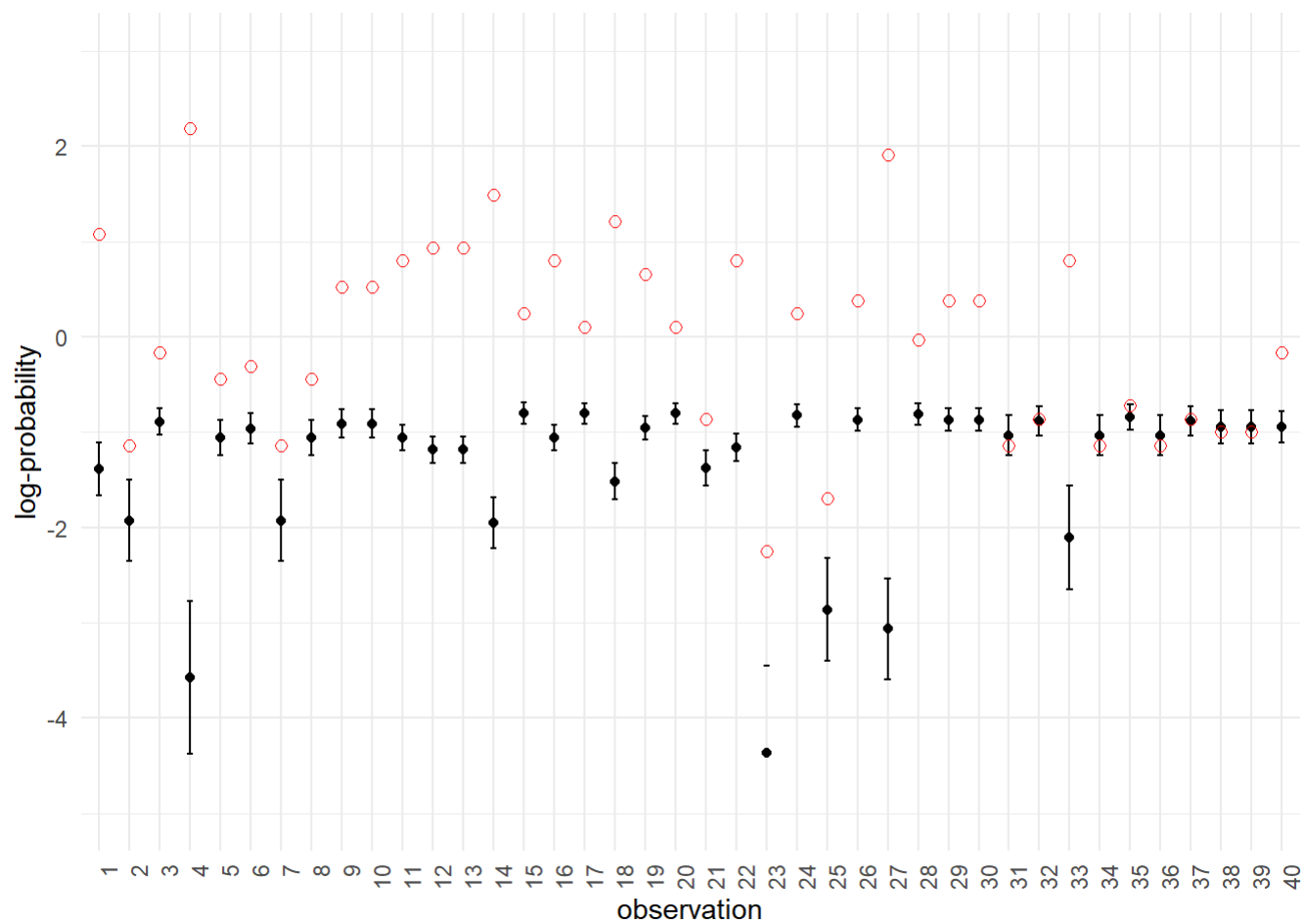
Plot simulated log-probabilities (points = mean, bars = standard deviations) of each observed Score

```
logprob_plot <- function(logprob_d) {
  ggplot(logprob_d, aes(x = observation, y = means)) +
    geom_point() +
    geom_errorbar(aes(ymin = means - sd, ymax = means + sd), width = 0.2) +
    geom_point(aes(y = d2$S), color = "red", size = 2, shape = 1) +
    labs(x = "observation", y = "log-probability") +
    ylim(-5, 3) +
    theme_minimal() +
    theme(axis.text.x = element_text(angle = 90, hjust = 1))
}
```

