

main

July 13, 2021

1 Quality control comparison between LIBD and public RNA-seq data

- CMC
- GTEx brain regions

```
[1]: library(tidyverse)
library(synapser)
library(ggpubr)
```

```
Attaching packages: tidyverse
1.3.1
```

```
ggplot2 3.3.5    purrr  0.3.4
tibble  3.1.2    dplyr  1.0.7
tidyr   1.1.3    stringr 1.4.0
readr   1.4.0    forcats 0.5.1
```

Conflicts

```
tidyverse_conflicts()
dplyr::filter() masks stats::filter()
dplyr::lag()    masks stats::lag()
```

New synapser version detected:

You are using synapser version 0.9.77.

synapser version 0.10.101 is detected at <http://ran.synapse.org>.

To upgrade to the latest version of synapser, please run the following command:

```
install.packages("synapser", repos="http://ran.synapse.org")
```

TERMS OF USE NOTICE:

When using Synapse, remember that the terms and conditions of use require that you:

1) Attribute data contributors when discussing these data or results from these data.

- 2) Not discriminate, identify, or recontact individuals or groups represented by the data.
- 3) Use and contribute only data de-identified to HIPAA standards.
- 4) Redistribute data only under these same terms of use.

1.1 Load metrics

1.1.1 Load Lieber RNA-seq metrics

```
[2]: libd = data.table::fread("/ceph/projects/v4_phase3_paper/inputs/phenotypes/_m/merged_phenotypes.csv") %>%
  select(-starts_with("snp"), -c("antipsychotics", "lifetime_antipsych")) %>%
  rename("Percent_Aligned"="overallMapRate", "rRNA_Rate"="rRNA_rate",
  ↪ "Brain_Region"="Region",
  ↪ "SampleID"="RNum")
libd %>% head(2)
```

| | SampleID | Sex | Race | Dx | Age | mitoRate | rRNA_Rate | totalAssignedC |
|----------------------|----------|-------|-------|-------|-------|-----------|--------------|----------------|
| | <chr> | <chr> | <chr> | <chr> | <dbl> | <dbl> | <dbl> | <dbl> |
| A data.table: 2 × 14 | R11135 | Male | EA | CTL | 18.77 | 0.2572796 | 0.0001690954 | 0.5231321 |
| | R11137 | Male | EA | CTL | 41.44 | 0.3840272 | 0.0000884558 | 0.5933431 |

1.1.2 Load CMC RNA-seq metrics

```
[3]: # Process functions
downloadFile_version <- function(id , version){
  data.table::fread(synGet(id, version = version)$path, data.table = F)
}
synLogin()

# Download clinical metadata
CLINICAL_ID = 'syn3354385'
clinical = downloadFile_version(CLINICAL_ID, version = 4)

# Download RNASeq metadata
METADATA_QC_DLPFC_ID = 'syn18358379'
metadata = downloadFile_version(METADATA_QC_DLPFC_ID, version = 3)

# Join clinical and RNASeq metadata
md = right_join(clinical, metadata, by = c("Individual ID" = "Individual_ID"))
↪ %>%
  mutate(Dx = fct_recode(Dx, AFF_BP = "BP", AFF_BP = "AFF", Other =
  ↪ "undetermined",
  ↪ Control = "Control", SCZ = "SCZ"))

# Compute read pair metrics and add Institution-Dx variable
```

```
md <- md %>%
  select(c("SampleID", "Dx", "Reported Gender", "Sex", "Ethnicity", "pH",
    ↪ "Age of Death",
    "Study", "Brain_Region", "Brodmann_Area", "RIN", "rRNA_Rate",
    ↪ "Percent_Aligned"))
colnames(md) <- gsub(' ', '_', colnames(md))
print(dim(md))
md %>% head(2)
```

Welcome, kj.benjamin!

NULL

[1] 991 13

| | | | | | | |
|----------------------|---|-------------------|-------------|--------------------------|--------------|--------------------|
| A data.frame: 2 × 13 | | SampleID <chr> | Dx <fct> | Reported_Gender <chr> | Sex <chr> | Ethnicity <chr> |
| | 1 | MSSM_RNA_PFC_155 | Control | Female | XX | African-American |
| | 2 | MSSM_RNA_PFC_280 | Control | Female | XX | Caucasian |

1.1.3 Load GTEx metrics and

```
[4]: gtex = data.table::fread(paste0("https://storage.googleapis.com/
  ↪ gtex_analysis_v8/annotations/",
  ↪
  ↪ "GTEx_Analysis_v8_Annotations_SampleAttributesDS.txt")) %>%
  select(c("SAMPID", "SMRIN", "SMTS", "SMTSD", "SMMAPRT", "SMRRNART")) %>%
  filter(SMTS == "Brain") %>%
  rename("RIN"="SMRIN", "Percent_Aligned"="SMMAPRT", "rRNA_Rate"="SMRRNART",
  ↪ "Brain_Region"="SMTSD",
  ↪ "SampleID"="SAMPID")
gtex %>% head()
```

| | | | | | | |
|---------------------|--|-------------------------------|--------------|---------------|------------------------------|--------|
| A data.table: 6 × 6 | | SampleID <chr> | RIN <dbl> | SMTS <chr> | Brain_Region <chr> | P < |
| | | GTEx-1117F-0011-R10a-SM-AHZ7F | NA | Brain | Brain - Frontal Cortex (BA9) | N |
| | | GTEx-1117F-0011-R10b-SM-CYKQ8 | 7.2 | Brain | Brain - Frontal Cortex (BA9) | N |
| | | GTEx-1117F-3226-SM-5N9CT | 6.2 | Brain | Brain - Cortex | 0. |
| | | GTEx-111FC-0011-R10a-SM-AHZ7K | NA | Brain | Brain - Frontal Cortex (BA9) | N |
| | | GTEx-111FC-0011-R10a-SM-CYKQ9 | 8.5 | Brain | Brain - Frontal Cortex (BA9) | N |
| | | GTEx-111FC-3126-SM-5GZZ2 | 6.1 | Brain | Brain - Cortex | 0. |

