

# Math 504 HW12

Jeff Gould

4/9/2020

2

a

$$\min_{\alpha} \sum_{i=1}^N |y_i - \sum_{j=1}^{K-4} \alpha_j b_j(x_i)|^2 + \rho \int_{x_{\min}}^{x_{\max}} \left( \sum_{j=1}^{K-4} \alpha_j b_j(z) \right)''^2 dz \quad (1)$$

From  $\sum_{j=1}^{K-4} \alpha_j b_j(x_i)$ , we have  $N \times K - 4$  values from  $b_j(x_i)$ . Let each  $b_j(x_i)$  be the  $ij^{th}$  entry in the matrix  $B$

Also, we can expand  $\sum_{j=1}^{K-4} \alpha_j b_j(x_i)$  as  $\alpha_1 b_1(x_i) + \alpha_2 b_2(x_i) + \dots + \alpha_{K-4} b_{K-4}(x_i) = S(x_i)$ . Thus, we can re-write

$$\sum_{i=1}^N |y_i - \sum_{j=1}^{K-4} \alpha_j b_j(x_i)|^2 = \sum_{i=1}^N |y_i - S(x_i)|^2 = \|y - B\alpha\|^2$$

where  $B$  is the  $N \times K - 4$  matrix as described above and  $\alpha$  is  $K - 4$  column vector.

Next, look at  $\rho \int_{x_{\min}}^{x_{\max}} \left( \sum_{j=1}^{K-4} \alpha_j b_j(z) \right)''^2 dz$ . Since  $\rho$  is a constant, we can ignore it for now. This leaves

$$\begin{aligned} \int_{x_{\min}}^{x_{\max}} \left( \sum_{j=1}^{K-4} \alpha_j b_j''(z) \right)^2 dz &= \int_{x_{\min}}^{x_{\max}} \left( \left( \sum_{j=1}^{K-4} \alpha_j b_j''(z) \right) \left( \sum_{i=1}^{K-4} \alpha_i b_i''(z) \right) \right) dz = \\ &= \int_{x_{\min}}^{x_{\max}} \sum_{j=1}^{K-4} \sum_{i=1}^{K-4} \alpha_j \alpha_i b_j''(z) b_i''(z) dz = \sum_{j=1}^{K-4} \sum_{i=1}^{K-4} \alpha_j \alpha_i \left( \int_{x_{\min}}^{x_{\max}} b_j''(z) b_i''(z) dz \right) \end{aligned}$$

Now define a  $K - 4$  square matrix  $\Omega$  such that each  $ji^{th}$  corresponds to  $\int_{x_{\min}}^{x_{\max}} b_j''(z) b_i''(z) dz$ . Then:

$$\sum_{j=1}^{K-4} \sum_{i=1}^{K-4} \alpha_j \alpha_i \left( \int_{x_{\min}}^{x_{\max}} b_j''(z) b_i''(z) dz \right) = \sum_{j=1}^{K-4} \sum_{i=1}^{K-4} \alpha_j \alpha_i \Omega_{ji} = \alpha^T \Omega \alpha$$

Putting this together, we get

$$\min_{\alpha} \sum_{i=1}^N |y_i - \sum_{j=1}^{K-4} \alpha_j b_j(x_i)|^2 + \rho \int_{x_{\min}}^{x_{\max}} \left( \sum_{j=1}^{K-4} \alpha_j b_j(z) \right)''^2 dz = \min_{\alpha} \|y - B\alpha\|^2 + \rho \alpha^T \Omega \alpha \quad (2)$$

Solve for  $\alpha$ :

$$L(\alpha) = \|y - B\alpha\|^2 + \rho \alpha^T \Omega \alpha = (y - B\alpha) \cdot (y - B\alpha) + \rho \alpha^T \Omega \alpha = y \cdot y - 2B\alpha \cdot y + B\alpha \cdot B\alpha + \rho \alpha^T \Omega \alpha \Rightarrow$$

$$\begin{aligned}\nabla_{\alpha} L(\alpha) &= -2B^T y + 2B^T B \alpha + 2\rho \Omega \alpha = 0 \longrightarrow B^T B \alpha + \rho \Omega \alpha = B^T y \rightarrow \\ (B^T B + \rho \Omega)^{-1} (B^T B + \rho \Omega) \alpha &= (B^T B + \rho \Omega)^{-1} B^T y \Rightarrow \\ \alpha &= (B^T B + \rho \Omega)^{-1} B^T y\end{aligned}$$

