Chapter 6

January 12, 2021

1 Housekeeping:

[2]:
```
sessionInfo()
options(repr.plot.width=14,repr.plot.antialias='subpixel',repr.plot.res=218)
update.packages()
```

```
R version 4.0.3 Patched (2020-10-12 r79333)
Platform: x86_64-apple-darwin17.0 (64-bit)
Running under: macOS Big Sur 10.16

Matrix products: default
BLAS:   /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRblas.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRlapack.dylib

locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

loaded via a namespace (and not attached):
 [1] compiler_4.0.3   ellipsis_0.3.1  IRdisplay_0.7.0 pbdZMQ_0.3-3
 [5] tools_4.0.3      htmltools_0.5.0 pillar_1.4.6    base64enc_0.1-3
 [9] crayon_1.3.4     uuid_0.1-4      IRkernel_1.1.1  jsonlite_1.7.1
[13] digest_0.6.25    lifecycle_0.2.0 repr_1.1.0      rlang_0.4.8
[17] evaluate_0.14
```

2 Back to OJ

[3]:
```
oj <- read.csv("oj.csv")
```

A log-log regression to get at elasiticities:

[4]:
```
basefit <- lm(log(sales) ~ log(price), data=oj)
coef(basefit)
```

(Intercept) 10.4234223275755 **log(price)** -1.60130655250769

Controlling for brands in OLS:

```
[5]: brandfit <- lm(log(sales) ~ brand + log(price), data=oj)
     coef(brandfit)
```

(Intercept) 10.8288215795649 **brandminute.maid** 0.87017465165164 **brandtropicana** 1.52994276420652 **log(price)** -3.13869142792174

Residulaiziing to show what partialing out things mean:

```
[6]: pricereg <- lm(log(price) ~ brand, data=oj)
     phat <- predict(pricereg, newdata=oj)
     presid <- log(oj$price)-phat
     coef( residfit <- lm( log(sales) ~ presid, data=oj) )
```

(Intercept) 9.16786399316262 **presid** -3.1386914279217

We get the same coefficient on the residual or the original variable if we control for the predicted value:

```
[7]: residfit2 <- lm( log(sales) ~ phat + log(price), data=oj)
     coef(residfit2)
```

(Intercept) 9.26268526156084 **phat** 3.0177588402107 **log(price)** -3.13869142792193

Traditionally, and for consistency, you would also residualize the left-hand side when you residualize the right-hand size. (You can also Google the Frisch-Waugh-Lowell Theorem. Frisch also shared the first Nobel Prize in economics.)

```
[8]: salesreg <- lm(log(sales) ~ brand, data=oj)
     shat <- predict(salesreg, newdata=oj)
     sresid <- log(oj$sales) - shat
     residfit3 <- lm( sresid ~ presid - 1)
     coef(residfit3)
```

presid: -3.138691427922

3 Not controling for abortion

Let's turn to a famous line of research, earning Levitt a Clark Medal (also Google Melissa Dell) and the Freakonomics franchise.

For this, let's load some data that is not in comma-separated plain text (csv) this time.

(`skip` says 'skip the first line of the file', `sep="/t"` says 'tab separated')

```
[9]: data <- read.table("abortion.dat", skip=1, sep="\t")
     names(data) <- c("state","year","pop","y_viol","y_prop","y_murd",
             "a_murd","a_viol","a_prop",'prison','police',
        'ur','inc','pov','afdc','gun','beer')
```

Some variable descriptions:

- prison: log of lagged prisoners per capita
- police: the log of lagged police per capita
- ur: the unemployment rate
- inc: per-capita income
- pov: the poerty rate
- AFDC: generosity at year t-15
- gun: dummy for concealed weapons law
- beer: beer consumption per capita

Let's drop some unusable parts of the data, and make the time and state variables

[10]:
```
data <- data[!(data$state%in%c(2,9,12)),] # AK, DC, HA are strange places
data <- data[data$year>84 & data$year<98,] # incomplete data outside these years
data$pop <- log(data$pop)
t <- data$year - 85
s <- factor(data$state) ## the states are numbered alphabetically
```

Here come the designated controls:

[11]:
```
controls <- data.frame(data[,c(3,10:17)])
```

Key: `y` is de-trended log crime rate, criminal-age-weighted prior abortion rate `a` is as described below. Note we also have violent and property crime versions for both.

[12]:
```
y <- data$y_murd
d <- data$a_murd
```

The abortion `a_` variables are weighted average of abortion rates where weights are determined by the fraction of the type of crime committed by various age groups. For example, if 60% of violent crime were committed by 18-year-olds and 40% were committed by 19 year olds in state `i`, the abortion rate for violent crime at time `t` in state `i` would be constructed as `.6` times the abortion rate in state `i` at time `t` `18` plus `.4` times the abortion rate in state `i` at time `t` `19`. See Donohue and Levitt (2001) for further detail.

We'll just look at murder. Note that for convenience here we've made `y,d,t` global: they are not in `controls`.

Let's win a Clark Medal:

[13]:
```
summary(orig <- glm(y ~ d + t + s +., data=controls) )$coef['d',]
```

Estimate -0.209811946154278 **Std. Error** 0.0410917700855323 **t value** -5.10593595061872 **Pr(>\textbar{}t\textbar{})** 4.50592549107522e-07

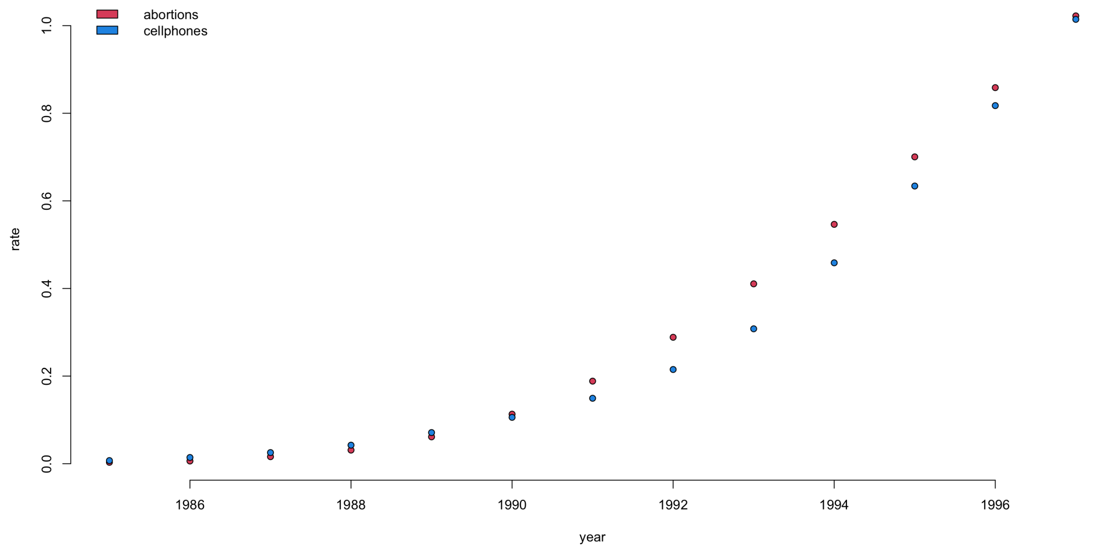
That abortion is only one factor influencing crime in the late 1980s points out the caution required in drawing any conclusions regarding an abortion-crime link based on time series evidence alone.