1.2 Clean and organize data

```
[5]: gtex = gtex %>% mutate("Dataset"="GTEx", "Dx"="Control",
  ↪ "Brain_Region"=gsub("Brain - ", "",
  ↪
  ↪ str_replace(gtex$Brain_Region, "\\(.*", ""))) %>%
  select("SampleID", "Dx", "Brain_Region", "RIN", "rRNA_Rate",
  ↪ "Percent_Aligned", "Dataset")
```

```
gtex$Brain_Region = gsub(" $", "", str_replace(gtex$Brain_Region, "Frontal_␣
↪Cortex", "DLPFC"))
gtex %>% head(2)
```

| | SampleID <chr> | Dx <chr> | Brain_Region <chr> | RIN <dbl> | rRNA_Rate <dbl> | P <dbl> |
|---------------------|-------------------------------|-------------|-----------------------|--------------|--------------------|------------|
| A data.table: 2 × 7 | GTEX-1117F-0011-R10a-SM-AHZ7F | Control | DLPFC | NA | NA | N |
| | GTEX-1117F-0011-R10b-SM-CYKQ8 | Control | DLPFC | 7.2 | NA | N |

```
[6]: cmc = md %>% select("SampleID", "Dx", "Brain_Region", "RIN", "rRNA_Rate", ␣
↪ "Percent_Aligned") %>%
      mutate("Dataset"="CMC")
cmc %>% head(2)
```

| | SampleID <chr> | Dx <fct> | Brain_Region <chr> | RIN <dbl> | rRNA_Rate <dbl> | Percent_␣ <dbl> |
|---------------------|--------------------|-------------|-----------------------|--------------|--------------------|--------------------|
| A data.frame: 2 × 7 | 1 MSSM_RNA_PFC_155 | Control | DLPFC | 8.4 | 0.000250992 | 0.9798915 |
| | 2 MSSM_RNA_PFC_280 | Control | DLPFC | 8.4 | 0.000373524 | 0.9688145 |

```
[7]: libd = libd %>% select("SampleID", "Dx", "Brain_Region", "RIN", "rRNA_Rate", ␣
↪ "Percent_Aligned") %>%
      mutate("Dataset"="LIBD", "Dx"=gsub("CTL", "Control", libd$Dx),
            "Brain_Region"=gsub("HIPPO", "Hippocampus", libd$Brain_Region))
libd %>% head(2)
```

| | SampleID <chr> | Dx <chr> | Brain_Region <chr> | RIN <dbl> | rRNA_Rate <dbl> | Percent_Aligned <dbl> | Dataset <chr> |
|---------------------|-------------------|-------------|-----------------------|--------------|--------------------|--------------------------|------------------|
| A data.table: 2 × 7 | R11135 | Control | Hippocampus | 5.9 | 0.0001690954 | 0.8746 | LIBD |
| | R11137 | Control | Hippocampus | 9.2 | 0.0000884558 | 0.9149 | LIBD |

```
[8]: df = bind_rows(libd, gtex, cmc) #>% mutate_if(is.character, as.factor)
df %>% head(2)
```

| | SampleID <chr> | Dx <chr> | Brain_Region <chr> | RIN <dbl> | rRNA_Rate <dbl> | Percent_Aligned <dbl> | Dataset <chr> |
|---------------------|-------------------|-------------|-----------------------|--------------|--------------------|--------------------------|------------------|
| A data.table: 2 × 7 | R11135 | Control | Hippocampus | 5.9 | 0.0001690954 | 0.8746 | LIBD |
| | R11137 | Control | Hippocampus | 9.2 | 0.0000884558 | 0.9149 | LIBD |

```
[9]: df$Brain_Region %>% unique
```

1. 'Hippocampus' 2. 'DLPFC' 3. 'Caudate' 4. 'Cortex' 5. 'Cerebellum' 6. 'Cerebellar Hemisphere'
7. 'Nucleus accumbens' 8. 'Putamen' 9. 'Hypothalamus' 10. 'Spinal cord' 11. 'Anterior cingulate
cortex' 12. 'Substantia nigra' 13. 'Amygdala'

1.3 Descriptive analysis

1.3.1 Check if NA present

RIN

```
[10]: rin = df %>% group_by(Dataset, Brain_Region) %>% count(is.na(RIN)) %>%
      pivot_wider(names_from=`is.na(RIN)`, values_from="n") %>%
      mutate("TRUE"=replace_na(`TRUE`,0), `RIN (%na)`=`TRUE`/(`FALSE`+`TRUE`))
      rin %>% head(2)
```