**b**

```
bone_mass <- read_delim("BoneMassData.txt", delim = " ")
females <- bone_mass %>% filter(gender == "female")
K <- 1000
min_x <- min(females$age)
max_x <- max(females$age)
myknots = seq(min_x, max_x, length.out = 1002)[2:1001]

h <- (max_x - min_x) / 2500
mygrid <- seq(min_x, max_x, h)

B <- splineDesign(knots = myknots, x = females$age, outer.ok = T)
Bpp <- splineDesign(knots = myknots, x = mygrid, derivs = 2, outer.ok = T)

Omega <- matrix(0, nrow = K-4, ncol = K-4)

test <- sum(Bpp[,10] * Bpp[,15] * h)

for(i in 1:(K-4)){
  for(j in 1:(K-4)){
    Omega[i,j] = sum(Bpp[,i] * Bpp[, j] * h)
  }
}
```

**c**

Show that  $B^T B$  is not invertible - simply show  $\det B^T B = 0$ :

```
det(t(B) %*% B) == 0
```

```
## [1] TRUE
```

To show that  $B^T B + \rho \Omega$  is invertible, first show that  $\Omega$  is invertible.  $\det(\Omega) = \infty$ . The matrix determinant lemma (reference) states that if  $A$  is an  $n \times n$  invertible matrix, and  $U$  and  $V$  are  $n \times m$  matrices, the  $\det(A + UV^T) = \det(I_m + V^T A^{-1} U) \det(A)$ . Applying to our data, we get  $\det(\Omega + B^T B) = \det(I_{259} + B \Omega^{-1} B^T) \det(\Omega) \rightarrow \det(\rho \Omega + B^T B) = \det(I_{259} + B \rho^{-1} \Omega^{-1} B^T) \det(\rho \Omega)$ . Since we know that  $\det(\Omega)$  is very large (R outputs it as  $\infty$ ), we simply need to show that  $\det(I_{259} + B \Omega^{-1} B^T) \neq 0$ :

```
I259 <- diag(nrow = 259, ncol = 259)
det(I259 + B %*% solve(Omega) %*% t(B))
```

