Exercises

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Part 1: Introduction to R and the R Synthax

Chapter 3: Data visualization

Load library ggplot2

```
library(ggplot2)
```

Load dataframe

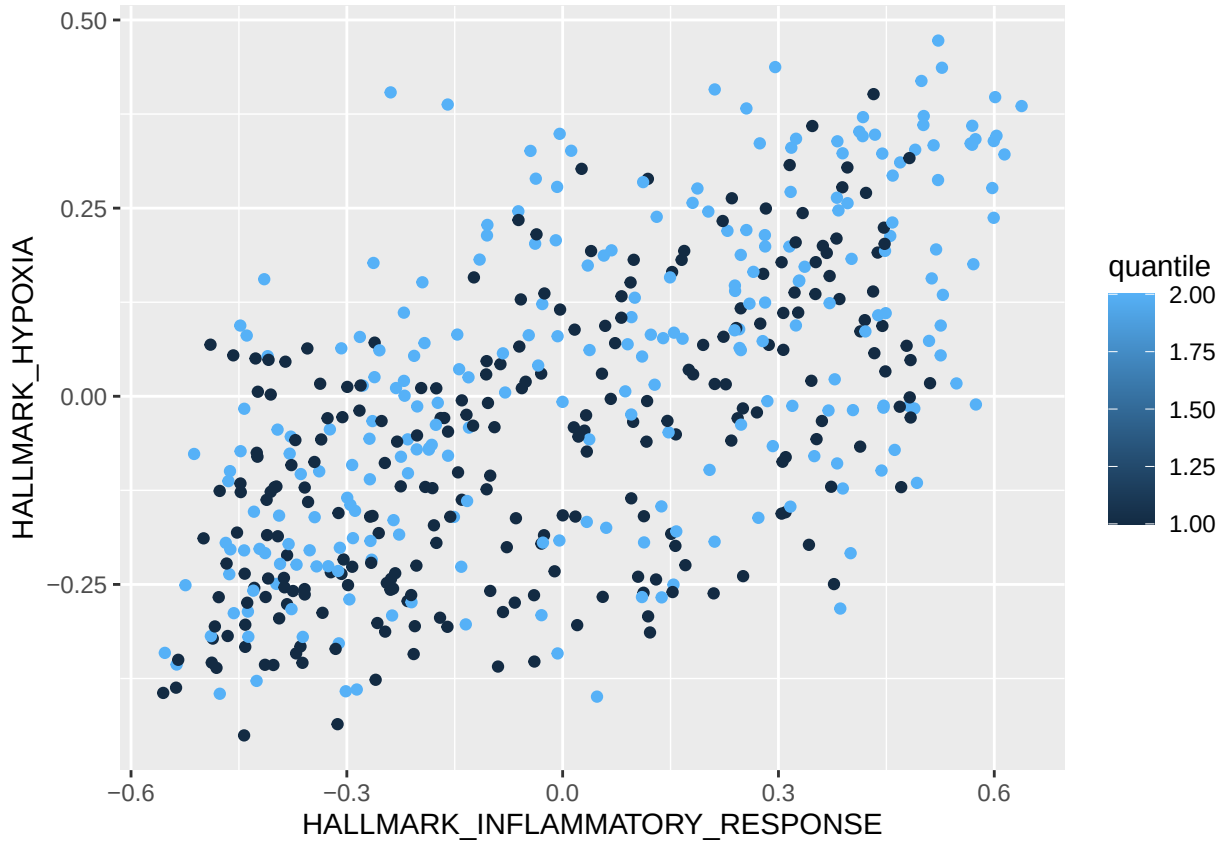
```
r2_gse62564_GSVA_Metadata <- readRDS("~/Desktop/r2_gse62564_GSVA_Metadata_exercise.rds")
```

Question 1

Use R plot functions to visualize the correlation between Hallmark Hypoxia and Hallmark Inflammatory Response

Solution: HALLMARK_INFLAMMATORY_RESPONSE vs. HALLMARK_HYPOXIA

```
qplot(HALLMARK_INFLAMMATORY_RESPONSE, HALLMARK_HYPOXIA,
      data = r2_gse62564_GSVA_Metadata,
      colour=quantile,
      ylab = "HALLMARK_HYPOXIA",
      xlab = "HALLMARK_INFLAMMATORY_RESPONSE")
```