As a cautionary example, let's repeat the analysis, but for cellphones rather than abortion:

[14]:
```
cell <- read.csv("us_cellphone.csv")
cellrate <- 5*cell[,2]/(1000*cell[,3]) # center on 1985 and scale by 1997-1985
```

A smart observation: there are many things that increased with similar (but non-linear) shapes over time (cellphone usage, yoga revenues, home prices, . . .). Is this loading onto abortion? What if we're just fitting a quadratic trend?

[15]:
```
par(mai=c(.9,.9,.1,.1))
plot(1985:1997, tapply(d, t, mean), bty="n", xlab="year", ylab="rate", pch=21,␣
  ↪bg=2)
points(1985:1997, cellrate, bg=4, pch=21)
legend("topleft", fill=c(2,4), legend=c("abortions","cellphones"), bty="n")
```



[16]:
```
phone <- cellrate[t+1]
summary(tech <- glm(y ~ phone + s + t+., data=controls))$coef['phone',]
1 - exp(-3.72e-01)
```

Estimate -0.372072322217271 **Std. Error** 0.069322615302163 **t value** -5.36725743244805 **Pr(>\textbar{}t\textbar{})** 1.16863650800927e-07

0.310645757475778

What is happening here is that murder has been increasing quadratically, and we have no other controls that do so. To be correct, you need to allow quadratic trends that could be caused by other confounding variables (e.g. technology). We also allow interaction between the controls, and interact the nation-wide phone variable with state dummies to allow for state specific tech adoption.

[17]:
```
t <- factor(t)
interact <- glm(y ~ d + t + phone*s + .^2, data=controls)
```

```
summary(interact)$coef["d",]
```

Estimate 0.279710654345324 **Std. Error** 0.180731113086339 **t value** 1.54766188050698 **Pr(>\textbar{}t\textbar{})** 0.122375348876949

The abortion effect has switched direction (and is insignificant)!

But we have very few observations relative to number of parameters:

```
[18]: dim(model.matrix(formula(interact), data=controls))
```

1. 624 2. 154

So we need a way to select only important controls. Try using a lasso (after refactoring state to have NA reference level):

```
[19]: library(gamlr)
      sna <- factor(s, levels=c(NA,levels(s)), exclude=NULL)
      x = sparse.model.matrix( ~ t + phone*sna + .^2, data=controls)[,-1]
      dim(x)

      ## naive lasso regression
      naive <- cv.gamlr(cbind(d,x),y)
      coef(naive)["d",] # effect is CV selected <0
```

```
Loading required package: Matrix
```

1. 624 2. 154

-0.118963279334163

To explicitly include confounder `dhat` confound, we first need a model to predict treatment (this is step `i` of Algorithm 14):

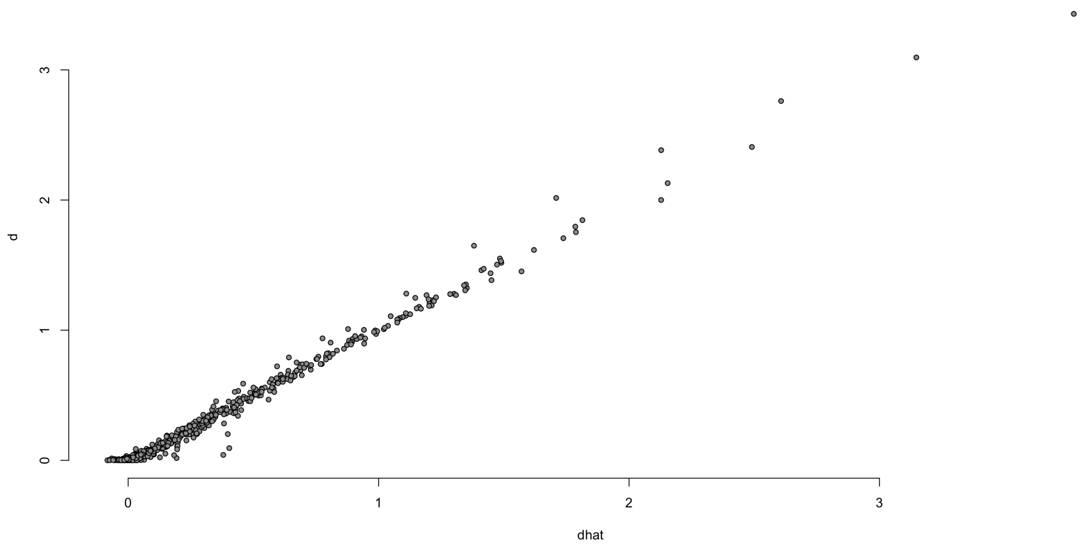
```
[20]: treat <- cv.gamlr(x,d, lmr=1e-4)
```

Save the predicted treatment. `type="response"` is redundant here (Gaussian model), but you'd want it if `d` was binary

```
[21]: dhat <- drop( predict(treat, x, select="min") )
```

Worrying sign: not much signal in `d` not predicted by `dhat` (that means we have little to resemble an experiment here. . .)

```
[22]: par(mai=c(.9,.9,.1,.1))
      plot(dhat,d,bty="n",pch=21,bg=8, cex=.8, yaxt="n")
      axis(2, at=c(0,1,2,3))
```



Check an In Sample R^2, which is what governs how much independent signal you have for estimating (which you see in the very similar OLS regressions below)

```
[23]: cor(drop(dhat),d)^2
```

0.989617332146834

```
[24]: summary( glm( y ~ I(d-dhat) ) )
      summary( glm( y ~ d + dhat) )
```

```
Call:
glm(formula = y ~ I(d - dhat))

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.5530  -0.4548   0.0899   0.5427   1.2888

Coefficients:
            Estimate Std. Error  t value Pr(>|t|)
(Intercept) -2.87706    0.02626 -109.572   <2e-16 ***
I(d - dhat)  0.32530    0.55353    0.588    0.557
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for gaussian family taken to be 0.4302084)

    Null deviance: 267.74  on 623  degrees of freedom
Residual deviance: 267.59  on 622  degrees of freedom
```

```
AIC: 1248.5

Number of Fisher Scoring iterations: 2



Call:
glm(formula = y ~ d + dhat)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.5476  -0.4438   0.0784   0.5415   1.3061

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -2.9080     0.0321 -90.601   <2e-16 ***
d             0.3164     0.5528   0.572    0.567
dhat         -0.2218     0.5562  -0.399    0.690
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for gaussian family taken to be 0.4289767)

    Null deviance: 267.74  on 623  degrees of freedom
Residual deviance: 266.39  on 621  degrees of freedom
AIC: 1247.7

Number of Fisher Scoring iterations: 2
```

Properly following Algorithm 14, we can re-run the lasso, with this prediction (the second column) included unpenalized.