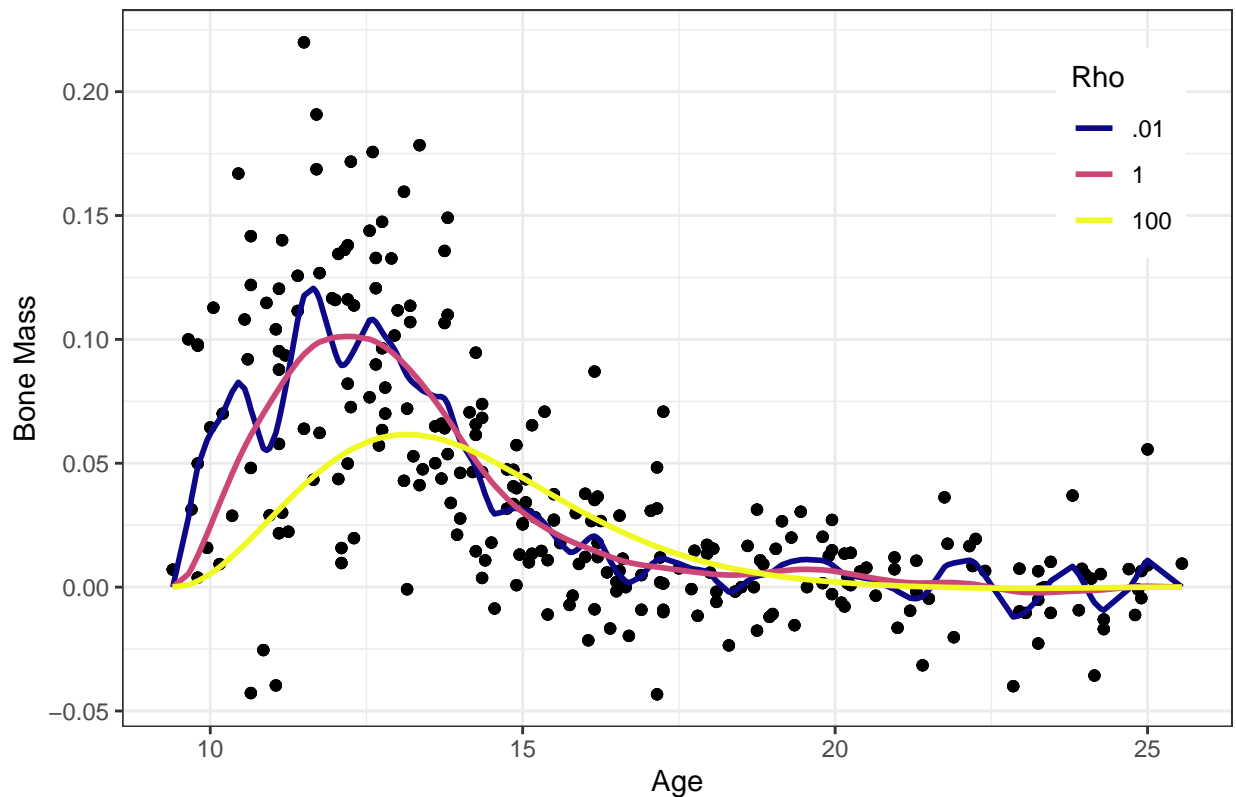
```
## [1] 7.181394e+13
```

Thus, since  $\det(\Omega + B^T B) = \det(I_{259} + B \Omega^{-1} B^T) \det(\Omega) \neq 0 \implies \Omega + B^T B$  is invertible, and if  $\rho > 0$ , then  $\det(\rho \Omega + B^T B) \neq 0$  and  $B^T B + \rho \Omega$  is invertible for  $\rho > 0$

d

```
solveAlpha <- function(rho, b = B, omega = Omega, y = females$spnbmd){  
  alpha <- solve(t(b) %*% b + rho * omega) %*% t(b) %*% y  
  return(alpha)  
}  
alpha.01 <- solveAlpha(rho = 0.01)  
alpha1 <- solveAlpha(rho = 1)  
alpha100 <- solveAlpha(rho = 100)  
  
spline_plot_data <- data.frame(x = females$age, boneMass = females$spnbmd,  
                              `01` = B %*% alpha.01,  
                              `1` = B %*% alpha1,  
                              `100` = B %*% alpha100)  
  
spline_test <- spline_plot_data %>%  
  pivot_longer(cols = 3:5,  
               names_to = "Rho",  
               values_to = "S_x") %>%  
  mutate(Rho = str_extract(Rho, "\\.[[:digit:]]+|[:digit:]+"))  
  
ggplot(data = spline_test, aes(x = x)) +  
  geom_point(aes(y = boneMass)) +  
  geom_line(aes(y = S_x, color = Rho), size = 1) +  
  scale_color_viridis(discrete = T, option = "C") +  
  theme_bw() +  
  labs(title = "1000 Knot Spline Regression with Varying Penalties",  
        x = "Age",  
        y = "Bone Mass") +  
  theme(legend.position = c(0.9,0.8))
```

### 1000 Knot Spline Regression with Varying Penalties



So we see that using too small of a  $\rho$  (blue-ish purple line) causes the regression to be overfit, with the regression line oscillating heavily in small intervals. A spline with a modest penalty of  $\rho = 1$  (magenta line), causes the spline regression to look similar to the one computed with two knots on our previous HW. It has a higher rise with the spike in data around ages 11-13 than a higher penalty, but it doesn't have heavy swings the way a lower penalty did. Meanwhile a highly penalized regression with  $\rho = 100$  (yellow line), the regression had smaller moves with the data, and perhaps penalized too much. It seems to have too small of a rise with the data from 11-13, and then too slow to drop with the data after age 15.

## 3

a

signal.R:

```
set.seed(1236)

# the "signal" that make up the rows of our matrix, with noise added.
sig <- seq(1,2,length.out = 10)
sig[5] <- -1

# each row of A will have the form: q*signal + noise
nsamples <- 500
A <- matrix(NA, ncol=10, nrow=nsamples)
```

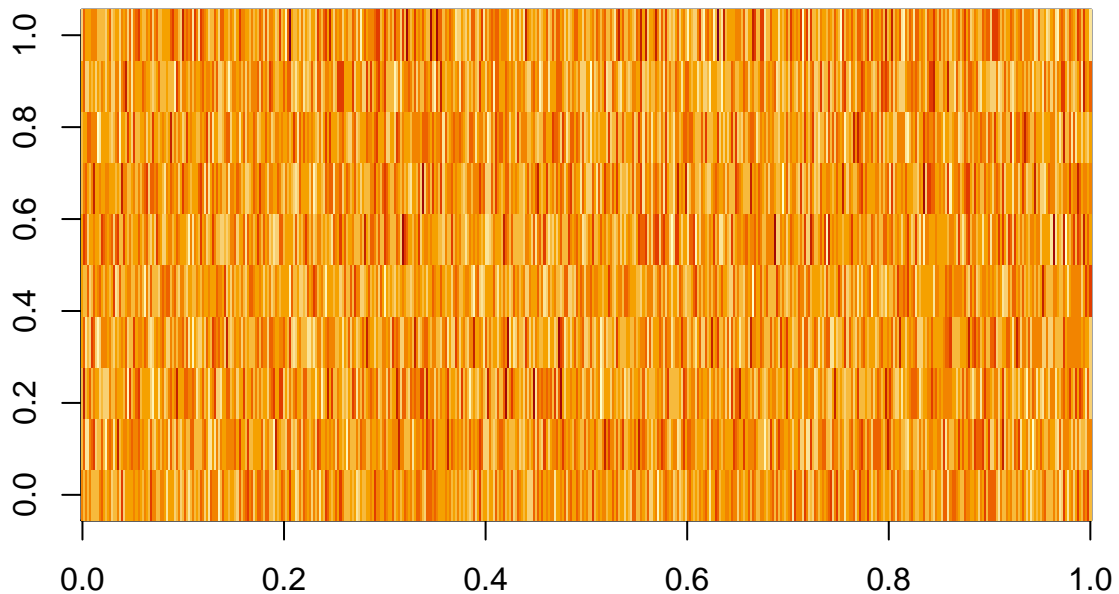
```

no_noise_A <- matrix(NA, ncol=10, nrow=nsamples)
q <- runif(nsamples, min=-3, max=3)
for (i in 1:nsamples) {
  noise <- rnorm(10, mean=0, sd=5)
  A[i,] <- q[i]*sig + noise
  no_noise_A[i,] <- q[i]*sig
}

write.table(no_noise_A, file="no_noise_A.txt", row.names = F, col.names = F)
write.table(A, file="A.txt", row.names = F, col.names = F)
write.table(q, file="q.txt", row.names=F, col.names=F)

image(A)

