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Tugas 2 Bootcamp R-Studio

1. Pengujian 3 model panel
    - Pooled/Common Effect Model

```
Pooling Model

Call:
plm(formula = model, data = paneldata, model = "pooling")

Balanced Panel: n = 5, T = 5, N = 25

Residuals:
    Min.  1st Qu.   Median  3rd Qu.     Max.
-1.82612 -0.78139 -0.12506  0.29285  4.04388

Coefficients:
             Estimate Std. Error t-value Pr(>|t|)
(Intercept) -6.134655   3.378708 -1.8157 0.083726 .
UK           0.094687   0.184124  0.5143 0.612443
K_IND       12.931823   3.883847  3.3296 0.003182 **
K_AUD        2.808153   2.214165  1.2683 0.218583
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Total Sum of Squares:    52.604
Residual Sum of Squares: 34.305
R-Squared:      0.34787
Adj. R-Squared: 0.25471
F-statistic: 3.73402 on 3 and 21 DF, p-value: 0.026995
```

    - Fixed Effect Model

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```
Oneway (individual) effect Within Model

Call:
plm(formula = model, data = paneldata, effect = "individual",
    model = "within")

Balanced Panel: n = 5, T = 5, N = 25

Residuals:
     Min.   1st Qu.    Median   3rd Qu.      Max.
-2.492108 -0.398168 -0.019114  0.301832  3.377892

Coefficients:
      Estimate Std. Error t-value Pr(>|t|)
UK     0.74465    1.51775  0.4906   0.6300
K_IND  2.09627   16.37727  0.1280   0.8997
K_AUD  1.87784    4.14993  0.4525   0.6566

Total Sum of Squares:    25.455
Residual Sum of Squares: 24.446
R-Squared:      0.039624
Adj. R-Squared: -0.35583
F-statistic: 0.233798 on 3 and 17 DF, p-value: 0.87156
```

- Random Effect Model

```
> summary(random)
Oneway (individual) effect Random Effect Model
   (Swamy-Arora's transformation)

Call:
plm(formula = model, data = paneldata, effect = "individual",
    model = "random")

Balanced Panel: n = 5, T = 5, N = 25

Effects:
                 var std.dev share
idiosyncratic 1.4380  1.1992 0.978
individual    0.0328  0.1811 0.022
theta: 0.05256

Residuals:
    Min.  1st Qu.   Median  3rd Qu.     Max.
-1.81924 -0.76288 -0.10512  0.28814  4.05076

Coefficients:
            Estimate Std. Error z-value Pr(>|z|)
(Intercept) -5.94050    3.49206 -1.7011 0.088916 .
UK           0.09607    0.19122  0.5024 0.615384
K_IND       12.54830    4.02239  3.1196 0.001811 **
K_AUD        2.74183    2.28931  1.1977 0.231046
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Total Sum of Squares:    49.825
Residual Sum of Squares: 33.939
R-Squared:      0.31884
Adj. R-Squared: 0.22154
Chisq: 9.82995 on 3 DF, p-value: 0.020068
>
```

2. Pengujian pemilihan model

- Chow Test (Pooled vs Fixed)

```
> chow_panel<-pFtest(fixed,pooled)
> chow_panel

        F test for individual effects

data:  model
F = 1.7139, df1 = 4, df2 = 17, p-value = 0.1933
alternative hypothesis: significant effects
```

Karena p-value>0,05 maka tolak H1 yang berarti Model Pooled lah yang terpilih

- Hausman Test(Random vs Fixed)

```
> hausman_panel<-phtest(fixed,random)
> hausman_panel

        Hausman Test

data:  model
chisq = 5.8357, df = 3, p-value = 0.1199
alternative hypothesis: one model is inconsistent
```

Karena p-value>0,05 maka tolak H1 yang berarti Model Random lah yang terpilih

- Breuschpagan Test(Pooled vs Random)

```
> bp_panel<-plmtest(pooled, type=c("bp"))
> bp_panel

        Lagrange Multiplier Test - (Breusch-Pagan)

data:  model
chisq = 0.78471, df = 1, p-value = 0.3757
alternative hypothesis: significant effects
```

Karena p-value>0,05 maka tolak H1 yang berarti Model Pooled lah yang terpilih.

Model pool terpilih 2 kali dari pengujian model diatas, maka akan dilakukan pengujian asumsi klasik terhadap model pool

3. Uji Asumsi Klasik

```
> check_collinearity(pooled)
# Check for Multicollinearity

Low Correlation

  Term  VIF   VIF 95% CI Increased SE Tolerance Tolerance 95% CI
    UK 4.07 [2.54, 7.11]         2.02      0.25     [0.14, 0.39]
 K_IND 1.48 [1.14, 2.61]         1.22      0.68     [0.38, 0.87]
 K_AUD 4.88 [2.98, 8.57]         2.21      0.21     [0.12, 0.34]
> residpooled<-pooled$residual
> shapiro.test(residpooled)

        Shapiro-Wilk normality test

data:  residpooled
W = 0.88379, p-value = 0.008283

> nortest::ad.test(residpooled)

        Anderson-Darling normality test

data:  residpooled
A = 0.74858, p-value = 0.04449

> check_autocorrelation(pooled)
Warning: Autocorrelated residuals detected (p = 0.014).> check_heteroscedasticity(pooled)
Warning: Heteroscedasticity (non-constant error variance) detected (p = 0.001).
>
```

Setelah diuji ternyata autokorelasi dan heteroskedasitasnya > 0,05. Yang berarti melanggar asums-asumsi tersebut

4. Transformasi Model

```
> #pcse
> ols <- lm(model, panel)
> pcse <- pcse(ols,groupN = panel$No, groupT = panel$Tahun)
> summary(pcse)

 Results:

               Estimate      PCSE    t value    Pr(>|t|)
(Intercept) -6.13465496 3.1354785 -1.9565291 0.063832138
UK           0.09468675 0.1304372  0.7259184 0.475902057
K_IND       12.93182311 4.5404761  2.8481205 0.009629681
K_AUD        2.80815269 1.8195566  1.5433170 0.137690060

 ------------------------------------------------

# Valid Obs = 25; # Missing Obs = 0; Degrees of Freedom = 21.
```

Dikarenakan model pooled melanggar asumsi heteroskedasitas dan autokorelasi secara simultan maka saya menggunakan model PCSE

5. Interpretasi

```
 Results:

               Estimate      PCSE    t value    Pr(>|t|)
(Intercept) -6.13465496 3.1354785 -1.9565291 0.063832138
UK           0.09468675 0.1304372  0.7259184 0.475902057
K_IND       12.93182311 4.5404761  2.8481205 0.009629681
K_AUD        2.80815269 1.8195566  1.5433170 0.137690060
```

Dari final model yang ditunjukkan diatas, dapat dilihat bahwa hanya K_IND lah yang mempengaruhi NP secara signifikan