A grouped_df: 2 × 5

| Dataset | Brain_Region | FALSE | TRUE | RIN (%na) |
|---------|--------------|-------|-------|-----------|
| <chr> | <chr> | <int> | <dbl> | <dbl> |
| CMC | DLPFC | 991 | 0 | 0 |
| GTEEx | Amygdala | 177 | 0 | 0 |

rRNA Rate

```
[11]: rrna = df %>% group_by(Dataset, Brain_Region) %>% count(is.na(rRNA_Rate)) %>%
      pivot_wider(names_from=`is.na(rRNA_Rate)`, values_from="n") %>%
      mutate("TRUE"=replace_na(`TRUE`,0), `rRNA Rate (%na)`=`TRUE`/
      ↪(`FALSE`+`TRUE`))
      rrna %>% head(2)
```

A grouped_df: 2 × 5

| Dataset | Brain_Region | FALSE | TRUE | rRNA Rate (%na) |
|---------|--------------|-------|-------|-----------------|
| <chr> | <chr> | <int> | <dbl> | <dbl> |
| CMC | DLPFC | 991 | 0 | 0.00000000 |
| GTEEx | Amygdala | 161 | 16 | 0.09039548 |

Percent Alignment

```
[12]: palign = df %>% group_by(Dataset, Brain_Region) %>% count(is.
      ↪na(Percent_Aligned)) %>%
      pivot_wider(names_from=`is.na(Percent_Aligned)`, values_from="n") %>%
      mutate("TRUE"=replace_na(`TRUE`,0), `Percent Aligned (%na)`=`TRUE`/
      ↪(`FALSE`+`TRUE`))
      palign %>% head(2)
```

A grouped_df: 2 × 5

| Dataset | Brain_Region | FALSE | TRUE | Percent Aligned (%na) |
|---------|--------------|-------|-------|-----------------------|
| <chr> | <chr> | <int> | <dbl> | <dbl> |
| CMC | DLPFC | 991 | 0 | 0.00000000 |
| GTEEx | Amygdala | 161 | 16 | 0.09039548 |

Combined summary

```
[13]: tbl = rin %>% select(-c(`FALSE`, `TRUE`)) %>%
      inner_join(select(rrna, -c(`FALSE`, `TRUE`)), by=c("Dataset",
      ↪"Brain_Region")) %>%
      inner_join(select(palign, -c(`FALSE`, `TRUE`)), by=c("Dataset",
      ↪"Brain_Region"))
      tbl %>% as.data.frame %>% data.table::fwrite("qc_metric_NAs_libd_gtex_cmc.csv")
      tbl
```

| | Dataset <chr> | Brain_Region <chr> | RIN (%na) <dbl> | rRNA Rate (%na) <dbl> | Percent Aligned <dbl> |
|----------------------|------------------|---------------------------|--------------------|--------------------------|--------------------------|
| A grouped_df: 17 × 5 | CMC | DLPFC | 0.000000000 | 0.00000000 | 0.00000000 |
| | GTEX | Amygdala | 0.000000000 | 0.09039548 | 0.09039548 |
| | GTEX | Anterior cingulate cortex | 0.000000000 | 0.06572770 | 0.06572770 |
| | GTEX | Caudate | 0.000000000 | 0.07560137 | 0.07560137 |
| | GTEX | Cerebellar Hemisphere | 0.000000000 | 0.06844106 | 0.06844106 |
| | GTEX | Cerebellum | 0.003355705 | 0.07718121 | 0.07718121 |
| | GTEX | Cortex | 0.000000000 | 0.13846154 | 0.13846154 |
| | GTEX | DLPFC | 0.287058824 | 0.48000000 | 0.48000000 |
| | GTEX | Hippocampus | 0.045267490 | 0.11934156 | 0.11934156 |
| | GTEX | Hypothalamus | 0.000000000 | 0.07203390 | 0.07203390 |
| | GTEX | Nucleus accumbens | 0.000000000 | 0.06859206 | 0.06859206 |
| | GTEX | Putamen | 0.000000000 | 0.05603448 | 0.05603448 |
| | GTEX | Spinal cord | 0.000000000 | 0.06043956 | 0.06043956 |
| | GTEX | Substantia nigra | 0.000000000 | 0.08536585 | 0.08536585 |
| | LIBD | Caudate | 0.000000000 | 0.00000000 | 0.00000000 |
| | LIBD | DLPFC | 0.000000000 | 0.00000000 | 0.00000000 |
| | LIBD | Hippocampus | 0.000000000 | 0.00000000 | 0.00000000 |

1.3.2 Summarize data

```
[14]: tbl = df %>% group_by(Dataset, Brain_Region) %>%
  summarise(RIN_mean=mean(RIN, na.rm=TRUE), RIN_sd=sd(RIN, na.rm=TRUE),
    rRNA_mean=mean(rRNA_Rate, na.rm=TRUE), rRNA_sd=sd(rRNA_Rate, na.
    ↪rm=TRUE),
    PercentAligned_mean=mean(Percent_Aligned, na.rm=TRUE),
    PercentAligned_sd=sd(Percent_Aligned, na.rm=TRUE))
tbl %>% as.data.frame %>% data.table::fwrite("qc_metric_summary_libd_gtex_cmc.
    ↪csv")
tbl
```

`summarise()` has grouped output by 'Dataset'. You can override using the `.groups` argument.