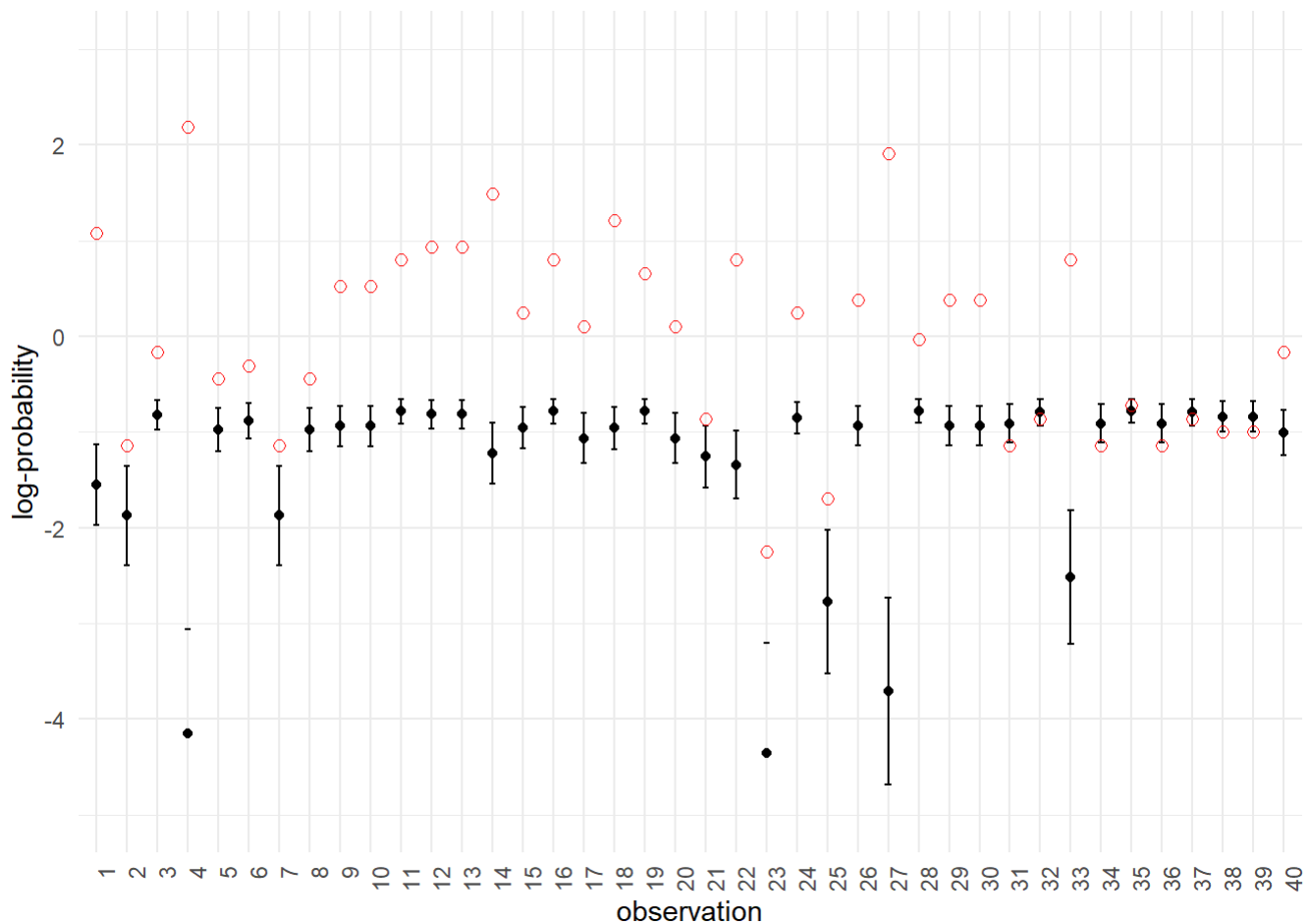
```
logprob_plot(logprob_lm_plot)
```



```
logprob_plot(logprob_qm_plot)
```



```
logprob_plot(logprob_sm_plot)
```