[25]:
```r
causal <- gamlr(cbind(d,dhat,x),y,free=2,lmr=1e-3)
coef(causal)["d",] # AICc says abortion has no causal effect.
```

0

Jumping ahead to other methods in the chapter, let's try orthoML on the abortion data. (with only 5 folds, the results are a bit unstable, but at least it does not matter for the signifiance of the effect)

[26]:
```r
source("orthoML.R")
dreg <- function(x,d){ cv.gamlr(x, d, lmr=1e-5) }

yreg <- function(x,y){ cv.gamlr(x, y, lmr=1e-5) }

resids <- orthoPLTE( x=x, d=d, y=y,
                                dreg=dreg, yreg=yreg, nfold=5)
```

```
Loading required package: AER
Loading required package: car

Loading required package: carData

Loading required package: lmtest

Loading required package: zoo


Attaching package: ‘zoo’


The following objects are masked from ‘package:base’:

    as.Date, as.Date.numeric


Loading required package: sandwich

Loading required package: survival


fold: 1  2  3  4  5
gamma (se) = 0.0180822 (0.147449)
```

Traditional two-sided p-value for the key treatment effect:

[27]:
```
2*(1-pnorm(0.120546/0.164335))
```

0.463230238315691

4 Sample-splitting and orthoML in the hockey data

[28]:
```
library(gamlr) # loads Matrix as well
data(hockey) # load the data
x <- cbind(config,team,player) # Combine the covariates all together
y <- goal$homegoal # build 'y': home vs away, binary response
fold <- sample.int(2,nrow(x),replace=TRUE)
nhlprereg <- gamlr(x[fold==1,], y[fold==1],
        free=1:(ncol(config)+ncol(team)),
        family="binomial", standardize=FALSE)
```

We can just take the selected variables (without the intercept, thus the `-1`), and fit an unpenalized model using them in the other half of the data.

[29]:
```
selected <- which(coef(nhlprereg)[-1,] != 0)
xnotzero <- as.data.frame(as.matrix(x[,selected]))
```

```
nhlmle <- glm( y ~ ., data=xnotzero,
                        subset=which(fold==2), family=binomial )
```

We can then interpret the coefficients and the (robust!) standard errors as causally.

[30]:
```
x[1,x[1,]!=0]
p <- predict(nhlmle, xnotzero[1,,drop=FALSE], type="response", se.fit=TRUE)
p$fit
p$se.fit
library(AER)
Vnhl <- vcovHC(nhlmle)
```

DAL.20022003 -1 **EDM.20022003** 1 **ERIC_BREWER** 1 **JASON_CHIMERA** 1 **ROB_DIMAIO** -1 **DERIAN_HATCHER** -1 **NIKO_KAPANEN** -1 **JERE_LEHTINEN** -1 **JUSSI_MARKKANEN** 1 **JANNE_NIINIMAA** 1 **RYAN_SMYTH** 1 **BRIAN_SWANSON** 1 **MARTY_TURCO** -1 **SERGEI_ZUBOV** -1

```
Warning message in predict.lm(object, newdata, se.fit, scale = residual.scale,
type = if (type == :
‘‘prediction from a rank-deficient fit may be misleading’’
```

1: 0.505982487615667

1: 0.068946009155856

Why did we get different numbers from the book? Could the random fold matter this much? Not really. Note that we use the original hockey specification here, when we don't penalize the configuration and team dummies. The book uses the slightly simpler example. (It is a bit surprising it matters this much.)

Let's pick a player as an example:

[31]:
```
WHO <- "SIDNEY_CROSBY"
Bhat <- coef(nhlmle)
exp(Bhat["SIDNEY_CROSBY"])
who <- grep(WHO,colnames(x))
```

SIDNEY_CROSBY: 1.60205026274221

We can repeat the propensity adjustment exercise:

[ ]:
```
treatreg <- gamlr(x[,-who], x[,who],
                                free=1:(ncol(config)+ncol(team)),
                                standardize=FALSE, lmr=1e-6)
plot(treatreg) # basically we're getting OLS here; signal is strong
```

[33]:
```
dhat <- predict(treatreg, x[,-who], type="response")
causereg <- gamlr(cbind(config,team,dhat,player), y,
                                free=1:(ncol(config)+ncol(team)+1),
                                family="binomial", standardize=FALSE)
coef(causereg)[WHO,]
```

1.11799427279508

Or just stick to ortogonal ML:

[34]:
```r
source("orthoML.R")
dreg <- function(x,d){
        gamlr(x, d, standardize=FALSE, lmr=1e-5) }

yreg <- function(x,d){
        gamlr(x, d, family="binomial", standardize=FALSE, lmr=1e-5) }

resids <- orthoPLTE( x=x[,-who], d=x[,who], y=y,
                                dreg=dreg, yreg=yreg, nfold=5)
```

```
fold: 1  2  3  4  5
gamma (se) = 0.255991 (0.0206741)
```

5 Heterogenous Treatment Effects

Back to the Oregon data:

[35]:
```r
library(foreign)

descr <- read.dta("OHIE_Public_Use_Files/OHIE_Data/oregonhie_descriptive_vars.
 ↪dta")
prgm <- read.dta("OHIE_Public_Use_Files/OHIE_Data/oregonhie_stateprograms_vars.
 ↪dta")
s12 <- read.dta("OHIE_Public_Use_Files/OHIE_Data/oregonhie_survey12m_vars.dta")

# nicely organized, one row per person
all(s12$person_id == descr$person_id)
all(s12$person_id == prgm$person_id)

P <- descr[,c("person_id","household_id", "numhh_list")]
P$medicaid <- as.numeric(prgm[,"ohp_all_ever_firstn_30sep2009"]=="Enrolled")
P$selected <- as.numeric(descr[,"treatment"]=="Selected")
levels(P$numhh_list) <- c("1","2","3+")

# 12 month is the survey that really matters
# need to control for household size interacted with survey return time
Y <- s12[,c("weight_12m",
        "doc_any_12m","doc_num_mod_12m",
        "er_any_12m","er_num_mod_12m",
        "hosp_any_12m","hosp_num_mod_12m")]
Y$doc_any_12m <- as.numeric(Y$doc_any_12m=="Yes")
Y$er_any_12m <- as.numeric(Y$er_any_12m=="Yes")
Y$hosp_any_12m <- as.numeric(Y$hosp_any_12m=="Yes")
```

```
# smk_ever_12m - num19_12m are sources of heterogeneity, plus descr
X <- s12[,121:147]
X$dt_returned <- factor(format(s12$dt_returned_12m, "%Y-%m"))

insurv <- which(s12$sample_12m_resp == "12m mail survey responder")
X <- X[insurv,]
Y <- Y[insurv,]
P <- P[insurv,]

sapply(Y,function(y) sum(is.na(y)))
nomiss <- which( !apply(Y,1, function(y) any(is.na(y))) )
X <- X[nomiss,]
Y <- Y[nomiss,]
P <- P[nomiss,]

# pull out the weights and attach doc_any to P
weights <- Y[,1]
Y <- Y[,-1]

# replace some ridiculous values in survey and drop num19
X$hhsize_12m[X$hhsize_12m>10] <- 10
X$num19_12m <- NULL

# organize to make it pretty for text
P$doc_any_12m <- Y$doc_any_12m # you can explore other responses if you want
P <- P[,c(1,2,6,5,4,3)]
names(P)[6] <- "numhh"
```

```
TRUE

TRUE

weight\_12m     0 doc\_any\_12m     249 doc\_num\_mod\_12m     300 er\_any\_12m     227
er\_num\_mod\_12m     260 hosp\_any\_12m     168 hosp\_num\_mod\_12m     202
```

5.1 Dealing with missingness

As often, make NA the reference level for all categories

[36]:
```
source("naref.R")
X <- naref(X)
```

Now take the numeric variables, flag them when they are missing, and impute zero for sparse variables and means for dense ones.

[37]:
```
xnum <- X[,sapply(X,class)%in%c("numeric","integer")]
xnum[66:70,]
colSums(is.na(xnum))
# flag missing
```

```
xnumna <- apply(is.na(xnum), 2, as.numeric)
xnumna[66:70,]
# impute the missing values
mzimpute <- function(v){
        if(mean(v==0,na.rm=TRUE) > 0.5) impt <- 0
        else impt <- mean(v, na.rm=TRUE)
        v[is.na(v)] <- impt
        return(v) }
xnum <- apply(xnum, 2,  mzimpute)
xnum[66:70,]

# replace/add the variables in new data frame
for(v in colnames(xnum)){
        X[,v] <- xnum[,v]
        X[,paste(v,"NA", sep=".")] <- xnumna[,v] }
X[144:147,]
```

A data.frame: 5 × 4

	smk_avg_mod_12m	birthyear_12m	hhinc_pctfpl_12m	hhsize_12m
	<int>	<int>	<dbl>	<dbl>
66	0	1974	NA	NA
67	15	1963	150.04617	1
68	NA	1962	150.04617	1
69	20	1964	61.44183	3
70	10	NA	14.71825	10

smk_avg_mod_12m 3356 **birthyear_12m** 518 **hhinc_pctfpl_12m** 2253 **hhsize_12m** 1175

A matrix: 5 × 4 of type dbl

smk_avg_mod_12m	birthyear_12m	hhinc_pctfpl_12m	hhsize_12m
0	0	1	1
0	0	0	0
1	0	0	0
0	0	0	0
0	1	0	0

A matrix: 5 × 4 of type dbl

smk_avg_mod_12m	birthyear_12m	hhinc_pctfpl_12m	hhsize_12m
0	1974.000	77.20707	2.987188
15	1963.000	150.04617	1.000000
0	1962.000	150.04617	1.000000
20	1964.000	61.44183	3.000000
10	1965.777	14.71825	10.000000

A data.frame: 4 × 31

	smk_ever_12m	smk_curr_12m	smk_avg_mod_12m	smk_quit_12m	female_12
	<fct>	<fct>	<dbl>	<fct>	<fct>
144	No	not at all	0	NA	Male
145	Yes	every day	14	No	Male
146	Yes	every day	6	Yes	Female
147	Yes	not at all	0	NA	Female

Now we just build the usual design matrix.

[38]:
```
xhte <- sparse.model.matrix(~., data=cbind(numhh=P$numhh, X))[,-1]
xhte[1:2,1:4]
dim(xhte)
```

```
2 x 4 sparse Matrix of class "dgCMatrix"
  numhh2 numhh3+ smk_ever_12mNo smk_ever_12mYes
1      .       .              .               1
2      .       .              1               .
```

1. 23107 2. 91

And interactions for an even larger design matrix:

[39]:
```
dxhte <- P$selected*xhte
colnames(dxhte) <- paste("d",colnames(xhte), sep=".")
htedesign <- cbind(xhte,d=P$selected,dxhte)
```

And now we can fix the interacted model, only we need to include the baseline treatment and its `numhh` controls without penalty.

[40]:
```
htefit <- gamlr(x=htedesign, y=P$doc_any_12m, free=c("numhh2","numhh3+","d"))
gam <- coef(htefit)[-(1:(ncol(xhte)+1)), ]
round(sort(gam)[1:6],4)
round(sort(gam, decreasing=TRUE)[1:6],4)
```

```
[1]   1   2 92
```

d.race_asian_12mYes -0.0446 **d.employ_hrs_12mwork 20-29 hrs/week** -0.0433
d.hhinc_cat_12m\$32501-\$35000 -0.0293 **d.hhinc_cat_12m\$27501-\$30000** -0.0232
d.hhinc_cat_12m\$15001-\$17500 -0.0195 **d.race_hisp_12mYes** -0.0173

d 0.0927 **d.race_pacific_12mYes** 0.0404 **d.hhinc_cat_12m\$2501-\$5000** 0.0221
d.hhinc_cat_12m\$5001-\$7500 0.0137 **d.live_other_12mYes** 0.0116
d.race_black_12mYes 0.0067

There is one extra complication here: as the interacting variables don't average to a zero shift of the treatment effect, the ATE is not just the coefficient on the `d` variable but also the weighted some of the heterogenous treatment effects. They can be collected by hand, or with a shorthand that certainly takes some time to learn.