| | Dataset <chr> | Brain_Region <chr> | RIN_mean <dbl> | RIN_sd <dbl> | rRNA_mean <dbl> | rRNA_sd <dbl> |
|----------------------|------------------|---------------------------|-------------------|-----------------|--------------------|------------------|
| A grouped_df: 17 × 8 | CMC | DLPFC | 7.595863 | 0.9002318 | 2.825332e-04 | 1.016402e- |
| | GTEEx | Amygdala | 6.594915 | 0.6356163 | 8.679170e-02 | 3.724921e- |
| | GTEEx | Anterior cingulate cortex | 6.683568 | 0.7626681 | 7.020330e-02 | 3.407544e- |
| | GTEEx | Caudate | 7.390034 | 0.8786767 | 6.669918e-02 | 2.858002e- |
| | GTEEx | Cerebellar Hemisphere | 7.457034 | 1.0033617 | 2.524327e-02 | 2.178709e- |
| | GTEEx | Cerebellum | 6.851852 | 0.7893323 | 2.060865e-02 | 1.212267e- |
| | GTEEx | Cortex | 6.588308 | 0.6811292 | 4.852958e-02 | 2.031282e- |
| | GTEEx | DLPFC | 7.168647 | 0.8580205 | 5.299829e-02 | 2.901991e- |
| | GTEEx | Hippocampus | 6.765517 | 0.7559981 | 7.530126e-02 | 3.385451e- |
| | GTEEx | Hypothalamus | 6.855085 | 0.7763085 | 6.479683e-02 | 3.499553e- |
| | GTEEx | Nucleus accumbens | 7.140433 | 0.8426733 | 7.279581e-02 | 3.489604e- |
| | GTEEx | Putamen | 7.085776 | 0.9074560 | 7.632170e-02 | 2.873567e- |
| | GTEEx | Spinal cord | 7.063187 | 0.7335050 | 4.625480e-02 | 2.817331e- |
| | GTEEx | Substantia nigra | 6.578659 | 0.7163100 | 7.752818e-02 | 3.039102e- |
| | LIBD | Caudate | 7.834483 | 0.8673440 | 5.759414e-05 | 3.599073e- |
| | LIBD | DLPFC | 7.779691 | 0.9663740 | 5.022716e-05 | 3.060435e- |
| | LIBD | Hippocampus | 7.723490 | 1.1208014 | 2.929714e-05 | 2.628273e- |

1.4 Plot metrics

```
[15]: save_ggplots <- function(fn, p, w, h){
      for(ext in c('.pdf', '.png', '.svg')){
        ggsave(paste0(fn, ext), plot=p, width=w, height=h)
      }
    }

[16]: bxp = df %>% ggboxplot(x="Brain_Region", y="RIN", color="Dataset", add='jitter',
      panel.labs.font=list(face='bold', size = 14),
      palette="npg",
      outlier.shape=NA, ylab='RIN', add.params=list(alpha=0.5),
      legend="bottom", xlab="Brain Region") +
      font("xy.text", size=14) + font("xy.title", size=16, face="bold") +
      font("legend.title", size=18, face="bold") + font("legend.text", size=18) +
      rotate_x_text(45)
      save_ggplots("boxplot_brain_region_comparison_rin", bxp, 12, 8)
      bxp
```

Warning message:

"Removed 134 rows containing non-finite values (stat_boxplot)."

Warning message:

"Removed 134 rows containing missing values (geom_point)."

Warning message:

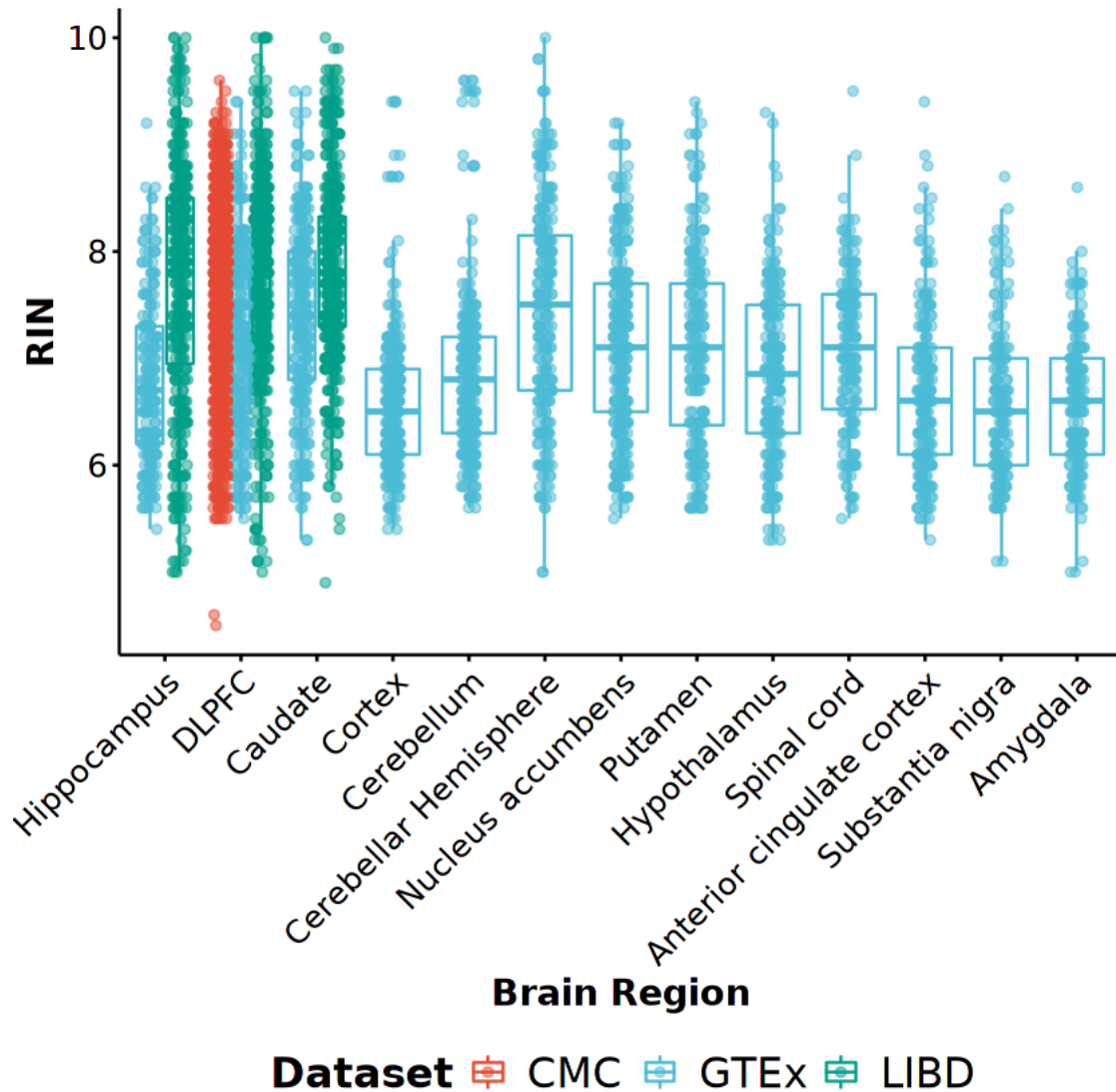
"Removed 134 rows containing non-finite values (stat_boxplot)."