Resume computing lppd

```
n <- 40
ns <- 10000

# for the 10,000 simulated log-probabilities of each observation (conditional on the model), exp
# onentiate each value, sum them, then take the log. subtract the log of the sample size from each
# (this divides the sum by the number of samples)

lppd_func <- function(i, logprob_d) {
  log_sum_exp(logprob_d[, i]) - log(ns)
}
```

Apply the function to compute lppd for each model (equivalent results to lppd())

```
sapply(1:n, function(i) lppd_func(i, logprob_lm)) |> sum()
```

```
## [1] -53.37836
```

```
sapply(1:n, function(i) lppd_func(i, logprob_qm)) |> sum()
```

```
## [1] -52.19257
```

```
sapply(1:n, function(i) lppd_func(i, logprob_sm)) |> sum()
```

```
## [1] -49.75263
```

The lppd score computed from training data improves with model complexity. Ideally, the lppd for each model can be computed for data the model was not trained on, and those scores can be compared to rank models by predictive accuracy. Information criterion and cross-validation are techniques to estimate this hypothetical out-of-sample lppd/deviance score.

Cross-validation re-fits the model on subsets of the data, and computes lppd (or deviance? I don't see a -2 multiplier in the formula, yet the magnitudes are very similar to WAIC which does estimate deviance) scores of each model on the observations that were left out. The lppd is then averaged for a final out-of-sample predictive accuracy estimate

PSIS approximates a LOOCV score without having to refit the model by weighing observations by their relative likelihood.

```
compare(lm, qm, sm, func=PSIS)
```

```
## Some Pareto k values are high (>0.5). Set pointwise=TRUE to inspect individual points.  
## Some Pareto k values are high (>0.5). Set pointwise=TRUE to inspect individual points.  
## Some Pareto k values are high (>0.5). Set pointwise=TRUE to inspect individual points.
```

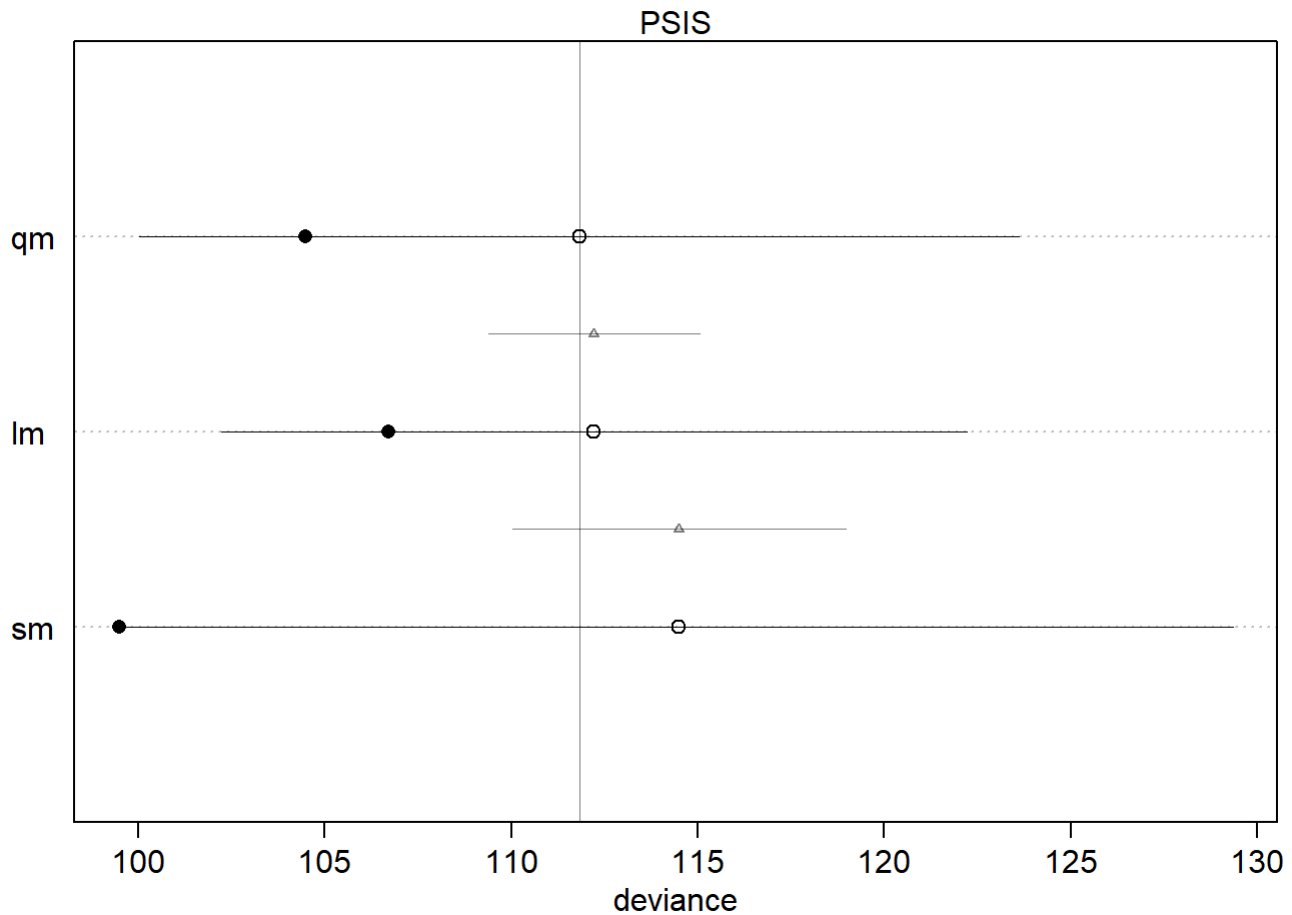
##	PSIS	SE	dPSIS	dSE	pPSIS	weight
## lm	111.8378	9.922361	0.00000000	NA	2.564240	0.4137051
## qm	111.8661	11.808815	0.02830084	2.928991	3.744569	0.4078922
## sm	113.5200	14.324100	1.68222007	5.999466	6.992820	0.1784027

