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 \<chr>	Sex \<chr>	Race \<chr>	Dx \<chr>	Age \<dbl>	mitoRate \<dbl>	rRNA_Rate \<dbl>	totalAssignedG \<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)
```

A data.table: 2 × 7

SampleID	Dx	Brain_Region	RIN	rRNA_Rate	P
<chr>	<chr>	<chr>	<dbl>	<dbl>	<
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)
```

A data.frame: 2 × 7

	SampleID	Dx	Brain_Region	RIN	rRNA_Rate	Percent_A
	<chr>	<fct>	<chr>	<dbl>	<dbl>	<dbl>
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)
```

A data.table: 2 × 7

SampleID	Dx	Brain_Region	RIN	rRNA_Rate	Percent_Aligned	Dataset
<chr>	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<chr>
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)
```

A data.table: 2 × 7

SampleID	Dx	Brain_Region	RIN	rRNA_Rate	Percent_Aligned	Dataset
<chr>	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<chr>
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]: 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))
```

	Dataset	Brain_Region	FALSE	TRUE
	\<chr\>	\<chr\>	\<int\>	\<dbl\>
	CMC	DLPFC	991	0
	GTEx	Amygdala	177	0
	GTEx	Anterior cingulate cortex	213	0
	GTEx	Caudate	291	0
	GTEx	Cerebellar Hemisphere	263	0
	GTEx	Cerebellum	297	1
	GTEx	Cortex	325	0
A grouped_df: 17 × 4	GTEx	DLPFC	303	122
	GTEx	Hippocampus	232	11
	GTEx	Hypothalamus	236	0
	GTEx	Nucleus accumbens	277	0
	GTEx	Putamen	232	0
	GTEx	Spinal cord	182	0
	GTEx	Substantia nigra	164	0
	LIBD	Caudate	464	0
	LIBD	DLPFC	453	0
	LIBD	Hippocampus	447	0

rRNA Rate

```
[11]: 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))
```

	Dataset	Brain_Region	FALSE	TRUE
	\<chr\>	\<chr\>	\<int\>	\<dbl\>
	CMC	DLPFC	991	0
	GTEx	Amygdala	161	16
	GTEx	Anterior cingulate cortex	199	14
	GTEx	Caudate	269	22
	GTEx	Cerebellar Hemisphere	245	18
	GTEx	Cerebellum	275	23
	GTEx	Cortex	280	45
A grouped_df: 17 × 4	GTEx	DLPFC	221	204
	GTEx	Hippocampus	214	29
	GTEx	Hypothalamus	219	17
	GTEx	Nucleus accumbens	258	19
	GTEx	Putamen	219	13
	GTEx	Spinal cord	171	11
	GTEx	Substantia nigra	150	14
	LIBD	Caudate	464	0
	LIBD	DLPFC	453	0
	LIBD	Hippocampus	447	0

Percent Alignment

```
[12]: 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))
```

	Dataset <chr>	Brain_Region <chr>	FALSE <int>	TRUE <dbl>
	CMC	DLPFC	991	0
	GTEx	Amygdala	161	16
	GTEx	Anterior cingulate cortex	199	14
	GTEx	Caudate	269	22
	GTEx	Cerebellar Hemisphere	245	18
	GTEx	Cerebellum	275	23
	GTEx	Cortex	280	45
A grouped_df: 17 × 4	GTEx	DLPFC	221	204
	GTEx	Hippocampus	214	29
	GTEx	Hypothalamus	219	17
	GTEx	Nucleus accumbens	258	19
	GTEx	Putamen	219	13
	GTEx	Spinal cord	171	11
	GTEx	Substantia nigra	150	14
	LIBD	Caudate	464	0
	LIBD	DLPFC	453	0
	LIBD	Hippocampus	447	0

1.3.2 Summarize data