[41]:
```
gam["d"] + colMeans(xhte)%*%gam[grep("d.", names(gam))]
```

A matrix: 1 × 1 of type dbl 0.05616546

6 Hold my beer

Load, explore and downsample the (cleaned) Dominick's beer data:

[42]:
```
load("dominicks-beer.rda")
```

```
# how many upcs?
length( upctab <- table(wber$UPC) )

# check data types
sapply(wber, class)

# create priceperoz
wber$lp <- log(12*wber$PRICE/upc[wber$UPC,"OZ"])

# smallbeer
set.seed(888)
ss <- sample.int(nrow(wber),5e3)
```

287

STORE	'character'	**UPC**	'character'	**WEEK**	'factor'	**PRICE**	'numeric'	**MOVE**	'integer'

See how you can get a small elasticity:

```
[43]: coef( margfit <- lm(log(MOVE) ~ lp, data=wber[ss,]) )
```

(Intercept)	1.04608661196579	**lp**	-0.658260564487543

Now, we better have some controls. Say, dummy indicators for beer type, week, and store:

```
[44]: wber$s <- factor(wber$STORE)
      wber$u <- factor(wber$UPC)
      wber$w <- factor(wber$WEEK)
      xs <- sparse.model.matrix( ~ s-1, data=wber)
      xu <- sparse.model.matrix( ~ u-1, data=wber)
      xw <- sparse.model.matrix( ~ w-1, data=wber)
```

We'll also collect some indicators for words in the description, and collect all controls:

```
[45]: #install.packages("tm")
      library(tm)
      descr <- Corpus(VectorSource(as.character(upc$DESCRIP)))
      descr <- DocumentTermMatrix(descr)
      descr <- sparseMatrix(i=descr$i,j=descr$j,x=as.numeric(descr$v>0), # convert␣
       ↪from stm to Matrix format
                    dims=dim(descr),dimnames=list(rownames(upc),colnames(descr)))

      descr[1:5,1:6]
      descr[287,descr[287,]!=0]

      controls <- cbind(xs, xu, xw, descr[wber$UPC,])
      dim(controls)
```

```
Loading required package: NLP
```

```
5 x 6 sparse Matrix of class "dgCMatrix"
           32oz beer budweiser n.r.b 6pk busch
1820000008    1    1         1     1   .     .
1820000016    .    1         1     .   1     .
1820000051    .    1         .     .   1     1
1820000106    .    1         1     .   1     .
1820000117    1    1         1     .   .     .
```

6pk 1 **red** 1 **ale** 1 **honey** 1 **oregon** 1

1. 1600572 2. 851

Here's the naive lasso. (Why don't we standardize here?)

```
[46]: naivefit <- gamlr(x=cbind(lp=wber$lp,controls)[ss,], y=log(wber$MOVE)[ss],␣
       ↪free=1, standardize=FALSE)
      print( coef(naivefit)[1:2,] )
```

```
intercept        lp
 0.128270 -1.980717
```

Let's do the double/orthogonal ML:

```
[47]: source("orthoML.R")
      dreg <- function(x,d){
              gamlr(x, d, standardize=FALSE, lmr=1e-5) }

      yreg <- function(x,y){
              gamlr(x, y, standardize=FALSE, lmr=1e-5) }

      resids <- orthoPLTE( x=controls[ss,], d=wber$lp[ss], y=log(wber$MOVE)[ss],␣
       ↪dreg=dreg, yreg=yreg, nfold=5)
```

```
fold: 1  2  3  4  5
gamma (se) = -3.60396 (0.121278)
```

Now here's a new trick: Actually, we can fit a big model after all, without penalty, but we would still need these fancy commands. Why? Because the standard commands work with matrices, which are horrendously large here if you want to include all the zeros everywhere. So let's you a trusty command that works with sparse matrices, only without penalties this time.

```
[48]: fullfit <- gamlr(x=cbind(lp=wber$lp,controls), y=log(wber$MOVE), lambda.start=0)
      print( coef(fullfit)["lp",] )
```

```
[1] -3.567488
```

Heterogenous treatment effects are great for beer, but complicated to build.

```
[49]: # interact items and text with price
      lpxu <- xu*wber$lp
      colnames(lpxu) <- paste("lp",colnames(lpxu),sep="")
```

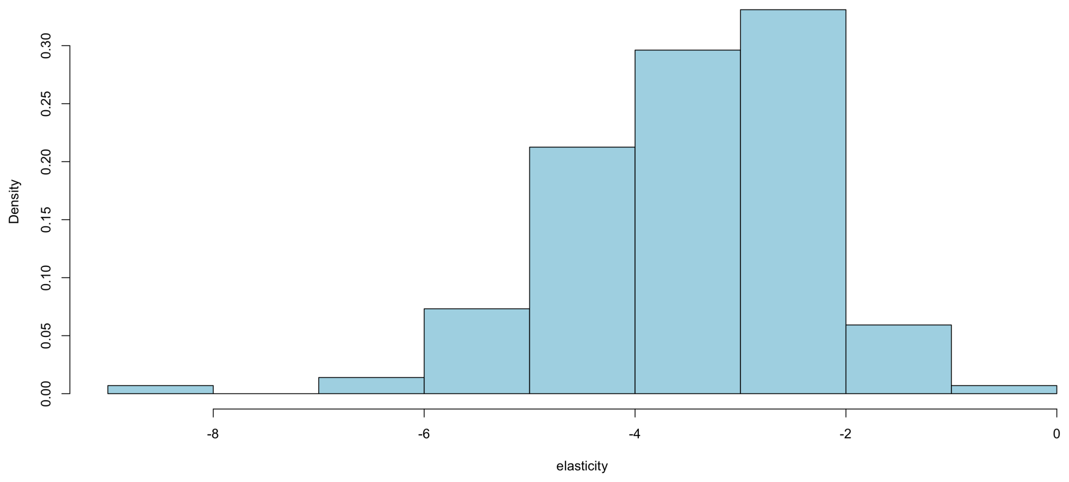
```
# create our interaction matrix
xhte <- cbind(BASELINE=1,descr[wber$UPC,])
d <- xhte*wber$lp
colnames(d) <- paste("lp",colnames(d),sep=":")

eachbeer <- xhte[match(rownames(upc),wber$UPC),]
rownames(eachbeer) <- rownames(upc)
```

Use these interactions in the fanciest model first:

```
[50]: dmlhte <- gamlr(x=xhte[ss,]*resids$dtil, y=resids$ytil, free=1,␣
       ↪standardize=FALSE)
      coef(dmlhte)[1:2]
      range( gamdml <- drop(eachbeer%*%coef(dmlhte)[-1,]) )
      hist(gamdml, main="", xlab="elasticity", col="lightblue", freq=FALSE)
```

1. -0.00172525179814379 2. -2.83651319832095

1. -8.43628254554082 2. -0.521001080730426



```
[51]: B <- coef(dmlhte)[-(1:2),]
      B <- B[B!=0]
      head(sort(round(B,2)))
      head(sort(round(B,2), decreasing=TRUE))
```

bonus	-4.22	**lager**	-3.04	**drft**	-2.24	**draft**	-1.44	**longneck**	-1.25	**30pk**	-1.19
sharp's	2.83	**state**	1.62	**n.a.**	1.55	**schlitz**	1.41	**dry**	1.23	**baderbrau**	1.2