Warning message:

"Removed 134 rows containing missing values (geom_point)."

Warning message:

"Removed 134 rows containing non-finite values (stat_boxplot)."
Warning message:
"Removed 134 rows containing missing values (geom_point)."
Warning message:
"Removed 134 rows containing non-finite values (stat_boxplot)."
Warning message:
"Removed 134 rows containing missing values (geom_point)."



```
[17]: bxp = df %>% ggboxplot(x="Brain_Region", y="rRNA_Rate", color="Dataset",
  ↪add='jitter',
  panel.labs.font=list(face='bold', size = 14),
  ↪palette="npg",
```



```

        outlier.shape=NA, ylab='rRNA Rate', add.
↪params=list(alpha=0.5),
        legend="bottom", xlab="Brain Region") +
    font("xy.text", size=14) + font("xy.title", size=16, face="bold") +
    font("legend.title", size=18, face="bold") + font("legend.text", size=18) +
    rotate_x_text(45)
save_ggplots("boxplot_brain_region_comparison_rRNA_rate", bxp, 12, 8)
bxp

```

Warning message:

"Removed 445 rows containing non-finite values (stat_boxplot)."

Warning message:

"Removed 445 rows containing missing values (geom_point)."

Warning message:

"Removed 445 rows containing non-finite values (stat_boxplot)."

Warning message:

"Removed 445 rows containing missing values (geom_point)."

Warning message:

"Removed 445 rows containing non-finite values (stat_boxplot)."

Warning message:

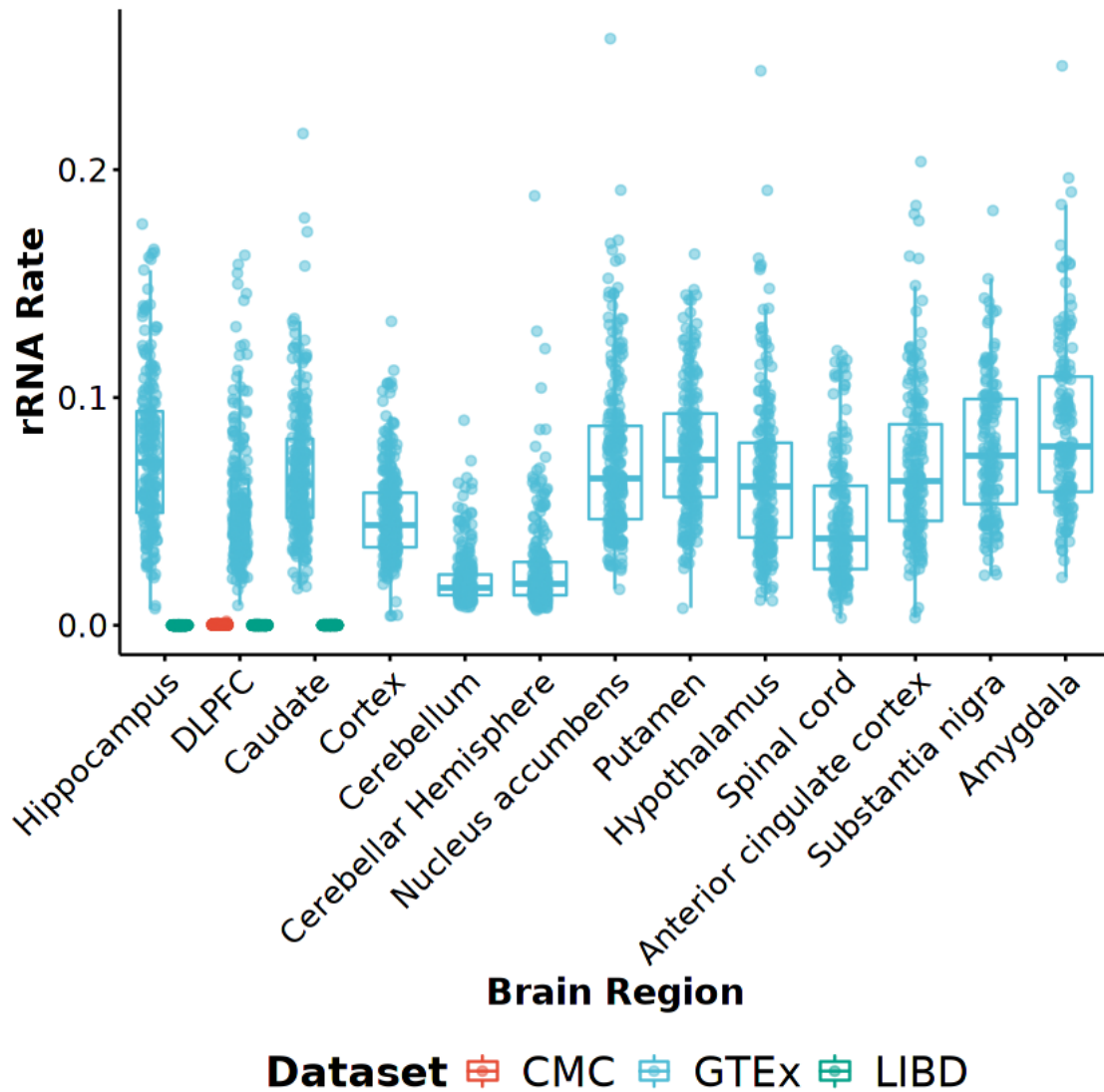
"Removed 445 rows containing missing values (geom_point)."