```
[13]: 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))
```

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

	Dataset	Brain_Region	RIN_mean	RIN_sd	rRNA_mean	rRNA_sd
	\<chr\>	\<chr\>	\<dbl\>	\<dbl\>	\<dbl\>	\<dbl\>
	CMC	DLPFC	7.595863	0.9002318	2.825332e-04	1.016402e-
	GTEx	Amygdala	6.594915	0.6356163	8.679170e-02	3.724921e-
	GTEx	Anterior cingulate cortex	6.683568	0.7626681	7.020330e-02	3.407544e-
	GTEx	Caudate	7.390034	0.8786767	6.669918e-02	2.858002e-
	GTEx	Cerebellar Hemisphere	7.457034	1.0033617	2.524327e-02	2.178709e-
	GTEx	Cerebellum	6.851852	0.7893323	2.060865e-02	1.212267e-
	GTEx	Cortex	6.588308	0.6811292	4.852958e-02	2.031282e-
A grouped_df: 17×8	GTEx	DLPFC	7.168647	0.8580205	5.299829e-02	2.901991e-
	GTEx	Hippocampus	6.765517	0.7559981	7.530126e-02	3.385451e-
	GTEx	Hypothalamus	6.855085	0.7763085	6.479683e-02	3.499553e-
	GTEx	Nucleus accumbens	7.140433	0.8426733	7.279581e-02	3.489604e-
	GTEx	Putamen	7.085776	0.9074560	7.632170e-02	2.873567e-
	GTEx	Spinal cord	7.063187	0.7335050	4.625480e-02	2.817331e-
	GTEx	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

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

```
[15]: 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
```
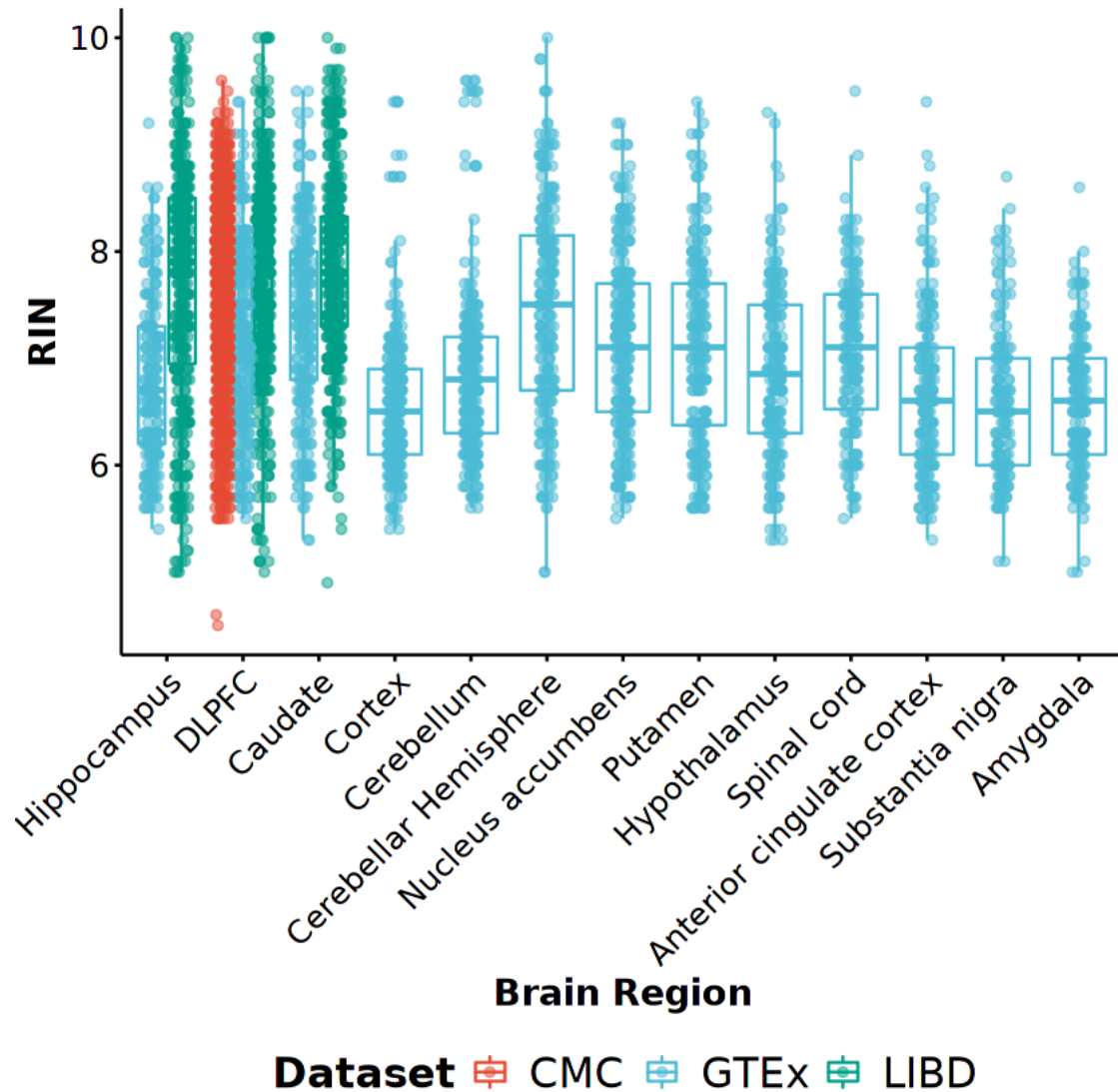
```
Warning message:
"Removed 134 rows containing non-finite values (stat_boxplot)."
Warning message:
"Removed 134 rows containing missing values (geom_point)."
Warning message:
"Removed 134 rows containing non-finite values (stat_boxplot)."
Warning message:
"Removed 134 rows containing missing values (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)."
```