Also can plot

```
plot(compare(lm, qm, sm, func=PSIS))
```

```
## Some Pareto k values are high (>0.5). Set pointwise=TRUE to inspect individual points.  
## Some Pareto k values are high (>0.5). Set pointwise=TRUE to inspect individual points.
```

```
## Some Pareto k values are very high (>1). Set pointwise=TRUE to inspect individual points.
```

The models are not reliably different in their predictive accuracy according to PSIS, given the largest dPSIS value is smaller than its corresponding dSE value (the standard error of the difference is larger than the difference itself). Though as expected, the penalty term (pPSIS) increases with model complexity. Some outliers may be disproportionately contributing to overfitting, and thus reduced predictive accuracy. We can inspect these with by specifying `pointwise=T`

```
PSIS_lm <- PSIS(lm, pointwise=T)
print(PSIS_lm)
```

##	PSIS	lppd	penalty	std_err	k
## 1	2.458048	-1.2290238	0.03539509	9.952468	1.050560e-01
## 2	4.562749	-2.2813745	0.19530268	9.952468	4.341976e-01
## 3	1.975464	-0.9877318	0.01831714	9.952468	1.496604e-01
## 4	6.568404	-3.2842022	0.34507855	9.952468	3.179761e-01
## 5	2.429411	-1.2147056	0.03553843	9.952468	1.254432e-01
## 6	2.175695	-1.0878474	0.02497772	9.952468	2.086926e-01
## 7	4.562749	-2.2813745	0.19530268	9.952468	4.341976e-01
## 8	2.429411	-1.2147056	0.03553843	9.952468	1.254432e-01
## 9	1.740704	-0.8703521	0.01474302	9.952468	-1.357465e-01
## 10	1.740704	-0.8703521	0.01474302	9.952468	-1.357465e-01
## 11	2.234952	-1.1174762	0.01541323	9.952468	-9.917332e-02
## 12	2.500257	-1.2501283	0.01894482	9.952468	4.499467e-02
## 13	2.500257	-1.2501283	0.01894482	9.952468	4.499467e-02
## 14	4.098498	-2.0492490	0.07535080	9.952468	3.160533e-01
## 15	1.675287	-0.8376434	0.01280221	9.952468	-2.909025e-05
## 16	2.234952	-1.1174762	0.01541323	9.952468	-9.917332e-02
## 17	1.658045	-0.8290224	0.01249244	9.952468	-5.556382e-02
## 18	3.188601	-1.5943005	0.03590804	9.952468	1.420809e-01
## 19	2.020601	-1.0103007	0.01375693	9.952468	-2.836459e-01
## 20	1.658045	-0.8290224	0.01249244	9.952468	-5.556382e-02
## 21	2.496741	-1.2483703	0.01513911	9.952468	1.764493e-01
## 22	2.577313	-1.2886564	0.01584464	9.952468	1.176185e-02
## 23	8.436067	-4.2180337	0.51650664	9.952468	3.048841e-01
## 24	1.763334	-0.8816670	0.01161416	9.952468	-1.519480e-01
## 25	5.256815	-2.6284074	0.15178837	9.952468	2.915764e-01
## 26	1.891682	-0.9458408	0.01099807	9.952468	-2.367892e-01
## 27	6.925632	-3.4628160	0.32690861	9.952468	4.811740e-01
## 28	1.653135	-0.8265674	0.01260027	9.952468	-2.726477e-02
## 29	1.891682	-0.9458408	0.01099807	9.952468	-2.367892e-01
## 30	1.891682	-0.9458408	0.01099807	9.952468	-2.367892e-01
## 31	2.409167	-1.2045837	0.04358855	9.952468	2.677485e-01
## 32	1.969546	-0.9847728	0.02456427	9.952468	1.658827e-01
## 33	3.710654	-1.8553269	0.14759971	9.952468	3.746881e-01
## 34	2.409167	-1.2045837	0.04358855	9.952468	2.677485e-01
## 35	1.827433	-0.9137163	0.01892561	9.952468	8.327044e-02
## 36	2.409167	-1.2045837	0.04358855	9.952468	2.677485e-01
## 37	1.969546	-0.9847728	0.02456427	9.952468	1.658827e-01
## 38	2.163190	-1.0815950	0.03256985	9.952468	2.341858e-01
## 39	2.163190	-1.0815950	0.03256985	9.952468	2.341858e-01
## 40	1.767506	-0.8837528	0.01468307	9.952468	2.611362e-01

```