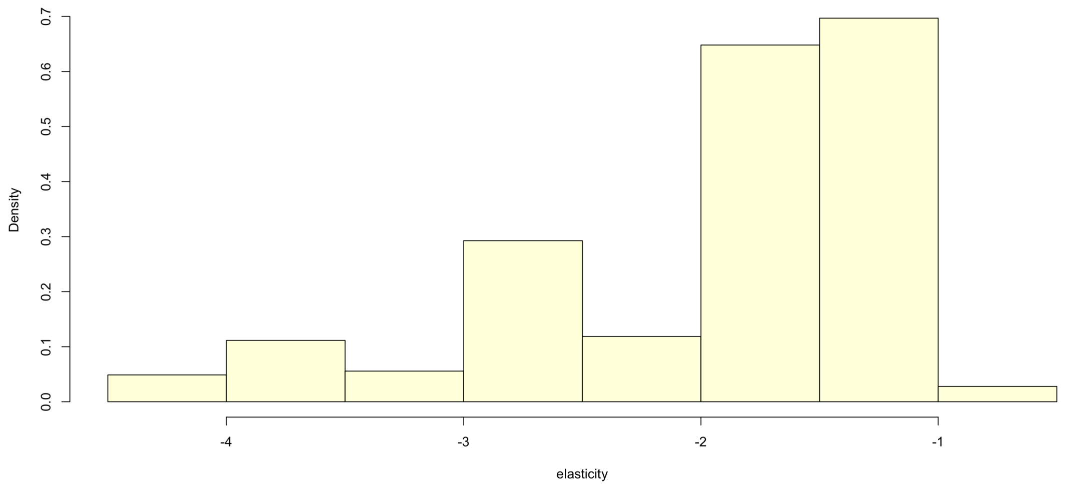
```
[52]: upc[names(sort(gamdml)[1:3]),]
```

A data.frame: 3 × 2

	DESCRIP <chr>	OZ <dbl>
7336097301	OLD STYLE LT BONUS 6 24pk	288
7336097305	OLD STYLE LT BONUS 6 24pk	288
3410015306	MILLER GENUINE DRFT 24pk	288

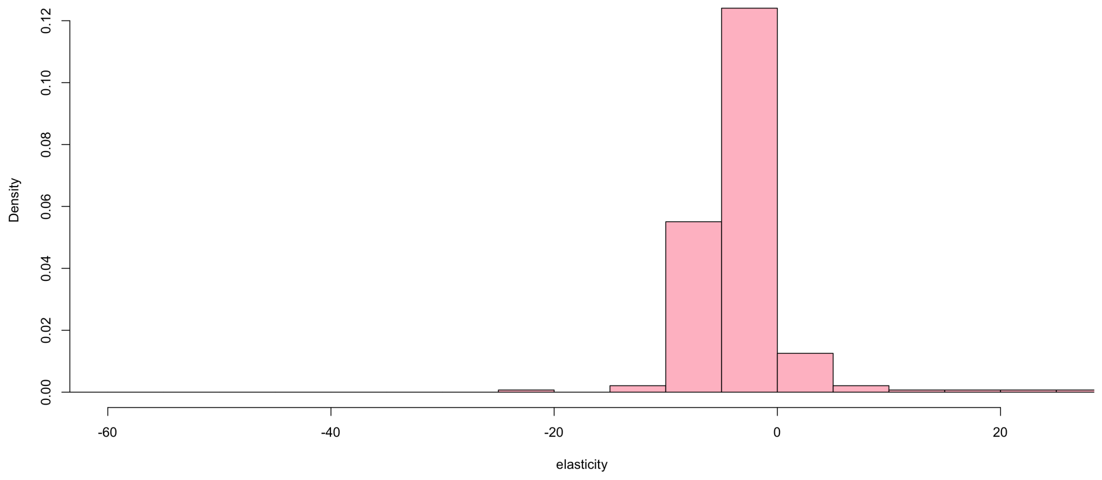
The other models performs much less sensibly with all these interactions, even the MLE that looked OK before.

[53]:
```r
d <- xhte*wber$lp
colnames(d) <- paste("lp",colnames(d),sep=":")
naivehte <- gamlr(x=cbind(d,controls)[ss,],
                                  y=log(wber$MOVE)[ss],
                                  free=1, standardize=FALSE)
gamnaive <- drop(eachbeer%*%coef(naivehte)[2:(ncol(d)+1),])
hist(gamnaive, main="", xlab="elasticity", col="lightyellow", freq=FALSE)
```



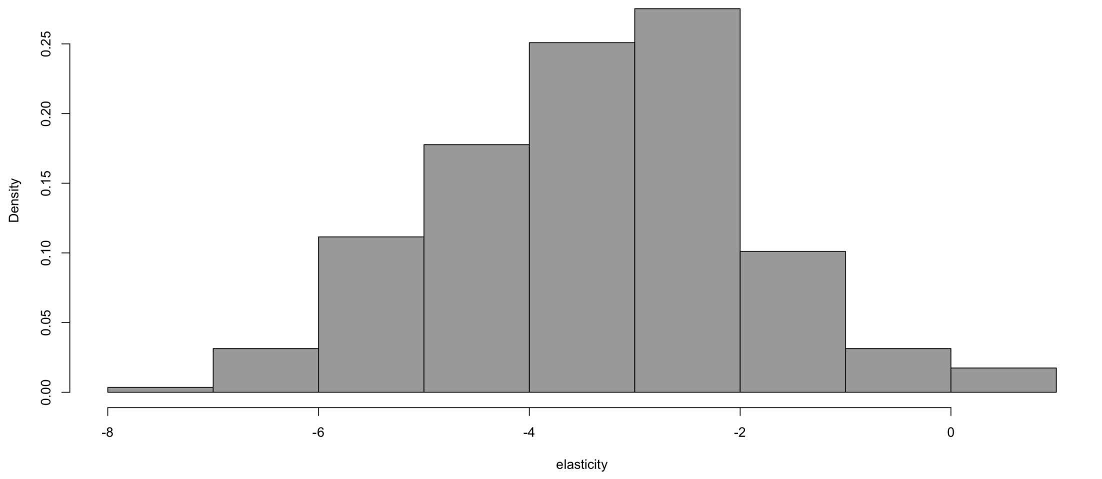
[54]:
```r
mlehte <- gamlr(x=cbind(d,controls)[ss,],
        y=log(wber$MOVE)[ss], lambda.start=0)
gamle <- drop(eachbeer%*%coef(mlehte)[2:(ncol(d)+1),])
hist(gamle, main="", xlab="elasticity", breaks=200, col="pink", xlim=c(-60,25),␣
 ↪freq=FALSE)
sort(gamle)[1:4]
```