```



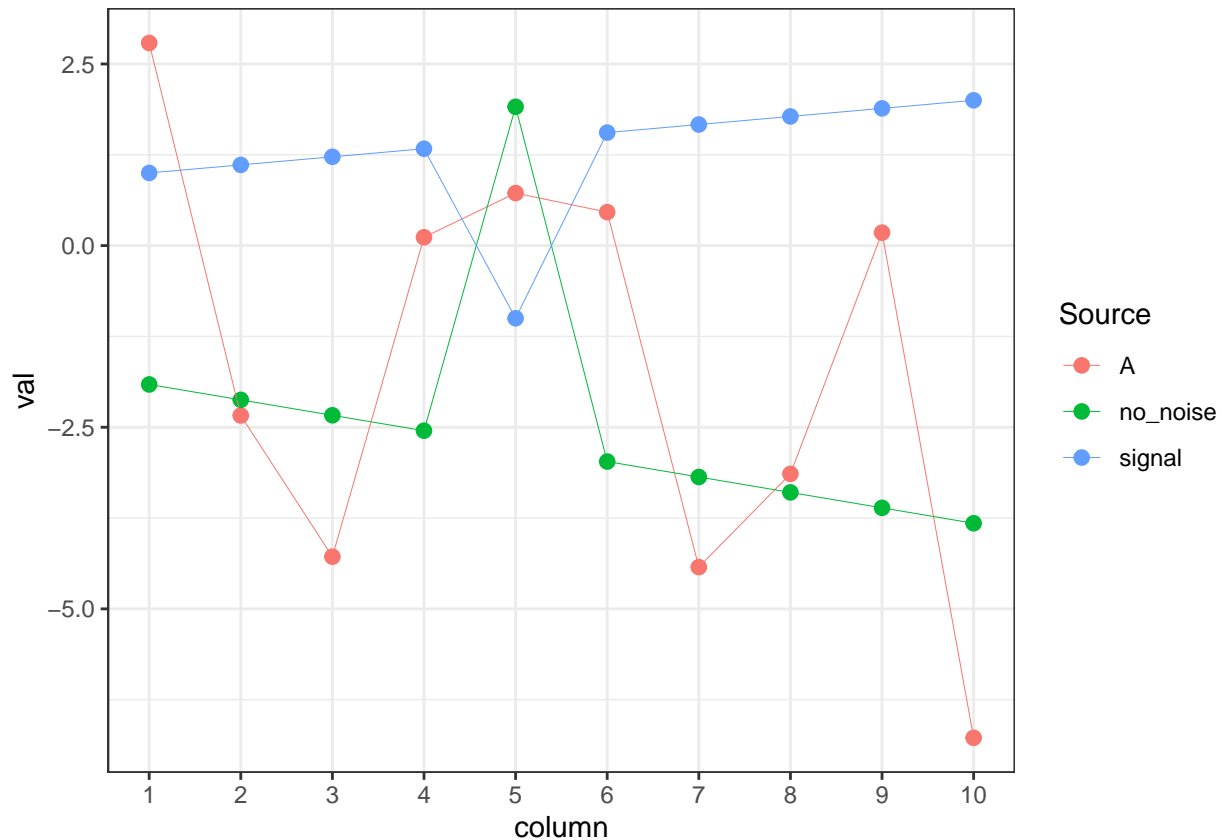
```

plot_data <- data.frame(
  column = seq(1,10,1),
  A = A[1,],
  no_noise = no_noise_A[1,],
  signal = sig
) %>%
  pivot_longer(cols = 2:4, names_to = "Source", values_to = "val")

ggplot(data = plot_data, aes(x = column, y = val)) +
  geom_point(aes(col = Source), size = 2.25) +