PSIS_qm <- PSIS(qm, pointwise=T)
```

```
## Some Pareto k values are high (>0.5). Set pointwise=TRUE to inspect individual points.
```

```
print(PSIS_qm)
```

##	PSIS	lppd	penalty	std_err	k
## 1	2.889229	-1.4446146	0.07552142	11.60725	0.527923351
## 2	4.001404	-2.0007022	0.17136120	11.60725	0.277701534
## 3	1.787760	-0.8938799	0.01619077	11.60725	0.178638209
## 4	7.973575	-3.9867875	0.63121183	11.60725	0.600954179
## 5	2.132315	-1.0661577	0.03141169	11.60725	0.178325824
## 6	1.932699	-0.9663495	0.02203499	11.60725	0.173221136
## 7	4.001404	-2.0007022	0.17136120	11.60725	0.277701534
## 8	2.132315	-1.0661577	0.03141169	11.60725	0.178325824
## 9	1.862810	-0.9314048	0.02254271	11.60725	0.134252653
## 10	1.862810	-0.9314048	0.02254271	11.60725	0.134252653
## 11	2.136631	-1.0683155	0.01707276	11.60725	-0.020081516
## 12	2.393672	-1.1968361	0.02085843	11.60725	0.159446215
## 13	2.393672	-1.1968361	0.02085843	11.60725	0.159446215
## 14	3.972279	-1.9861397	0.07353197	11.60725	0.506478070
## 15	1.626900	-0.8134498	0.01196954	11.60725	-0.171695557
## 16	2.136631	-1.0683155	0.01707276	11.60725	-0.020081516
## 17	1.627004	-0.8135019	0.01125560	11.60725	-0.252376038
## 18	3.069947	-1.5349734	0.03722432	11.60725	0.258299893
## 19	1.932007	-0.9660033	0.01485077	11.60725	-0.100345803
## 20	1.627004	-0.8135019	0.01125560	11.60725	-0.252376038
## 21	2.814379	-1.4071895	0.03842275	11.60725	0.204466222
## 22	2.334760	-1.1673802	0.02279713	11.60725	-0.004430421
## 23	9.870581	-4.9352905	0.86216858	11.60725	0.670596153
## 24	1.665468	-0.8327340	0.01224136	11.60725	-0.202060658
## 25	6.098108	-3.0490541	0.29539484	11.60725	0.383400608
## 26	1.754854	-0.8774271	0.01320457	11.60725	-0.129248993
## 27	6.427377	-3.2136883	0.30098057	11.60725	0.645402533
## 28	1.640145	-0.8200726	0.01147451	11.60725	-0.235684340
## 29	1.754854	-0.8774271	0.01320457	11.60725	-0.129248993
## 30	1.754854	-0.8774271	0.01320457	11.60725	-0.129248993
## 31	2.140016	-1.0700081	0.04339945	11.60725	0.145994831
## 32	1.801181	-0.9005905	0.02234520	11.60725	0.128054767
## 33	4.482068	-2.2410340	0.28301891	11.60725	0.367047783
## 34	2.140016	-1.0700081	0.04339945	11.60725	0.145994831
## 35	1.713104	-0.8565520	0.01661851	11.60725	0.106453847
## 36	2.140016	-1.0700081	0.04339945	11.60725	0.145994831
## 37	1.801181	-0.9005905	0.02234520	11.60725	0.128054767
## 38	1.943344	-0.9716718	0.03115662	11.60725	0.141716469
## 39	1.943344	-0.9716718	0.03115662	11.60725	0.141716469
## 40	1.903270	-0.9516352	0.02557425	11.60725	0.280339964

```
PSIS_sm <- PSIS(sm, pointwise=T)
```

```
## Some Pareto k values are very high (>1). Set pointwise=TRUE to inspect individual points.
```

```
print(PSIS_sm)
```