73692011121 -918.809201244423 **7336043668** -23.695480005504 **8797501350** -11.1158949438684 **7336097301** -10.3412562421114



If you use the entire data, even MLE could work (under ignorability):

[64]:
```
fullhte <- gamlr(x=cbind(d,controls), y=log(wber$MOVE), lambda.start=0)
gamfull <- drop(eachbeer%*%coef(fullhte)[2:(ncol(d)+1),])
hist(gamfull, main="", xlab="elasticity", ,
                                   col="darkgrey", freq=FALSE)
```



But this is not a great sign:

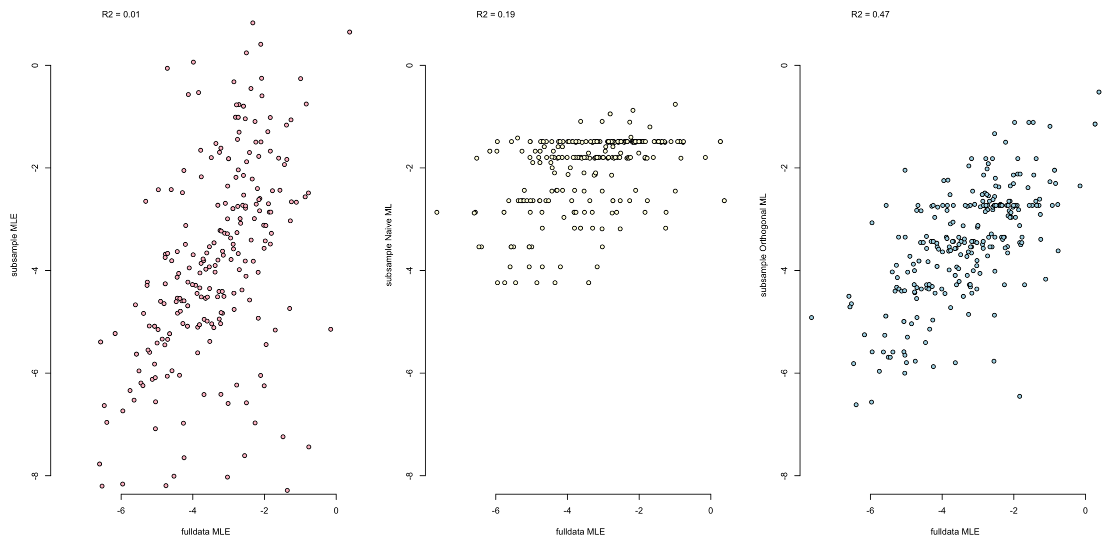
[56]:
```
upc[which(gamfull>0),]
```

A data.frame: 5 × 2

	DESCRIP <chr>	OZ <dbl>
3410000304	MILLER SHARP'S N/A C 6pk	72
3410010505	MILLER SHARP'S N/A L 6pk	72
5230000035	OLD MILWAUKEE N.A. C 6pk	72
5230001300	OLD MILWAUKEE N.A. B 6pk	72
5230001301	OLD MILWAUKEE N.A. B 6pk	72

Compare the elasticity estimates:

```
[57]: ylim <- c(-8,1)
par(mai=c(.7,.7,.1,.1), mfrow=c(1,3))
plot(gamfull, gammle, pch=21, bg="pink", xlab="fulldata MLE", ylab="subsample␣
 ↪MLE", bty="n", ylim=ylim)
text(x=-6,y=1, sprintf("R2 = %.02f",summary(lm(gamfull~gammle))$r.squared))
plot(gamfull, gamnaive, pch=21, bg="lightyellow", xlab="fulldata MLE",␣
 ↪ylab="subsample Naive ML", bty="n", ylim=ylim)
text(x=-6,y=1, sprintf("R2 = %.02f",summary(lm(gamfull~gamnaive))$r.squared))
plot(gamfull, gamdml, pch=21, bg="lightblue", xlab="fulldata MLE",␣
 ↪ylab="subsample Orthogonal ML", bty="n", ylim=ylim)
text(x=-6,y=1, sprintf("R2 = %.02f",summary(lm(gamfull~gamdml))$r.squared))
```



7 Synthetic controls

You are welcome to tune into the Chamberlain Seminar, by the way.

Just work with the OG data for this:

[58]:
```r
#install.packages(c("Synth","tidyr"))
library(Synth)
library(tidyr)
data(basque)
```

```
##
## Synth Package: Implements Synthetic Control Methods.


## See http://www.mit.edu/~jhainm/software.htm for additional information.




Attaching package: ‘tidyr’


The following object is masked _by_ ‘.GlobalEnv’:

    who


The following objects are masked from ‘package:Matrix’:

    expand, pack, unpack
```

Collect outcomes for treated region pre and post, and for all control.

[59]:
```r
y <- basque[,1:4] %>% spread(year, gdpcap)
rownames(y) <- y$regionname
y <- y[c(17,2:16,18), -(1:2)]
y <- y[,1:35]
```

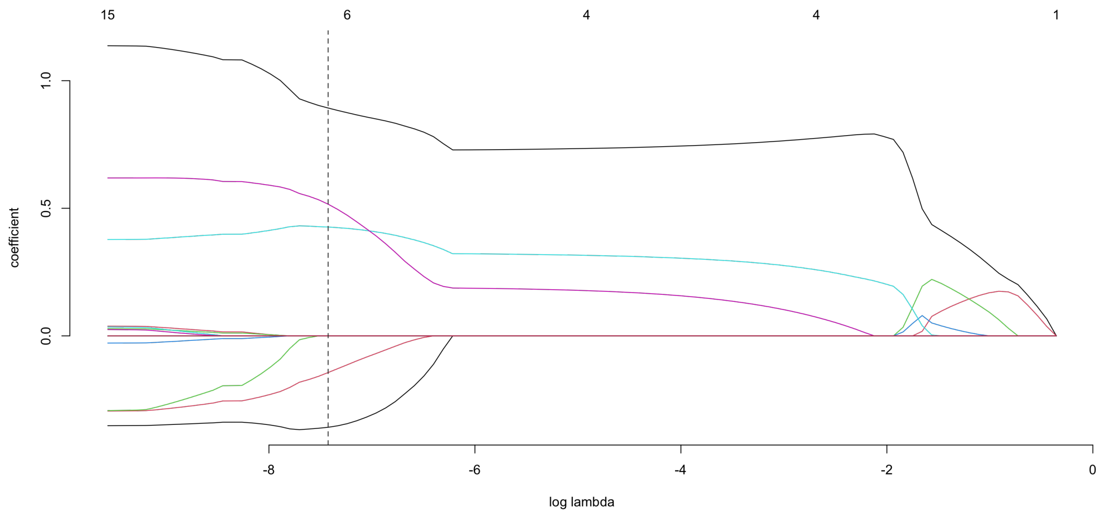
We can define a function that runs an ML prediction routine to predict a control. This hard codes the treated year here.