Warning message:

"Removed 445 rows containing non-finite values (stat_boxplot)."

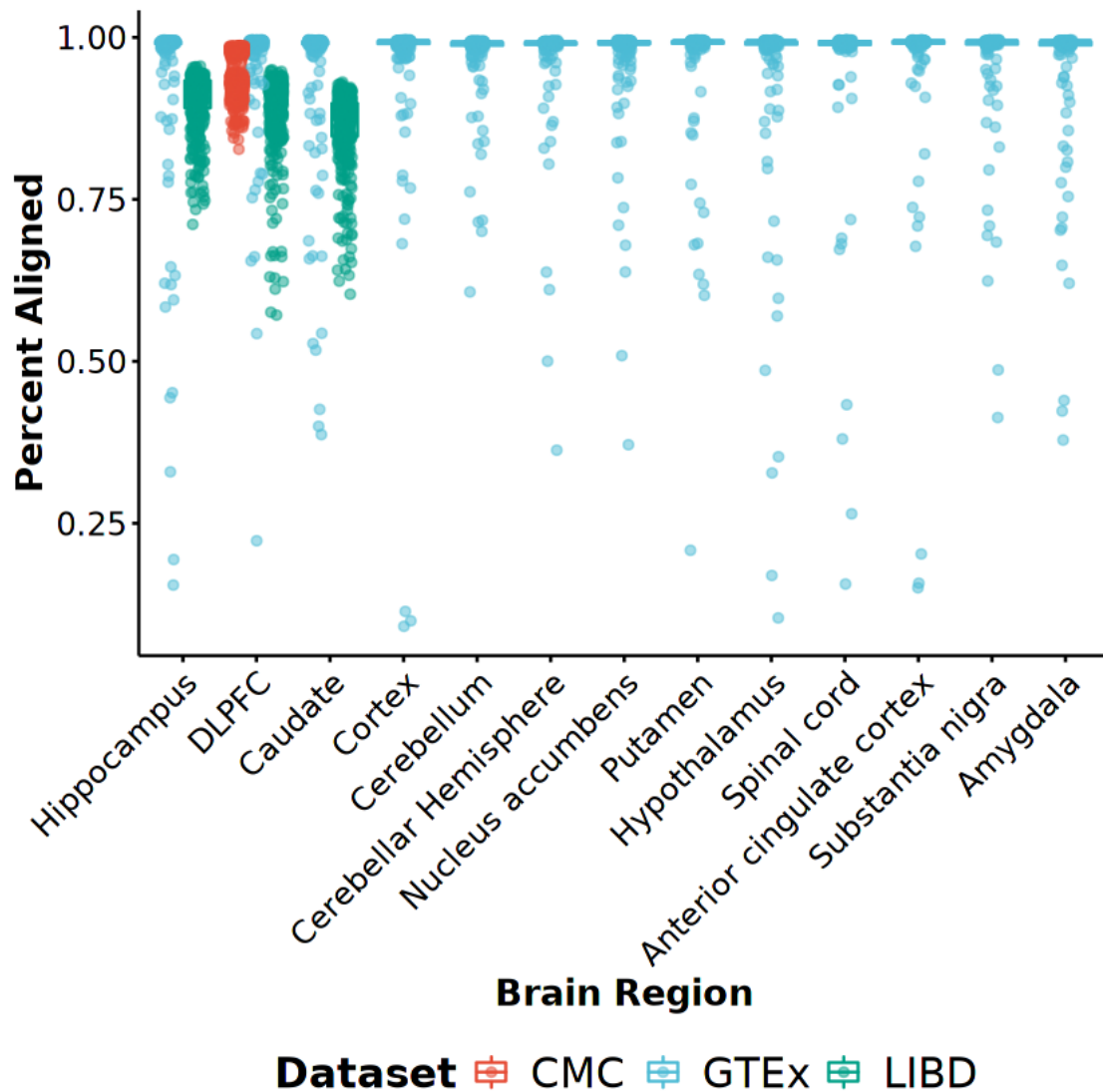
Warning message:

"Removed 445 rows containing missing values (geom_point)."



```
[18]: bxp = df %>% ggboxplot(x="Brain_Region", y="Percent_Aligned", color="Dataset",
  ↪add='jitter',
  panel.labs.font=list(face='bold', size = 14),
  ↪palette="npg",
  outlier.shape=NA, ylab='Percent Aligned', add.
  ↪params=list(alpha=0.5),
  legend="bottom", xlab="Brain Region") +
  font("xy.text", size=14) + font("xy.title", size=16, face="bold") +
  font("legend.title", size=18, face="bold") + font("legend.text", size=18) +
  rotate_x_text(45)
save_ggplots("boxplot_brain_region_comparison_Percent_Aligned", bxp, 12, 8)
bxp
```

Warning message:
 "Removed 445 rows containing non-finite values (stat_boxplot)."
 Warning message:
 "Removed 445 rows containing missing values (geom_point)."
 Warning message:
 "Removed 445 rows containing non-finite values (stat_boxplot)."
 Warning message:
 "Removed 445 rows containing missing values (geom_point)."
 Warning message:
 "Removed 445 rows containing non-finite values (stat_boxplot)."
 Warning message:
 "Removed 445 rows containing missing values (geom_point)."
 Warning message:
 "Removed 445 rows containing non-finite values (stat_boxplot)."
 Warning message:
 "Removed 445 rows containing missing values (geom_point)."



1.5 Session Info

```
[19]: Sys.time()
proc.time()
options(width = 120)
sessioninfo::session_info()
```

```
[1] "2021-07-13 16:31:02 EDT"
```

```
   user  system elapsed
19.208   1.168   17.527
```

Session info

setting value

version R version 4.0.3 (2020-10-10)

os Arch Linux

system x86_64, linux-gnu

ui X11

language (EN)

collate en_US.UTF-8

ctype en_US.UTF-8

tz America/New_York

date 2021-07-13

Packages

| package | * version | date | lib | source |
|------------|-----------|------------|-----|----------------|
| abind | 1.4-5 | 2016-07-21 | [1] | CRAN (R 4.0.2) |
| assertthat | 0.2.1 | 2019-03-21 | [1] | CRAN (R 4.0.2) |
| backports | 1.2.1 | 2020-12-09 | [1] | CRAN (R 4.0.2) |
| base64enc | 0.1-3 | 2015-07-28 | [1] | CRAN (R 4.0.2) |
| broom | 0.7.8 | 2021-06-24 | [1] | CRAN (R 4.0.3) |
| Cairo | 1.5-12.2 | 2020-07-07 | [1] | CRAN (R 4.0.2) |
| car | 3.0-11 | 2021-06-27 | [1] | CRAN (R 4.0.3) |
| carData | 3.0-4 | 2020-05-22 | [1] | CRAN (R 4.0.2) |
| cellranger | 1.1.0 | 2016-07-27 | [1] | CRAN (R 4.0.2) |
| cli | 3.0.0 | 2021-06-30 | [1] | CRAN (R 4.0.3) |
| codetools | 0.2-16 | 2018-12-24 | [2] | CRAN (R 4.0.3) |
| colorspace | 2.0-2 | 2021-06-24 | [1] | CRAN (R 4.0.3) |
| crayon | 1.4.1 | 2021-02-08 | [1] | CRAN (R 4.0.3) |
| curl | 4.3.2 | 2021-06-23 | [1] | CRAN (R 4.0.3) |
| data.table | 1.14.0 | 2021-02-21 | [1] | CRAN (R 4.0.3) |
| DBI | 1.1.1 | 2021-01-15 | [1] | CRAN (R 4.0.2) |
| dbplyr | 2.1.1 | 2021-04-06 | [1] | CRAN (R 4.0.3) |
| digest | 0.6.27 | 2020-10-24 | [1] | CRAN (R 4.0.2) |
| dplyr | * 1.0.7 | 2021-06-18 | [1] | CRAN (R 4.0.3) |
| ellipsis | 0.3.2 | 2021-04-29 | [1] | CRAN (R 4.0.3) |

