Relationship between alcohol and health

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Our goal is to figure out the relationship between alcohol use and health condition. First, we use the regular way: running OLS.

```
% Title:  Matlab script for group project, STATS 506
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% Funtion: explore the relationship between health condition and drinking
%          alcohol, using data NHANES 2005—2006 data.
% Date: 11/30/2019

% load data
alq = xptread('ALQ_D.XPT');
demo = xptread('DEMO_D.XPT');
hsq = xptread('HSQ_D.XPT');

% select variables
alq = alq(:, {'SEQN', 'ALQ120Q'});
demo = demo(:, {'SEQN', 'RIAGENDR', 'RIDAGEYR', 'DMDEDUC2', 'INDFMPIR'});
hsq = hsq(:, {'SEQN', 'HSD010'});

% merge data
dt = join(alq, demo, 'Keys', 'SEQN');
dt = join(dt, hsq, 'Keys', 'SEQN');

% rename columns
dt.Properties.VariableNames = ...
["id", "alcohol", "sex", "yr", "edu", "pir", "health"];

% drop invalid values
dt = rmmissing(dt);
dt(dt.alcohol > 365, :) = [];
dt(dt.yr < 21, :) = [];
dt(dt.edu > 5, :) = [];
dt(dt.health > 3, :) = [];

% centralize and factorize
dt.alcohol = (dt.alcohol - mean(dt.alcohol)) ./ std(dt.alcohol);
dt.sex = categorical(dt.sex);
dt.yr = (dt.yr - mean(dt.yr)) ./ std(dt.yr);
dt.edu = categorical(dt.edu);
dt.pir = (dt.pir - mean(dt.pir)) ./ std(dt.pir);
dt.health = categorical(dt.health);
dt.health = reordercats(dt.health, {'3','2','1'});

% run OLS
md = fitlm(dt, 'alcohol ~ sex + yr + edu + pir + health');

% extract fitted values and residuals
fit = predict(md, dt(:, 3:7));
res = md.Residuals.Raw;

% calculate observed coverage probability
df = height(dt) - width(dt) -1;
se = sqrt(sum(res .^2) / df);
ci = [fit - tinv(0.95, df) * se, fit + tinv(0.95, df) * se];
cover = sum(dt.alcohol > ci(:,1) & dt.alcohol < ci(:,2)) / length(ci);

% plot residuals
plot(1:length(ci), res, 'x'), title('residuals of OLS')
```
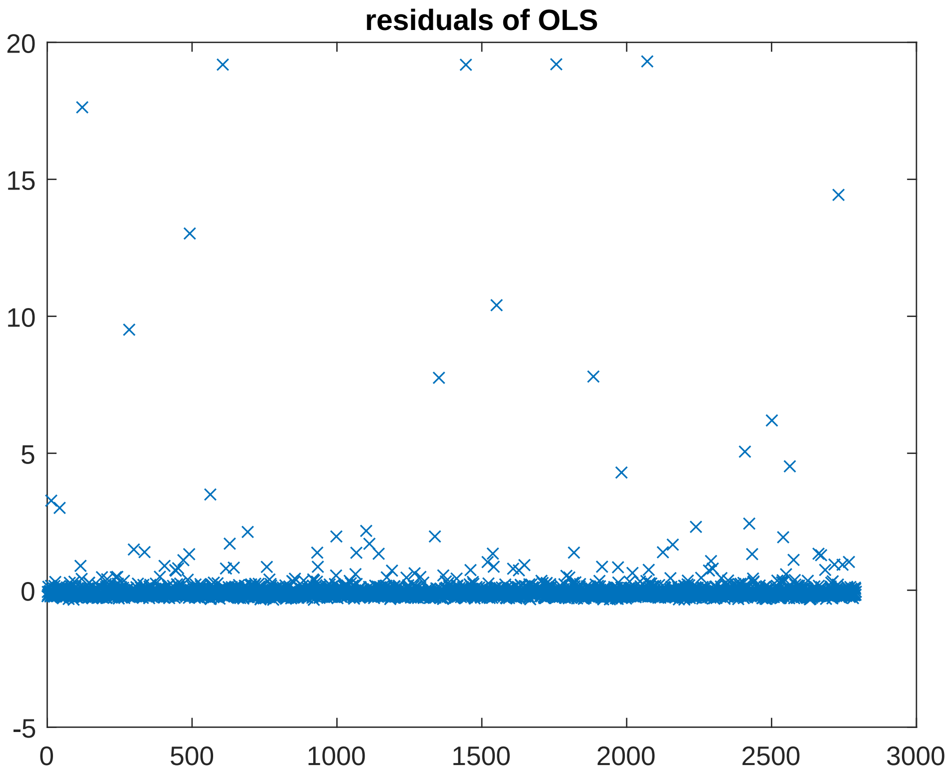
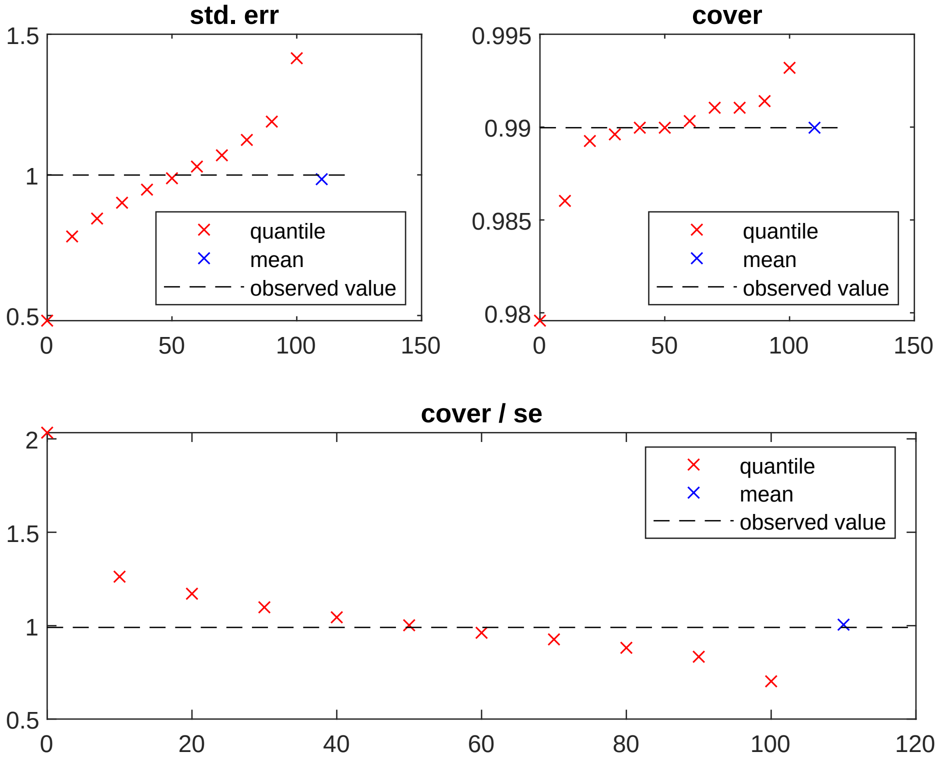