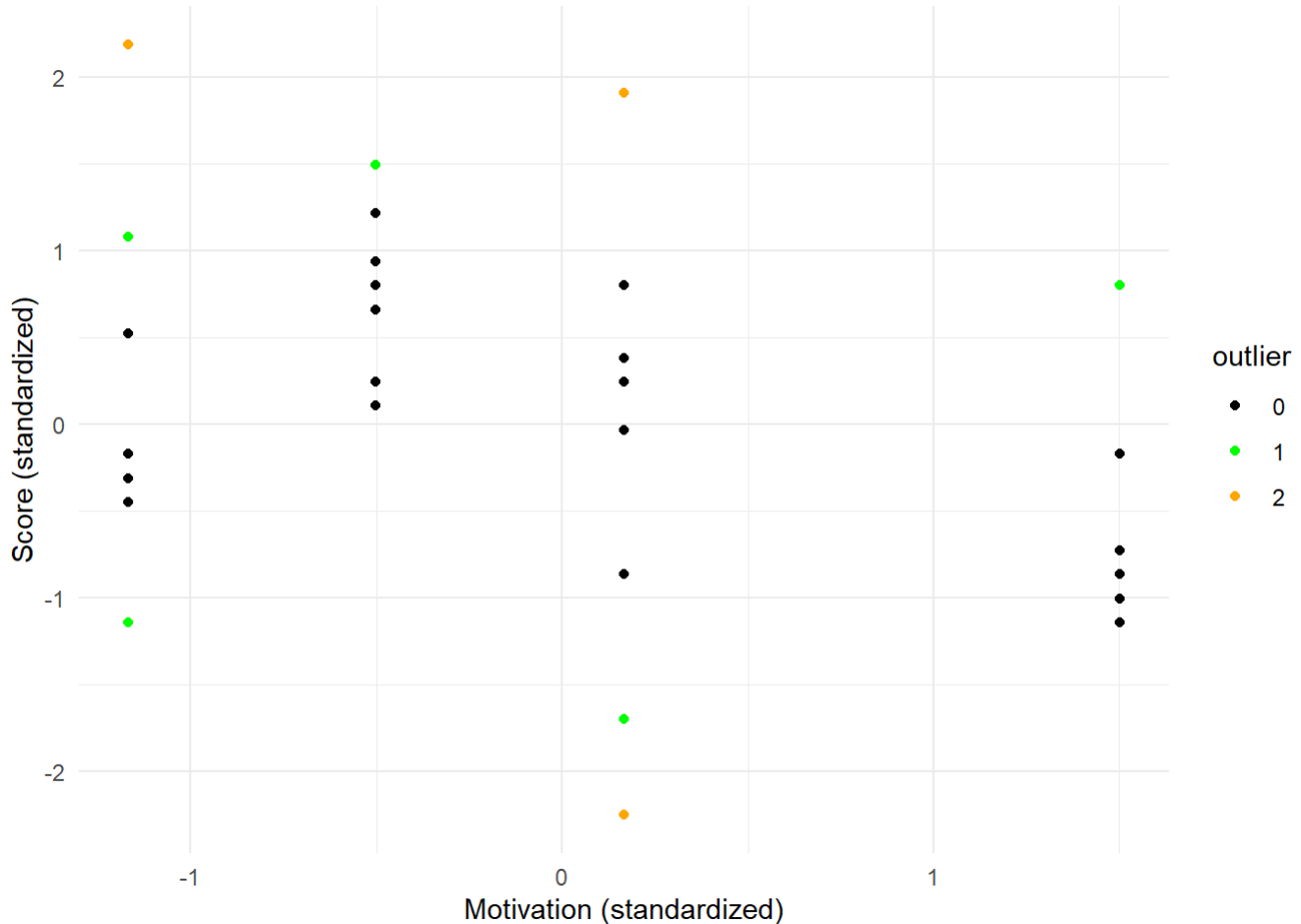
##	PSIS	lppd	penalty	std_err	k
## 1	3.348199	-1.6740996	0.19312234	15.83132	0.3019114
## 2	4.120033	-2.0600167	0.31201883	15.83132	0.5509001
## 3	1.665927	-0.8329635	0.02464702	15.83132	0.3296279
## 4	10.985977	-5.4929886	1.77458969	15.83132	1.0604277
## 5	2.010766	-1.0053830	0.05665834	15.83132	0.3403047
## 6	1.805343	-0.9026717	0.03733315	15.83132	0.3236438
## 7	4.120033	-2.0600167	0.31201883	15.83132	0.5509001
## 8	2.010766	-1.0053830	0.05665834	15.83132	0.3403047
## 9	1.932839	-0.9664197	0.04451048	15.83132	-0.0224463
## 10	1.932839	-0.9664197	0.04451048	15.83132	-0.0224463
## 11	1.573328	-0.7866639	0.01759750	15.83132	0.1137148
## 12	1.636803	-0.8184017	0.02180068	15.83132	0.1826908
## 13	1.636803	-0.8184017	0.02180068	15.83132	0.1826908
## 14	2.529502	-1.2647510	0.09056159	15.83132	0.2616447
## 15	1.948204	-0.9741021	0.04337020	15.83132	0.2274368
## 16	1.573328	-0.7866639	0.01759750	15.83132	0.1137148
## 17	2.202024	-1.1010122	0.06305797	15.83132	0.2835409
## 18	1.953793	-0.9768964	0.04422888	15.83132	0.1180806
## 19	1.572377	-0.7861887	0.01739921	15.83132	0.2042313
## 20	2.202024	-1.1010122	