# Your Turn

head(Puromycin)

This data set is the Puromycin data in R. The goal is to create a regression model about the rate of an enzymatic reaction as a function of the substrate concentration.

```
## conc rate state
## 1 0.02 76 treated
## 2 0.02 47 treated
## 3 0.06 97 treated
## 4 0.06 107 treated
## 5 0.11 123 treated
## 6 0.11 139 treated
```

```
dim(Puromycin)
```

## [1] 23 3

```
ggplot(Puromycin) +
  geom_point(aes(conc, rate))
```

```
ggplot(Puromycin) +
  geom_point(aes(log(conc), (rate)))
```



#### 2.1.4 Standard regression

```
m0 <- lm(rate ~ conc, data = Puromycin)
plot(m0)
summary(m0)</pre>
```

```
##
## Call:
## lm(formula = rate ~ conc, data = Puromycin)
##
## Residuals:
##
      Min
               10 Median
                               3Q
                                      Max
## -49.861 -15.247 -2.861 15.686 48.054
##
## Coefficients:
##
              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 93.92 8.00 11.74 1.09e-10 ***
## conc
               105.40 16.92 6.23 3.53e-06 ***
## ___
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 28.82 on 21 degrees of freedom
## Multiple R-squared: 0.6489, Adjusted R-squared: 0.6322
## F-statistic: 38.81 on 1 and 21 DF, p-value: 3.526e-06
confint(m0)
##
                 2.5 %
                         97.5 %
## (Intercept) 77.28643 110.5607
## conc
             70.21281 140.5832
m1 <- lm(rate ~ log(conc), data = Puromycin)</pre>
plot(m1)
summary(m1)
##
## Call:
```

## lm(formula = rate ~ log(conc), data = Puromycin)

```
##
## Residuals:
              1Q Median 3Q
##
      Min
                                    Max
## -33.250 -12.753 0.327 12.969 30.166
##
## Coefficients:
##
              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 190.085 6.332 30.02 < 2e-16 ***
## log(conc)
              33.203
                          2.739 12.12 6.04e-11 ***
## ___
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 17.2 on 21 degrees of freedom
## Multiple R-squared: 0.875, Adjusted R-squared: 0.869
## F-statistic: 146.9 on 1 and 21 DF, p-value: 6.039e-11
```

confint(m1)

 ##
 2.5 % 97.5 %

 ## (Intercept) 176.91810 203.2527

 ## log(conc)
 27.50665 38.8987

 # Fisher Infernation.







### 2.1.5 Paired bootstrap

```
# Your turn
library(boot)
reg_func <- function(dat, idx) {
    # write a regression function that returns fitted beta
}
    gr write your our is fre.
# use the boot function to get the bootstrap samples
# examing the bootstrap sampling distribution, make histograms
# get confidence intervals for beta_0 and beta_1 using boot.ci
```

### 2.1.6 Bootstrapping the residuals

```
# Your turn
library(boot)
reg_func_2 <- function(dat, idx) {
    # write a regression function that returns fitted beta
    # from fitting a y that is created from the residuals
}
# use the boot function to get the bootstrap samples
# examing the bootstrap sampling distribution, make histograms
# get confidence intervals for beta_0 and beta_1 using boot.ci
```

## **3** Bootstrapping Dependent Data

Suppose we have dependent data  $\boldsymbol{y} = (y_1, \ldots, y_n)$  generated from some unknown distribution  $F = F_{\boldsymbol{Y}} = F_{(Y_1, \ldots, Y_n)}$ .

No longer assuming Y, ,..., Y, independent. Les could be time serves, spatial, network, etc.

Goal:

Challenge:

Since Yi's are dependent it is inappropriate to use The iid bootstrap.  
Bootstrapped samples would no longer reproduce the data genoting process.  
(and sampling independenting from 
$$\hat{F}_n$$
 no longer mimics drawing original sample from F).