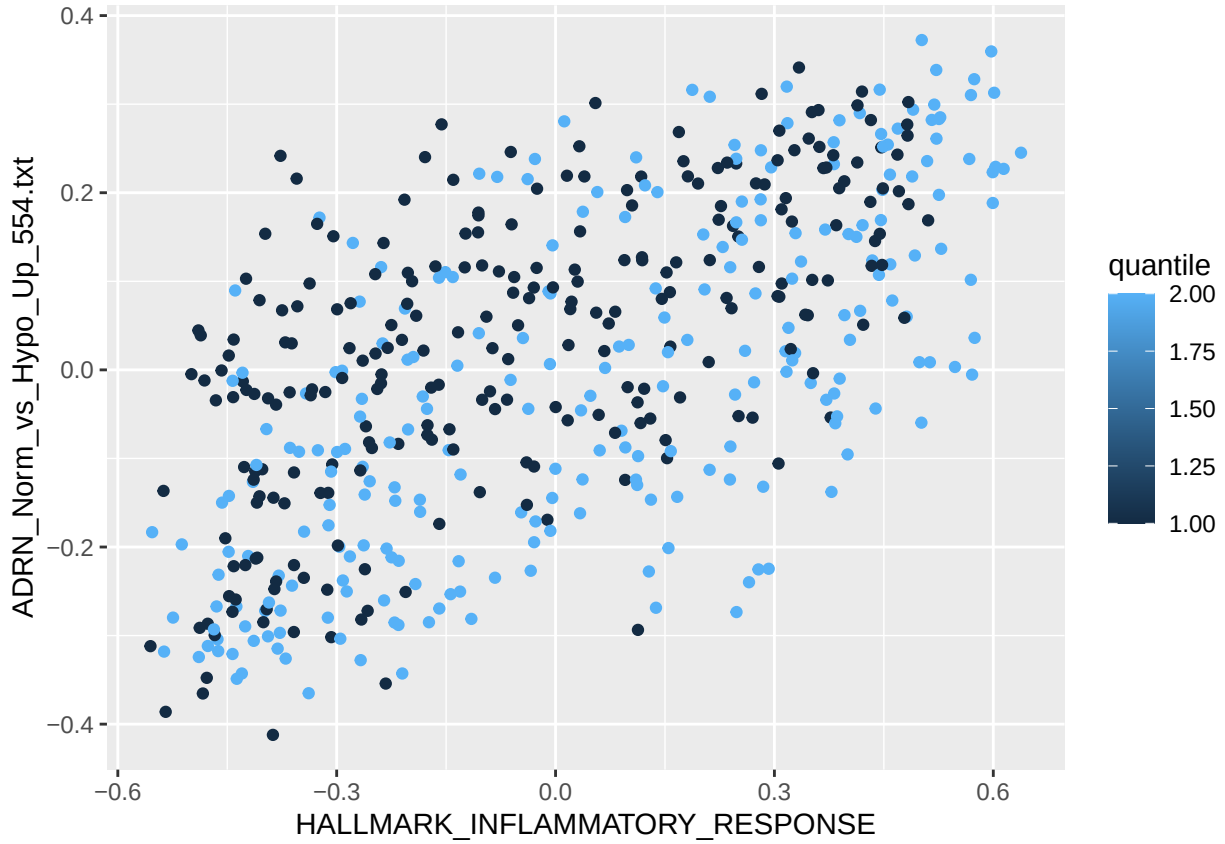


Question 1

Use R plot functions to visualize the correlation between Hallmark Hypoxia and Hallmark Inflammatory Response

Solution: HALLMARK_INFLAMMATORY_RESPONSE vs. ADRN_Norm_vs_Hypo_Up_554.txt

```
qplot(HALLMARK_INFLAMMATORY_RESPONSE, ADRN_Norm_vs_Hypo_Up_554.txt,
      data = r2_gse62564_GSVA_Metadata,
      colour=quantile,
      xlab = "HALLMARK_INFLAMMATORY_RESPONSE",
      ylab = "ADRN_Norm_vs_Hypo_Up_554.txt")
```



Question 1

Use R plot functions to visualize the correlation between Hallmark Hypoxia and Hallmark Inflammatory Response

Solution: HALLMARK_INFLAMMATORY_RESPONSE vs. ADRN_Norm_vs_Hypo_Down_635.txt

```
qplot(HALLMARK_INFLAMMATORY_RESPONSE, ADRN_Norm_vs_Hypo_Down_635.txt,
      data = r2_gse62564_GSVA_Metadata,
      colour=quantile,
      ylab = "ADRN_Norm_vs_Hypo_Down_635.txt",
      xlab = "HALLMARK_INFLAMMATORY_RESPONSE")
```