homework

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2018년 8월 23일

```r
library(tidyr)
library(dplyr)
```

```
## Warning: package 'dplyr' was built under R version 3.5.1

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
library(OpenMx)
```

```
## Warning: package 'OpenMx' was built under R version 3.5.1

## OpenMx is not compiled to take advantage of computers with multiple cores.
```

```r
library(broom)
```

```
## Warning: package 'broom' was built under R version 3.5.1
```

```r
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 3.5.1
```

```r
data(twinData)
twinData <- as_tibble(twinData)
```

8번

compare weight this time. You should be able to recycle almost all code chunks.

이번에는 몸무게를 비교하십시오. 거의 모든 코드 덩어리를 재활용 할 수 있어야합니다

```r
condition = twinData %>%
  group_by(cohort,zygosity) %>%
  do(tidy( cor.test(~ ht1 + ht2, alternative = "greater" , data = . ))) %>%
  filter(estimate >= 0.5)

twinData$significantly_similar[twinData$cohort %in% condition$cohort &
                               twinData$zygosity %in% condition$zygosity] = '>=.5'
```
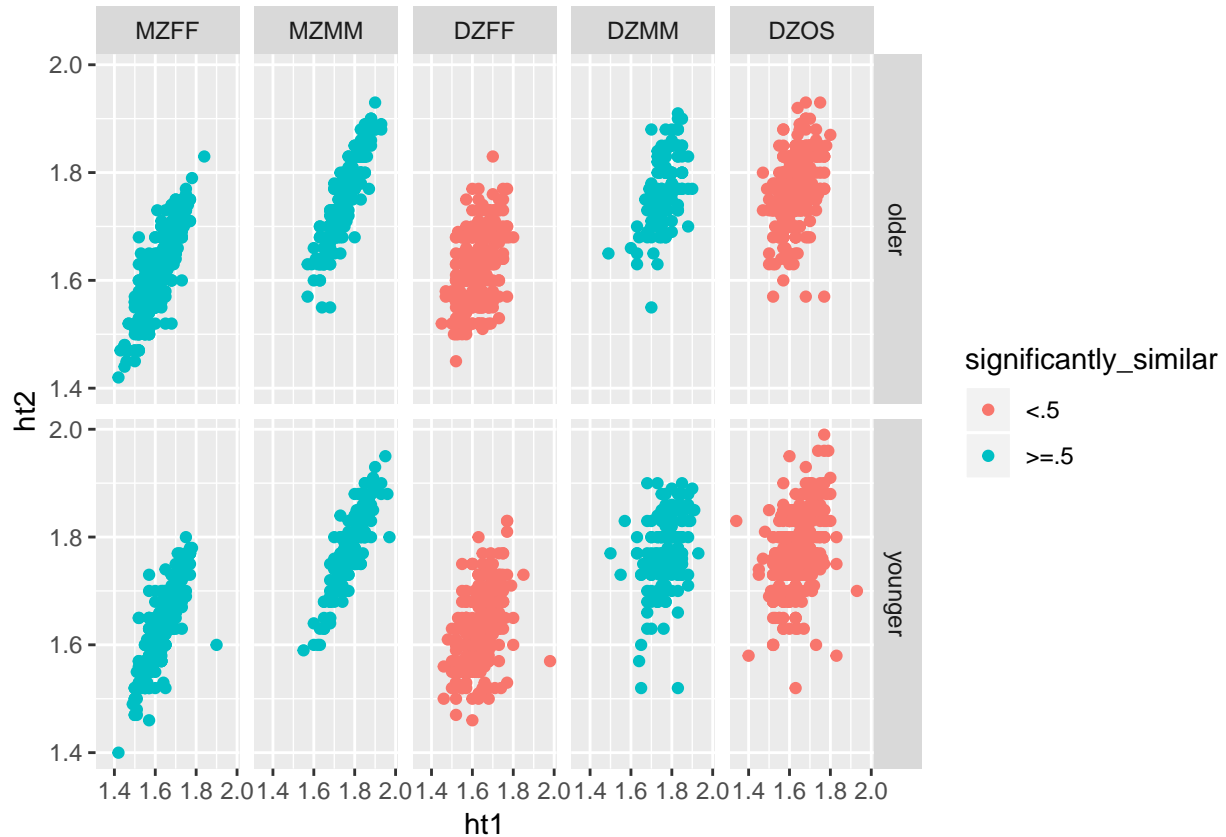
```
## Warning: Unknown or uninitialised column: 'significantly_similar'.
```

```r
twinData$significantly_similar[!(twinData$cohort %in% condition$cohort &
                               twinData$zygosity %in% condition$zygosity)] = '<.5'

twinData %>% na.omit() %>% ggplot(mapping = aes(ht1, ht2, color = significantly_similar)) +
```

```
  geom_point() +
  facet_grid(rows = vars(cohort), cols = vars(zygosity))
```


9번

8번과 동일하되 ht1, ht2 대신에 wt1, wt2로 해라.

```
condition2 = twinData %>%
  group_by(cohort,zygosity) %>%
  do(tidy( cor.test(~ wt1 + wt2, alternative = "greater" , data = . ))) %>%
  filter(estimate >= 0.5)


twinData$significantly_similar2[twinData$cohort %in% condition2$cohort &
                        twinData$zygosity %in% condition2$zygosity] = '>=.5'
```

Warning: Unknown or uninitialised column: 'significantly_similar2'.

```
twinData$significantly_similar2[!(twinData$cohort %in% condition2$cohort &
                        twinData$zygosity %in% condition2$zygosity)] = '<.5'


twinData %>% na.omit() %>% ggplot(mapping = aes(wt1, wt2, color = significantly_similar2)) +
  geom_point() +
  facet_grid(rows = vars(cohort), cols = vars(zygosity))
```