| | | | | | |
|----------------|---------|------------|-----|-------|-----------|
| evaluate | 0.14 | 2019-05-28 | [1] | CRAN | (R 4.0.2) |
| fansi | 0.5.0 | 2021-05-25 | [1] | CRAN | (R 4.0.3) |
| farver | 2.1.0 | 2021-02-28 | [1] | CRAN | (R 4.0.3) |
| forcats | * 0.5.1 | 2021-01-27 | [1] | CRAN | (R 4.0.2) |
| foreign | 0.8-80 | 2020-05-24 | [2] | CRAN | (R 4.0.3) |
| fs | 1.5.0 | 2020-07-31 | [1] | CRAN | (R 4.0.2) |
| generics | 0.1.0 | 2020-10-31 | [1] | CRAN | (R 4.0.2) |
| ggplot2 | * 3.3.5 | 2021-06-25 | [1] | CRAN | (R 4.0.3) |
| ggpubr | * 0.4.0 | 2020-06-27 | [1] | CRAN | (R 4.0.2) |
| ggsci | 2.9 | 2018-05-14 | [1] | CRAN | (R 4.0.2) |
| ggsignif | 0.6.2 | 2021-06-14 | [1] | CRAN | (R 4.0.3) |
| glue | 1.4.2 | 2020-08-27 | [1] | CRAN | (R 4.0.2) |
| gtable | 0.3.0 | 2019-03-25 | [1] | CRAN | (R 4.0.2) |
| haven | 2.4.1 | 2021-04-23 | [1] | CRAN | (R 4.0.3) |
| hms | 1.1.0 | 2021-05-17 | [1] | CRAN | (R 4.0.3) |
| htmltools | 0.5.1.1 | 2021-01-22 | [1] | CRAN | (R 4.0.2) |
| httr | 1.4.2 | 2020-07-20 | [1] | CRAN | (R 4.0.2) |
| IRdisplay | 1.0 | 2021-01-20 | [1] | CRAN | (R 4.0.2) |
| IRkernel | 1.2 | 2021-05-11 | [1] | CRAN | (R 4.0.3) |
| jsonlite | 1.7.2 | 2020-12-09 | [1] | CRAN | (R 4.0.2) |
| labeling | 0.4.2 | 2020-10-20 | [1] | CRAN | (R 4.0.2) |
| lifecycle | 1.0.0 | 2021-02-15 | [1] | CRAN | (R 4.0.3) |
| lubridate | 1.7.10 | 2021-02-26 | [1] | CRAN | (R 4.0.3) |
| magrittr | 2.0.1 | 2020-11-17 | [1] | CRAN | (R 4.0.2) |
| modelr | 0.1.8 | 2020-05-19 | [1] | CRAN | (R 4.0.2) |
| munsell | 0.5.0 | 2018-06-12 | [1] | CRAN | (R 4.0.2) |
| openxlsx | 4.2.4 | 2021-06-16 | [1] | CRAN | (R 4.0.3) |
| pack | 0.1-1 | 2021-02-23 | [1] | local | |
| pbdbZMQ | 0.3-5 | 2021-02-10 | [1] | CRAN | (R 4.0.3) |
| pillar | 1.6.1 | 2021-05-16 | [1] | CRAN | (R 4.0.3) |
| pkgconfig | 2.0.3 | 2019-09-22 | [1] | CRAN | (R 4.0.2) |
| purrr | * 0.3.4 | 2020-04-17 | [1] | CRAN | (R 4.0.2) |
| PythonEmbedInR | 0.6.76 | 2021-02-23 | [1] | local | |
| R6 | 2.5.0 | 2020-10-28 | [1] | CRAN | (R 4.0.2) |
| Rcpp | 1.0.7 | 2021-07-07 | [1] | CRAN | (R 4.0.3) |
| readr | * 1.4.0 | 2020-10-05 | [1] | CRAN | (R 4.0.2) |
| readxl | 1.3.1 | 2019-03-13 | [1] | CRAN | (R 4.0.2) |
| repr | 1.1.3 | 2021-01-21 | [1] | CRAN | (R 4.0.2) |
| reprex | 2.0.0 | 2021-04-02 | [1] | CRAN | (R 4.0.3) |
| rio | 0.5.27 | 2021-06-21 | [1] | CRAN | (R 4.0.3) |
| rlang | 0.4.11 | 2021-04-30 | [1] | CRAN | (R 4.0.3) |
| rstatix | 0.7.0 | 2021-02-13 | [1] | CRAN | (R 4.0.3) |
| rstudioapi | 0.13 | 2020-11-12 | [1] | CRAN | (R 4.0.2) |
| rvest | 1.0.0 | 2021-03-09 | [1] | CRAN | (R 4.0.3) |
| scales | 1.1.1 | 2020-05-11 | [1] | CRAN | (R 4.0.2) |
| sessioninfo | 1.1.1 | 2018-11-05 | [1] | CRAN | (R 4.0.2) |
| stringi | 1.6.2 | 2021-05-17 | [1] | CRAN | (R 4.0.3) |
| stringr | * 1.4.0 | 2019-02-10 | [1] | CRAN | (R 4.0.2) |

| | | | | |
|-------------|----------|------------|-----|----------------|
| svglite | 2.0.0 | 2021-02-20 | [1] | CRAN (R 4.0.3) |
| synapser | * 0.9.77 | 2021-02-23 | [1] | local |
| systemfonts | 1.0.2 | 2021-05-11 | [1] | CRAN (R 4.0.3) |
| tibble | * 3.1.2 | 2021-05-16 | [1] | CRAN (R 4.0.3) |
| tidyr | * 1.1.3 | 2021-03-03 | [1] | CRAN (R 4.0.3) |
| tidyselect | 1.1.1 | 2021-04-30 | [1] | CRAN (R 4.0.3) |
| tidyverse | * 1.3.1 | 2021-04-15 | [1] | CRAN (R 4.0.3) |
| utf8 | 1.2.1 | 2021-03-12 | [1] | CRAN (R 4.0.3) |
| uuid | 0.1-4 | 2020-02-26 | [1] | CRAN (R 4.0.2) |
| vctrs | 0.3.8 | 2021-04-29 | [1] | CRAN (R 4.0.3) |
| withr | 2.4.2 | 2021-04-18 | [1] | CRAN (R 4.0.3) |
| xml2 | 1.3.2 | 2020-04-23 | [1] | CRAN (R 4.0.2) |
| zip | 2.2.0 | 2021-05-31 | [1] | CRAN (R 4.0.3) |

[1] /home/jbenja13/R/x86_64-pc-linux-gnu-library/4.0

[2] /usr/lib/R/library