```

```
geom_line(aes(col = Source), size = .125) +
scale_x_continuous(breaks = seq(1,10,1), minor_breaks = NULL) +
theme_bw()
```



You can't derive the signal just using one observation of *A* and *no\_noise\_A*, as at a single row observation level the noise is too strong and causes *A* to not follow a tight enough window to derive the noise. As the first row of *no\_noise\_A* is derived from multiplying  $q_1 = -1.911$  times the signal, we would expect to be able to derive the signal by dividing the first row by  $-1.911$ , but doing so with *A* does not give a result reminiscent of our signal:

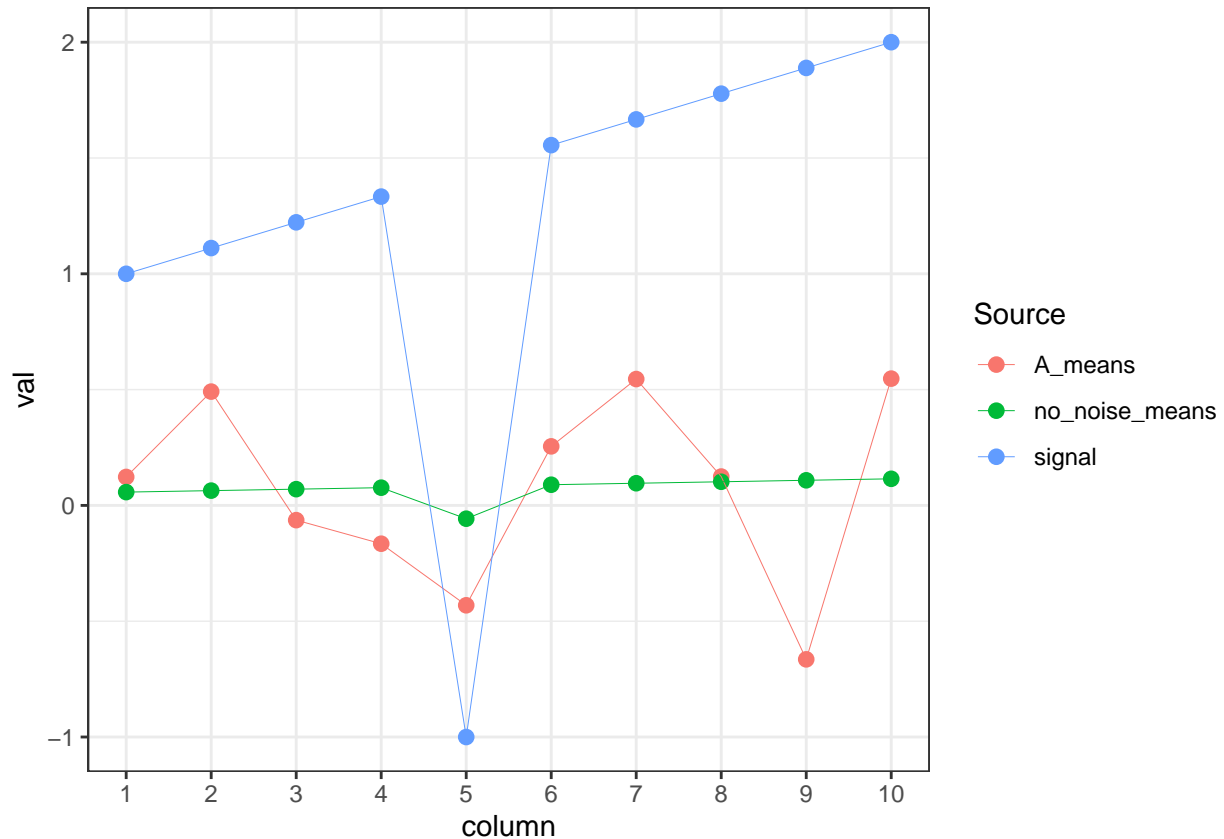
-1.4594568, 1.2235123, 2.2406375, -0.0602157, -0.3782986, -0.2410538, 2.3155057, 1.6442113, -0.093381, 3.5449524

Can we find the signal in *A* using the column means though?

```
col_means_A <- colMeans(A)
col_no_noise_A <- colMeans(no_noise_A)
plot_data_2 <- data.frame(
  column = seq(1,10,1),
  A_means = col_means_A,
  no_noise_means = col_no_noise_A,
  signal = sig
) %>%
  pivot_longer(cols = 2:4, names_to = "Source", values_to = "val")

ggplot(data = plot_data_2, aes(x = column, y = val)) +
  geom_point(aes(col = Source), size = 2.25) +
```

```
geom_line(aes(col = Source), size = .125) +
scale_x_continuous(breaks = seq(1,10,1), minor_breaks = NULL) +
theme_bw()
```



By taking the column means we can see the muted signal in `no_noise_A`, however the signal in `A` is still suppressed by the random noise added to the matrix generation.