We could learn from this plot that the residuals are skewed. As a result, the regular way to estimate SE may fail. So we use bootstrap method to estimate σ^2 by resampling residuals.

```
% bootstrap
rng(506);
nboot = 1000;

func_se = @(x)sqrt(sum(x .^2) / df);
se_boot = bootstrp(nboot, func_se, res);
cover_boot = zeros(nboot, 1);

for i=1:nboot
    ci_boot = [fit - tinv(0.95, df) * se_boot(i), ...
        fit + tinv(0.95, df) * se_boot(i)];
    cover_boot(i) = sum(dt.alcohol > ci_boot(:,1) & ...
        dt.alcohol < ci_boot(:,2)) / length(ci);
end

% consider 0, 10, ... , 100 quantile, mean and the original observed value
% as estimate candidates
se_list = ([quantile(se_boot, (0:10) / 10), mean(se_boot), se])' ;
cover_list = zeros(13, 1);

for i=1:13
    ci_list = [fit - tinv(0.95, df) * se_list(i), ...
        fit + tinv(0.95, df) * se_list(i)];
    cover_list(i) = sum(dt.alcohol > ci_list(:,1) & ...
        dt.alcohol < ci_list(:,2)) / length(ci);
end

ratio_list = cover_list ./ se_list;

% plot se
subplot(2,2,1)
plot(linspace(0,100,11), se_list(1:11), 'rx', ...
     110, se_list(12), 'bx', ...
     linspace(0,120,13), se_list(13) * ones(13,1), 'k--'), ...
     title('std. err'), ...
     legend('quantile', 'mean', 'observed value', 'Location','southeast')

% plot coverage (probability)
subplot(2,2,2)
plot(linspace(0,100,11), cover_list(1:11), 'rx', ...
     110, cover_list(12), 'bx', ...
     linspace(0,120,13), cover_list(13) * ones(13,1), 'k--'), ...
     title('cover'), ...
     legend('quantile', 'mean', 'observed value', 'Location','southeast')

% plot cover / se
```

```
subplot(2,2,[3,4])
plot(linspace(0,100,11), ratio_list(1:11), 'rx', ...
     110, ratio_list(12), 'bx', ...
     linspace(0,120,13), ratio_list(13) * ones(13,1), 'k--'), ...
     title('cover / se'), ...
     legend('quantile', 'mean', 'observed value', 'Location','northeast')
```