0.06305797	15.83132	0.2835409
## 21	2.632978	-1.3164891	0.11193574	15.83132	0.2212944
## 22	2.848291	-1.4241455	0.13415296	15.83132	0.4017957
## 23	11.414518	-5.7072592	1.84338481	15.83132	0.9367735
## 24	1.734389	-0.8671943	0.02809994	15.83132	0.1695657
## 25	6.410359	-3.2051793	0.66793945	15.83132	0.7012296
## 26	1.911771	-0.9558855	0.04301096	15.83132	0.2221699
## 27	9.784468	-4.8922339	1.53252243	15.83132	1.1008131
## 28	1.572227	-0.7861135	0.01502485	15.83132	0.1774367
## 29	1.911771	-0.9558855	0.04301096	15.83132	0.2221699
## 30	1.911771	-0.9558855	0.04301096	15.83132	0.2221699
## 31	1.867635	-0.9338175	0.04158665	15.83132	0.1227378
## 32	1.608570	-0.8042848	0.01854359	15.83132	0.1193239
## 33	5.748140	-2.8740701	0.53607983	15.83132	0.6714781
## 34	1.867635	-0.9338175	0.04158665	15.83132	0.1227378
## 35	1.576288	-0.7881438	0.01594062	15.83132	0.1134536
## 36	1.867635	-0.9338175	0.04158665	15.83132	0.1227378
## 37	1.608570	-0.8042848	0.01854359	15.83132	0.1193239
## 38	1.705285	-0.8526425	0.02682874	15.83132	0.1322557
## 39	1.705285	-0.8526425	0.02682874	15.83132	0.1322557
## 40	2.088625	-1.0443123	0.06036727	15.83132	0.2592917