[60]:
```r
library(gamlr)
synthc <- function(j, tyear=1968, ...){
        y0t <- t(y[,1:(tyear-1954)])
        fit <- gamlr( y0t[,-j], y0t[,j], ...)
        plot(fit)
        y0hat <- predict(fit, t(y[-j,]))[,1]
        return(list(w=coef(fit)[,1], y0hat=y0hat ) )
}
```

And run it.

[61]:
```
sc <- synthc(1, lmr=1e-4)
sc$w
```

intercept 0.832492340851006 **Andalucia** 0 **Aragon** 0 **Principado De Asturias** 0 **Baleares (Islas)** -0.143662241431167 **Canarias** 0 **Cantabria** 0 **Castilla Y Leon** 0.515992402831998 **Castilla-La Mancha** 0 **Cataluna** 0 **Comunidad Valenciana** -0.358177982636518 **Extremadura** 0 **Galicia** 0 **Madrid (Comunidad De)** 0.426397880130771 **Murcia (Region de)** 0.892844824789896 **Navarra (Comunidad Foral De)** 0 **Rioja (La)** 0



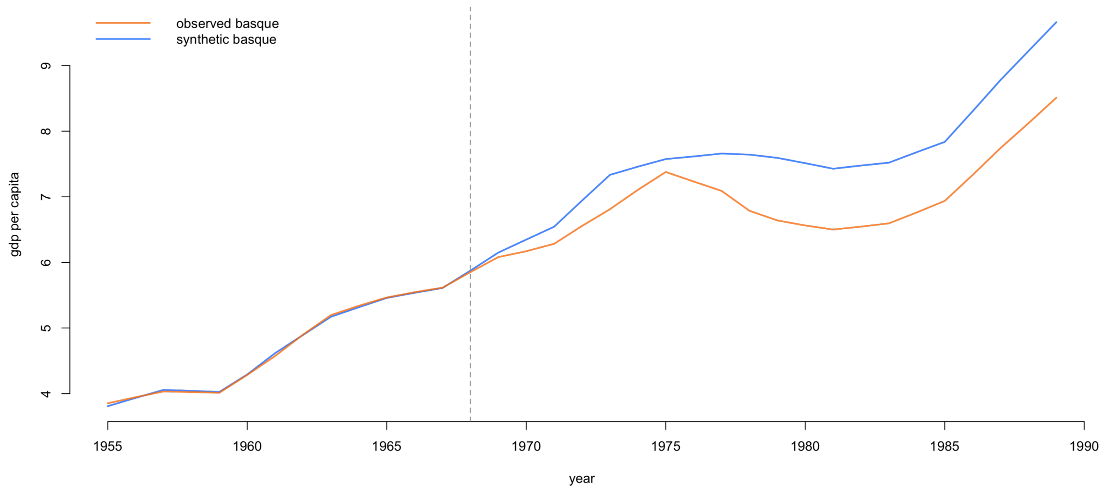
We can do a permutation test for untreated regions, and this is typically a task that can be parallelized.

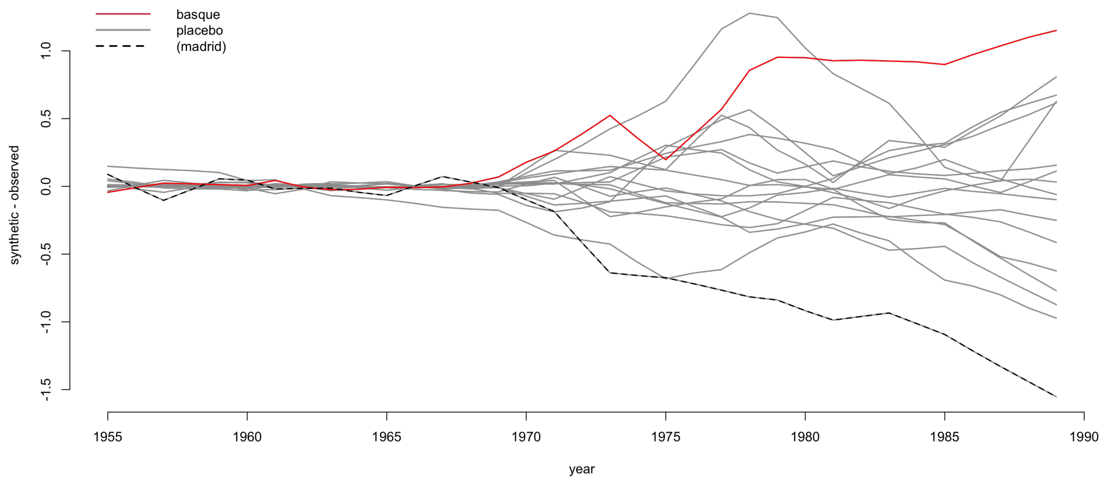
[62]:
```
library(parallel)
cl <- makeCluster(detectCores())
clusterExport(cl, c("y", "gamlr", "synthc"))

gety0 <- function(j){ synthc(j, lmr=1e-4)$y0hat }
Ysynth <- parSapply(cl, 1:nrow(y), gety0)
diff <- Ysynth - t(y)
```

Aaaaand plots!

[63]:
```
year <- as.numeric(colnames(y))
plot(year, sc$y0hat, type="l", ylab="gdp per capita",
        col=rgb(.1,.5,1,0.8), ylim=range(c(y[1,],sc$y0hat)), bty="n", lwd=2)
abline(v=1968, col=8, lty=2)
lines(year, y[1,], col=rgb(1,.5,0,.8), lwd=2)
legend("topleft", bty="n", legend=c("observed basque","synthetic basque"),
        lwd=2, col=c(col=rgb(1,.5,0,.8),rgb(.1,.5,1,0.8)) )
```

```r
matplot(year, diff, type="l", lwd=1.5,
        xlab="year", ylab="synthetic - observed",
         col=8, lty=1, bty="n")
lines(year, diff[,1], lwd=1.5, col="red")
lines(year, diff[,14], lwd=1.5, lty=2, col=1)
legend("topleft", bty="n",
        legend=c("basque", "placebo", "(madrid)"),
        lty=c(1,1,2), lwd=2, col=c(2,8,1))
```


observed basque
synthetic basque
gdp per capita
year


basque
placebo
(madrid)
synthetic - observed
year