The plot indicates that the length of SE varies widely, from 0.5 to 1.5. On the other hand, the range of coverage probability are relatively small, which is about 0.02.

The mean and median of bootstrap statistics perform almost the same as the observed values. In fact, there is a platform from 10 quantile to 90 quantile, and the statistics change sharply on 0 and 100 quantile.

There are serval criterions to choose estimators. If we focus on coverage probability, the maximum (100 quantile) of bootstrap sample is the desired estimator. If we define the ratio of coverage and SE as the efficiency of estimator, and the bigger the better, then we can conclude that the minimum (0 quantile) has the best performance. Otherwise, the observed value will just be fine.

It is natural that the maximum has the biggest coverage probability, and the mean and median perform similarly to the observed value. However, it remains unclear that whether the minimum is always the most efficient estimator. To address this problem, we use Monte Carlo to assess the power.

```
%test
nrep = 1000;

count = 0;

for i=1:nrep
    se_boot = bootstrp(nboot, func_se, res);
    cover_boot = zeros(nboot, 1);

    for j=1:nboot
        ci_test = [fit - tinv(0.95, df) * se_boot(j), ...
            fit + tinv(0.95, df) * se_boot(j)];
        cover_boot(j) = sum(dt.alcohol > ci_test(:,1) & ...
            dt.alcohol < ci_test(:,2)) / length(ci);
    end

    se_list = ([quantile(se_boot, (0:10) / 10), mean(se_boot), se])' ;
    cover_list = zeros(13, 1);

    for j=1:13
        ci_list = [fit - tinv(0.95, df) * se_list(j), ...
        fit + tinv(0.95, df) * se_list(j)];
        cover_list(j) = sum(dt.alcohol > ci_list(:,1) & ...
        dt.alcohol < ci_list(:,2)) / length(ci);
    end

    ratio_list = cover_list ./ se_list;

    if( max(ratio_list) == ratio_list(1) )
        count = count +1;
    end
end

prob = count / nrep;
```

```
prob =

     1
```

Indeed, the minimum is always the best. Intuitively, we could learn from the residual plot that, most points are concentrated around 0, but there are some outliers far away from 0. Each of them could make RSS bigger dramatically. So the best way to improve robustness is to avoid using them, which means choosing the minimum of SE in empirical distribution.