```
[16]: 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)."
```
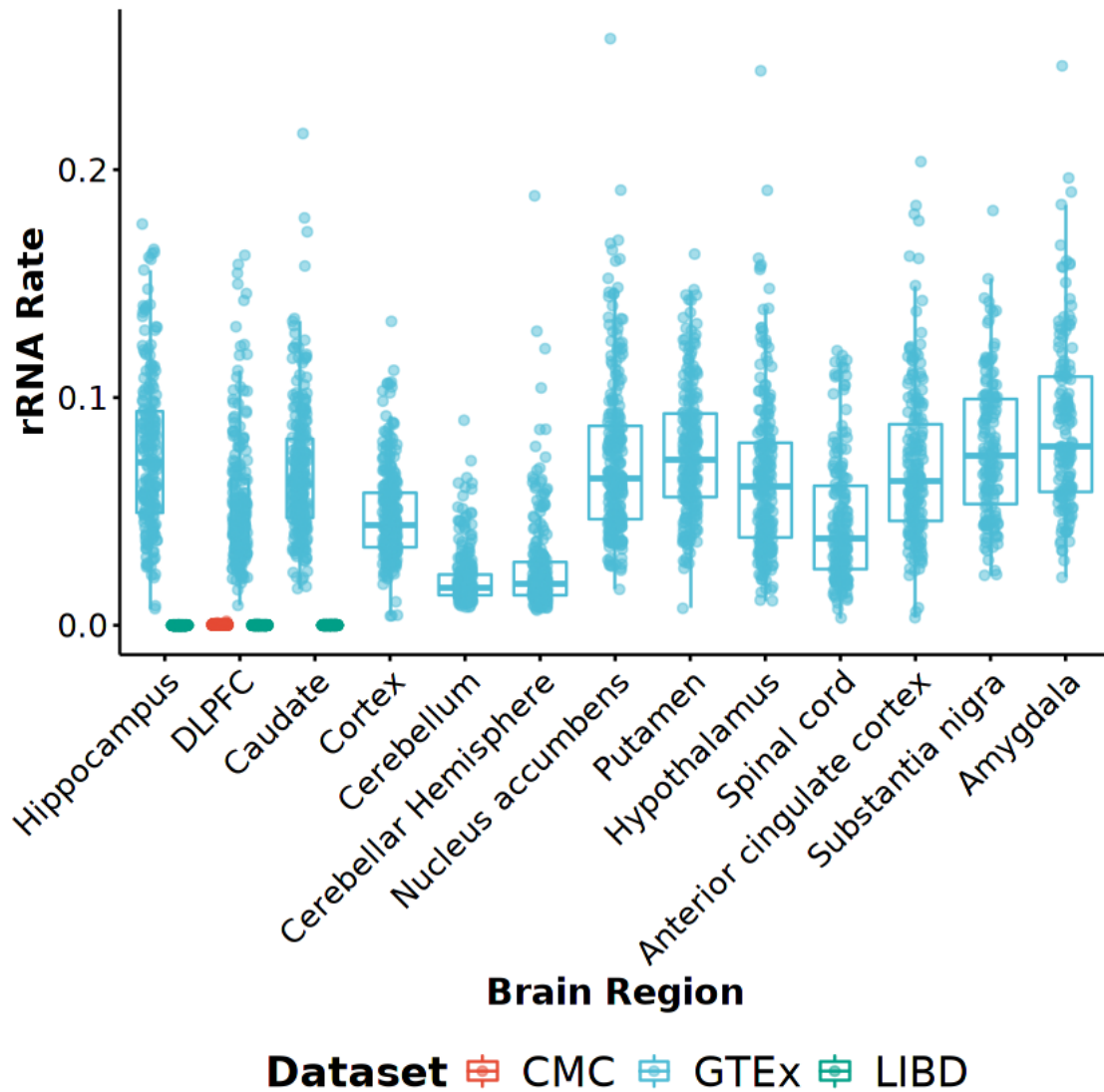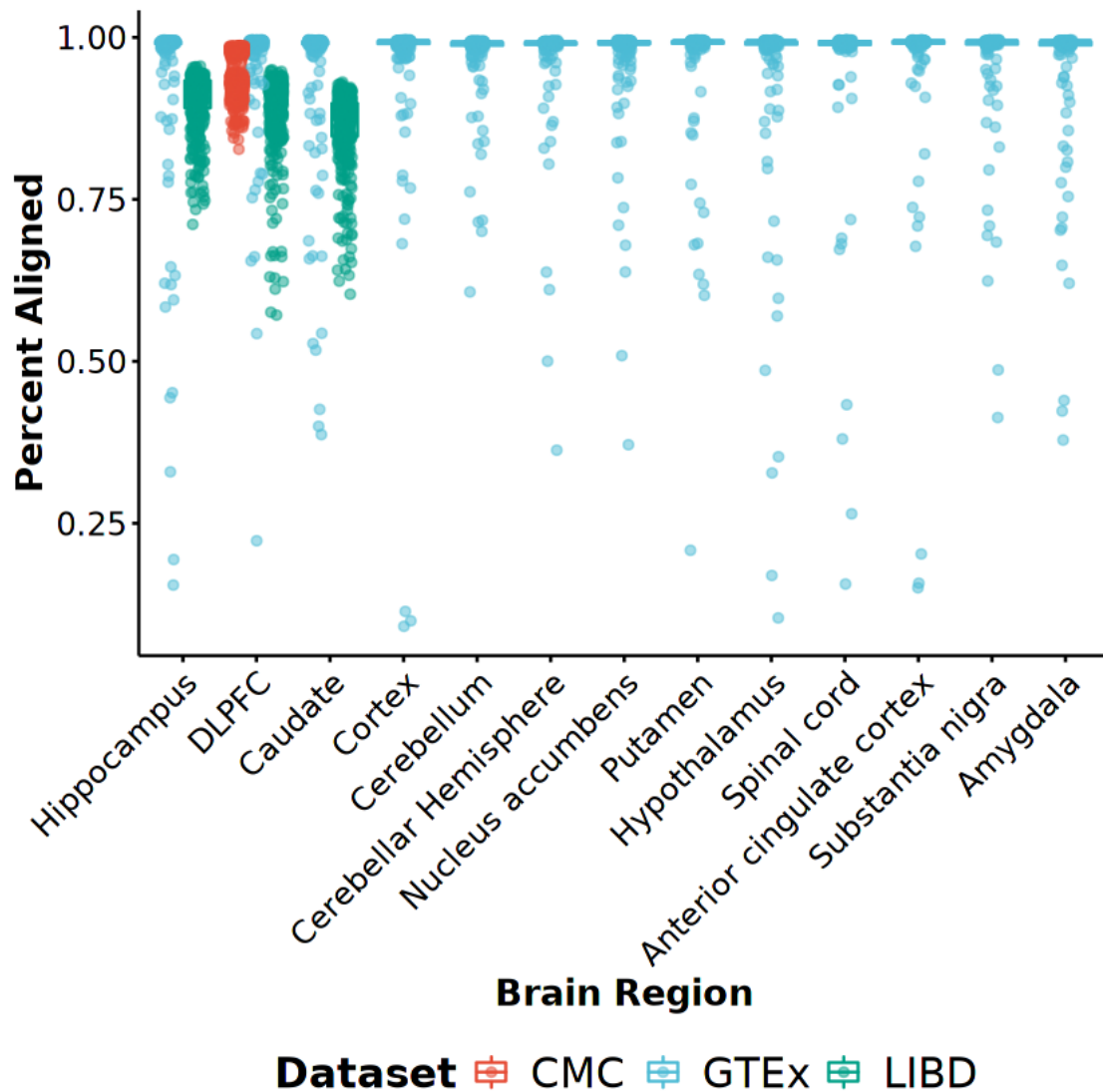
```
[17]: bxp = df %>% ggboxplot(x="Brain_Region", y="Percent_Aligned", color="Dataset",
      ↪add='jitter',
                             panel.labs.font=list(face='bold', size = 14),
      ↪palette="npg",
                             outlier.shape=NA, ylab='Percent Aligned', add.
      ↪params=list(alpha=0.5),
                             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

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

```
[1] "2021-07-13 15:45:22 EDT"

   user  system elapsed
 18.684   0.762  16.663

 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
pbdZMQ          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)
```

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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
```