We will consider 2 approaches

Model -based (parametric).
 Block bootstrap (nonperametric).

**Example 3.1** Suppose we observe a time series  $\mathbf{Y} = (Y_1, \ldots, Y_n)$  which we assume is generated by an AR(1) process, i.e.,

This was for m-dependent process, which is a very strong assumption! Under more realistic process, may be even worse.

### **3.1 Model-based approach**

If we assume an AR(1) model for the data, we can consider a method similar to bootstrapping residuals for linear regression.

(1) Estimate à from data (fit the model). (a) before estimated "innovations"  $\hat{e}_t = Y_t - \hat{\alpha} Y_{t-1}, t = 2,..., n$ and  $\hat{e} = \frac{1}{n-1} \hat{\Sigma} \hat{e}_{\pm}$ (3) Define the residuals as cartered Mnovations  $\hat{\mathcal{E}}_{t} = \hat{\mathcal{E}}_{\perp} - \overline{\hat{\mathcal{E}}} \quad \left[ E\mathcal{E}_{i} = o \right]$ (4) For r=1,..,R a) Create a bootstrap sample  $\hat{\xi}_{0,...,}^{\star}$   $\hat{\xi}_{n}^{\star}$  by randomly sampling n+1 values for the n-1 values  $\hat{\mathcal{E}}_{4}$ ,  $t=\lambda_{1-n}$ . b) Construct perudo data Y\*= (y\*, ..., y\*) from  $y_0^* = \hat{\xi}_0^*, \quad y_t^* = \hat{d} y_{t-1}^* + \hat{\xi}_t^*, \quad t = l_{1-y_1}^*.$ c) define at as the estimate of a from "" (5) Isn of a " is bootstrap estimate of dan of a.

**Model-based** – the performance of this approach depends on the model being appropriate for the data.

As we know, this may not always be a good assumption.

## **3.2** Nonparametric approach

To deal with dependence in the data, we will employ a nonparametric *block* bootstrap.

Idea:

resample data in blocks to preserve the dependence structure within the blocks.

### 3.2.1 Nonoverlapping Blocks (NBB) Carlstein (1986).

Consider splitting  $\mathbf{Y} = (Y_1, \ldots, Y_n)$  in b consecutive blocks of length  $\ell$ .

We can then rewrite the data as  $\boldsymbol{Y} = (\boldsymbol{B}_1, \dots, \boldsymbol{B}_b)$  with  $\boldsymbol{B}_k = (Y_{(k-1)\ell+1}, \dots, Y_{k\ell}), k = 1, \dots, b.$ 

() Sample nonovelapping blocks B<sup>\*</sup>\_{i},..., B<sup>\*</sup>\_{b} independently from B<sub>1,-3</sub>B<sub>10</sub> with replacement to form puendo data set Y<sup>\*</sup> = (B<sup>\*</sup><sub>1</sub>,..., B<sup>\*</sup><sub>b</sub>).

(a) estimate statistic of interest from 
$$Y^*$$
 to get  $\hat{\partial}^*$ .  
(3) Repeat D-Q R times to obtain  $\hat{\partial}^{*(1)}_{,...,\hat{\partial}} \hat{\sigma}^{*(R)}$  to estimate day of  $\hat{\partial}$ .

Note, the order of data within the blocks must be maintained, but the order of the blocks that are resampled does not matter.

## Künsch (1989) 3.2.2 Moving Blocks (MBB) Lin Esingh (1992).

Now consider splitting  $\mathbf{Y} = (Y_1, \ldots, Y_n)$  into overlapping blocks of adjacent data points of length  $\ell$ .

Now we have more blocks the choose firm!  $(N = n - e + 1 \text{ us. } b = \lfloor \frac{n}{e} \rfloor)$ .