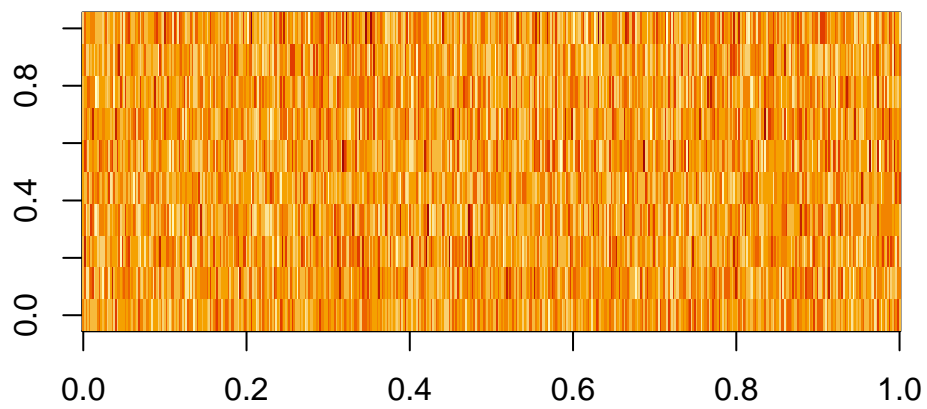
**b**

While Singular Value Decomposition says an  $m \times n$  matrix  $A$ ,  $m > n$  can be expressed as  $A = USV^T$ , where  $U$  is an  $m \times m$  matrix composed of the eigenvectors of  $AA^T$ , when using R's `svd` function, it returns  $U$  as an  $m \times n$  matrix. This is because the eigenvalues beyond the  $n^{th}$  eigenvector are pretty much 0, so the added information from the corresponding eigenvectors is minimal, and we can instead shorten our SVD to  $A \approx U'SV^T$ , where  $U'$  is the  $m \times n$  matrix generated by R's `svd` function. Additionally,  $S$  dfnow becomes an  $n \times n$  diagonal matrix instead of an  $m \times n$  diagonal matrix.

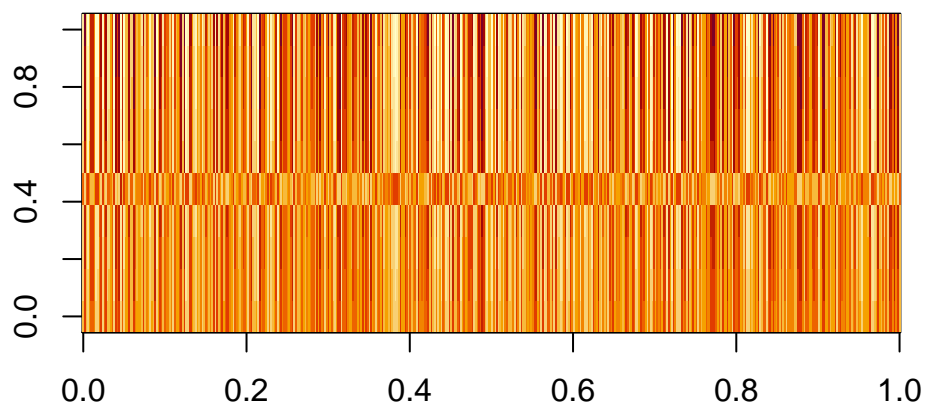
```
svd_A <- svd(A)
U <- svd_A$u
V <- svd_A$v
S <- diag(svd_A$d)

A_1 <- S[1,1] * U[,1] %*% t(V[,1])

image(A)
```

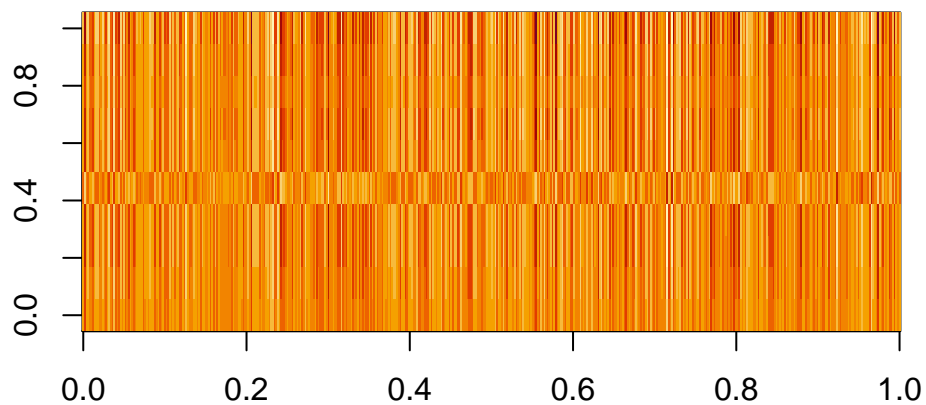


```
image(no_noise_A)
```



```
image(A_1)
```