Each model has identified different points as outliers. We will flag all points over 0.50 across models and highlight these in a plot.

```
d2$outlier_lm <- ifelse(PSIS_lm$k > 0.5, 1, 0)
d2$outlier_qm <- ifelse(PSIS_qm$k > 0.5, 1, 0)
d2$outlier_sm <- ifelse(PSIS_sm$k > 0.5, 1, 0)
d2$outlier <- rowSums(d2[, c("outlier_lm", "outlier_qm", "outlier_sm")])
d2$outlier <- d2$outlier |> as.factor()
```

Plot raw standardized data, and color code by how many models a point has been identified as an outlier in (0-3).

```
ggplot(d2, aes(x=M, y=S, color=outlier)) +  
  geom_point() +  
  labs(x = "Motivation (standardized)", y = "Score (standardized)") +  
  scale_color_manual(values = c("0"="black", "1"="green", "2"="orange", "3"="red")) +  
  theme_minimal()
```



This helps visualize which points in the data are most contributing to overfitting.

Information criterion estimates the out-of-sample deviance by considering the complexity of the model in a penalty term (in AIC, that is the number of parameters). In WAIC, the penalty term is defined by the variance in log-probabilities of each observation, given the model.

```
compare(lm, qm, sm, func=WAIC)
```

##		WAIC	SE	dWAIC	dSE	pWAIC	weight
##	qm	111.4046	11.433730	0.0000000	NA	3.527496	0.4329670
##	lm	112.0747	9.750818	0.6701453	2.761222	2.665950	0.3096953
##	sm	112.4451	13.748585	1.0405453	4.139801	6.465284	0.2573376

The models are not reliably different in terms of predictive accuracy, using the WAIC. The PSIS and WAIC results converge, suggesting these results are reliable.

In conclusion, of the 3 models compared, the quadratic model *might* have the best predictive accuracy, but if so, not by much. Thus, there is no support for the inverted-U shape of Performance ~ Motivation, as the quadratic model does not reliably outperform the linear model.

Question 3

Explain Bayes Rule.

Bayes theorem: $P(A|B) = P(B|A) * P(A) / P(B)$

In the context of Bayesian statistics, Bayes rule provides the logical way to update a model's probability distributions (i.e., your initial hypothesis) based on new evidence. The model initially has a prior probability distribution which, represents your initial belief about the world (a hypothesis; $P(H)$). The upon observing new data, you update your model accordingly.

The posterior distribution, $P(A|B)$, is the product of the likelihood of the data given the prior distribution, and the prior distribution, over the average probability of the data.

What does McElreath mean when he distinguishes between small-world and large-world?

My interpretation of what McElreath means when he distinguishes between small-world and large-world is analagous to the map versus the territory. The territory / large-world refers to nature, in all her complexity, down to the last subatomic particle. The map / small-world refers to models of nature, which we use to simplify a particular set of phenomena, facilitating comprehension and prediction, and thus informing decision making.

Give an example of the distinction between small-world and large-world based on your area of research interest.

An example of this can be found in psychiatric diagnosis and nosology. The phenomena we call 'mental disorders' refers to a wide and heterogeneous range and collection of experiences and behaviors that revolve around subjective suffering (and many times associated with physiological degradation or neurological dysfunction). These collections of experiences can have complex and diverse phenomenologies, behavioral manifestations, causes, risk factors, severities, interpretations, and timescales. Yet, to facilitate understanding through research, and ultimately treatment, we deploy a simplified diagnostic system to categorize these experiences. The reality of individual suffering and dysfunction constitute the large-world of mental disorders, and the constructed classification system of the DSM constitute the small-world.