We can then write the blocks as  $B_k = (Y_k, \ldots, Y_{k+\ell-1}), k = 1, \ldots, n-\ell+1$ .

$$\mu^{\mu}(\text{collect brocks} C - (D_{1,..,B_N}) \text{ sempling } B_{1,..,B_0}^* \text{ from } C, b = [\overline{z}], \text{ put together to get } Y^{m} = (B_{1,..,B_n}^*).$$

Alternative but  
equivalent formulation but 
$$I_{1,m-1} I_{b}$$
 but tid of  $P(T_{1}=j) = \frac{1}{N}$ ,  $j = 1,..., N$  of  $B_{1}^{k} = B_{T_{1}}^{k}$ ,  $i = 1,..., b$ .  
 $E_{X}$ : but  $\hat{b}_{n} = \overline{Y}_{n}$ , but MBB sample mean perform  $\overline{Y}_{m}^{k} = \sum_{i=1}^{N} Y_{i}^{k} f_{m}^{k}$ , Find  $E_{X}(\overline{y}_{m}^{k})$  and  $Var_{X}(\overline{y}_{m}^{k})$  which estimate  
 $N_{0}te: \overline{Y}_{m}^{k} = \frac{1}{b} \stackrel{b}{\leq} \overline{y}_{T}^{k}$  (sample mean  $f_{1}^{k}$   
 $N_{0}te: \overline{Y}_{m}^{k} = \frac{1}{b} \stackrel{b}{\leq} \overline{y}_{T}^{k}$  (sample mean  $f_{1}^{k}$   
 $N_{0}te: \overline{Y}_{m}^{k} = \frac{1}{b} \stackrel{b}{\leq} \overline{y}_{T}^{k}$  ( $\overline{y}_{T}^{k}$ )  $= E_{X}(\overline{y}_{T}^{k})$   
 $(\widehat{P} = \sum_{i=1}^{N} \sqrt{y_{T}^{k}}) = \frac{1}{b} \stackrel{b}{\leq} \overline{z}_{i} (\overline{y}_{T}^{k}) = E_{X}(\overline{y}_{T}^{k})$   
 $(\widehat{P} = \sum_{i=1}^{N} \sqrt{y_{T}^{k}}) = \frac{1}{b} \stackrel{b}{z}_{i=1}^{k} E_{X}(\overline{y}_{T}^{k}) = E_{X}(\overline{y}_{T}^{k})$   
 $(\widehat{P} = \sum_{i=1}^{N} \sqrt{y_{T}^{k}}) = Var_{X}(\overline{y}_{T}^{k}) = E_{X}(\overline{y}_{T}^{k})$   
 $(\widehat{P} = \frac{1}{N} \stackrel{b}{z}_{i=1}^{k} \frac{1}{b} \frac{b}{y} = Var_{X}(\overline{y}_{T}^{k})$   
 $(\widehat{P} = \frac{1}{N} \stackrel{b}{z}_{i=1}^{k} \frac{b}{b} \frac{b}{i})$   
 $(\widehat{P} = \frac{1}{N} \stackrel{b}{z}_{i=1}^{k} \frac{b}{b} \frac{b}{i})$   
 $(\widehat{P} = \frac{1}{N} \stackrel{b}{z}_{i=1}^{k} \frac{b}{b} \frac{b}{i})$   
 $(\widehat{P} = \frac{1}{N} \stackrel{b}{z}_{i=1}^{k} \frac{b}{b} \frac{b$ 

This directly estimates the virial of simple mean of legth & block Jey;

NOTE: The MBB recision of  $\overline{V_n}(\overline{Y_n} - M) = \overline{V_n}(\overline{Y_n} - \overline{EY_n})$  is NOT  $\overline{V_m}(\overline{Y_m} - \overline{Y_n})!$ is actually  $\overline{V_m}(\overline{Y_m} - \overline{E_x}\overline{Y_m}) = \overline{V_m}(\overline{Y_m} - \widehat{M}) + \frac{\overline{V_n}}{\overline{V_n}}\overline{\overline{Y_n}}.$  Both NBB and MBB fix the resione issue from page 35.