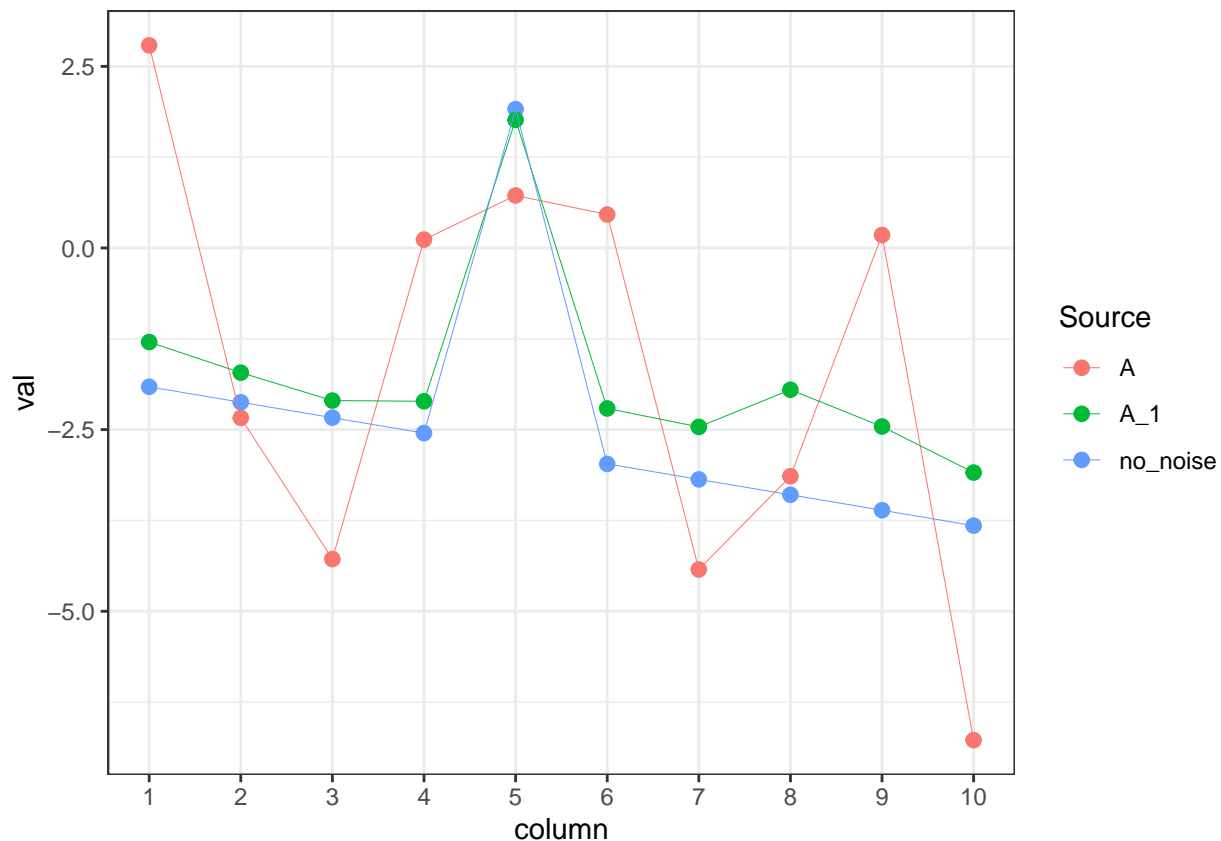


We see that the first singular values remove most of the noise from  $A$ , as  $A_1$  looks much closer to `no_noise_A` than  $A$ , and in particular we are able to see the clear negative value from the signal at the fifth signal entry.

Compare first rows of  $A$ ,  $A_1$ , `no_noise_A`:

```
plot_data <- data.frame(
  column = seq(1,10,1),
  A = A[1,],
  no_noise = no_noise_A[1,],
  A_1 = A_1[1,]
) %>%
  pivot_longer(cols = 2:4, names_to = "Source", values_to = "val")

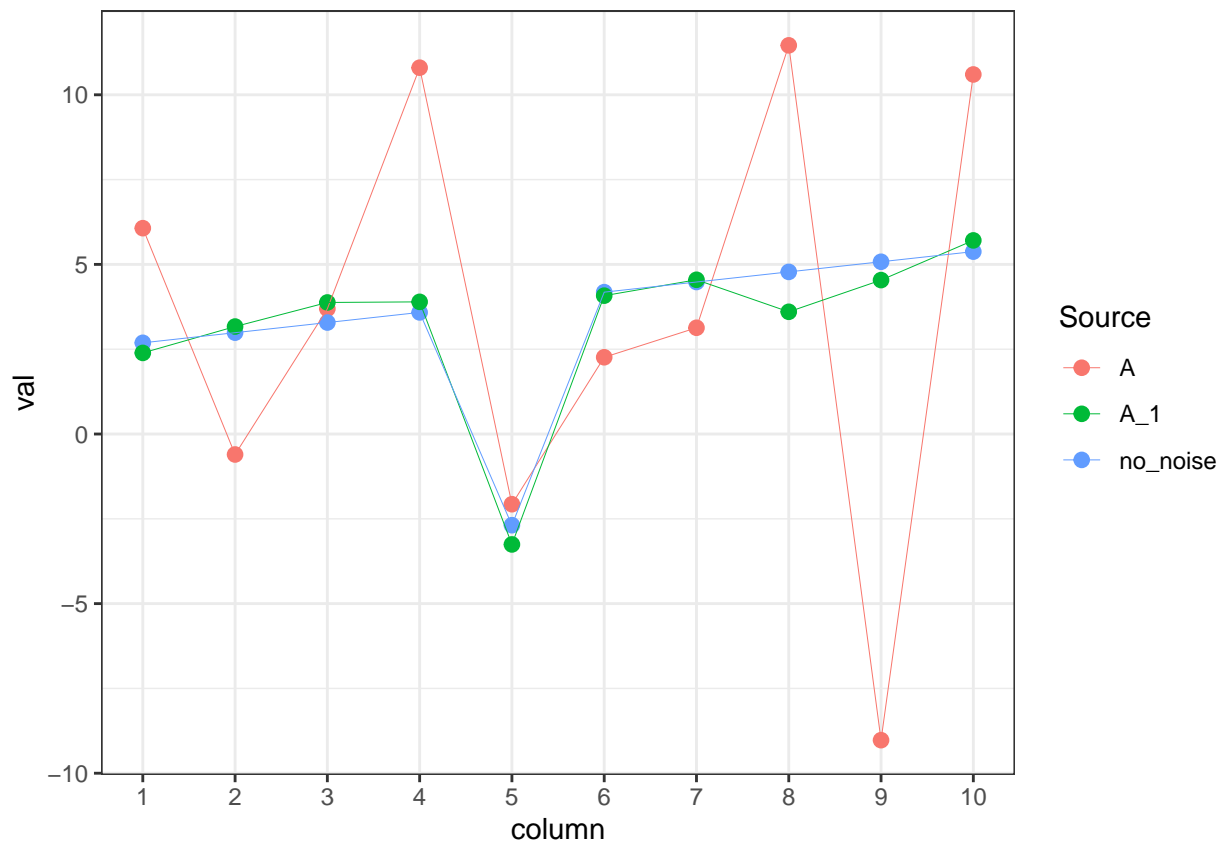
ggplot(data = plot_data, aes(x = column, y = val)) +
  geom_point(aes(col = Source), size = 2.25) +
  geom_line(aes(col = Source), size = .125) +
  scale_x_continuous(breaks = seq(1,10,1), minor_breaks = NULL) +
  theme_bw()
```



We see that the first row of  $A_1$  closely matches that of `no_noise_A`, suggesting that the first singular values do a good job of filtering out most of the noise in  $A$  and capture much of the signal. Now pick a row at random and see if we are able to make a similar observation.

```
sample_row <- sample(c(1:500), 1)
plot_data <- data.frame(
  column = seq(1,10,1),
  A = A[sample_row,],
  no_noise = no_noise_A[sample_row,],
  A_1 = A_1[sample_row,]
) %>%
  pivot_longer(cols = 2:4, names_to = "Source", values_to = "val")

ggplot(data = plot_data, aes(x = column, y = val)) +
  geom_point(aes(col = Source), size = 2.25) +
  geom_line(aes(col = Source), size = .125) +
  scale_x_continuous(breaks = seq(1,10,1), minor_breaks = NULL) +
  theme_bw()
```



While still not perfect, row 453 still closely follows the pattern of `no_noise_A`, this time tracking `no_noise_A` even more closely than in the first row. It is pretty evident that  $v^{(1)}$ ,  $s_1$ , and  $u^{(1)}$  filter out most of the noise in  $A$  and capture most of the relationship between  $q$  and  $sig$