DNEasy Analysis

UCLA STURM LAB

DATA AND DEPENDENCIES

```
# dependencies

library(ggplot2)
library(tibble)
library(ggpubr)

# data

cr8_names <- c("ur_native", "ur_decell", "bld_native", "bld_decell")

cr8 <- list(c(74.93, 75.50, 70.29, 67.94),
            c(5.506, 4.470, 4.429, 4.191),
            c(62.51, 64.29, 67.07, 65.78),
            c(2.774, 2.450, -0.8232, 2.413)
            )

cr9_names <- c("bld_native", "bld_dcdet", "ur_native", "ur_dcdet")

cr9 <- list(c(96.24, 114.5, 115.7, 119.7),
            c(0.06801, 5.518, 3.522, 0.5096),
            c(16.70, 18.83, 22.96, 25.47),
            c(34.64, 33.71, 30.87, 32.36)
            )

# ug/ul to ug/g

amounts_cr8 <- c(0.014, 0.0128, 0.0118, 0.0125)

cr8 <- as.data.frame(lapply(1:4, function(x){
  (cr8[[x]] / 1000) / amounts_cr8[x]
}))

names(cr8) <- cr8_names


amounts_cr9 <- c(0.012, 0.0106, 0.0105, 0.0116)

cr9 <- as.data.frame(lapply(1:4, function(x){
  (cr9[[x]] / 1000) / amounts_cr9[x]
}))
```

```r
names(cr9) <- cr9_names

cr8
```

```
##   ur_native ur_decell bld_native bld_decell
## 1  5.352143 0.4301563   5.297458   0.221920
## 2  5.392857 0.3492187   5.448305   0.196000
## 3  5.020714 0.3460156   5.683898  -0.065856
## 4  4.852857 0.3274219   5.574576   0.193040
```

```r
cr9
```

```
##   bld_native   bld_dcdet ur_native ur_dcdet
## 1   8.020000 0.006416038  1.590476 2.986207
## 2   9.541667 0.520566038  1.793333 2.906034
## 3   9.641667 0.332264151  2.186667 2.661207
## 4   9.975000 0.048075472  2.425714 2.789655
```

FUNCTION SETUP

```r
get_stats <- function(nat, decell) {
  list(
    nat = nat,
    decell = decell,
    p = t.test(nat, decell)$p.value,
    foldchange = decell/nat,
    percent_dec = (nat - decell) / nat * 100
  )
}
```

CR8 Pre-Pubertal

```r
#getting figures
cr8_stats <- list(
  ur = get_stats(cr8$ur_native, cr8$ur_decell),
  bld = get_stats(cr8$bld_native, cr8$bld_decell)
)

cr8_df <- rbind(data.frame(cr8_stats$ur[-3]), cr8_stats$bld[-3])
cr8_df <- cbind("Tissue" = c(rep("UR", nrow(cr8)), rep("BLD", nrow(cr8))),
                cr8_df)

# summary
knitr::kable(cr8_df, caption = "CR8 Pre-Pubertal Summary")
```

Table 1: CR8 Pre-Pubertal Summary

Tissue	nat	decell	foldchange	percent_dec
UR	5.352143	0.4301563	0.0803708	91.96292
UR	5.392857	0.3492187	0.0647558	93.52442
UR	5.020714	0.3460156	0.0689176	93.10824
UR	4.852857	0.3274219	0.0674699	93.25301
BLD	5.297458	0.2219200	0.0418918	95.81082
BLD	5.448305	0.1960000	0.0359745	96.40255
BLD	5.683898	-0.0658560	-0.0115864	101.15864
BLD	5.574576	0.1930400	0.0346286	96.53714

```
# p values
cr8_stats$ur$p
```

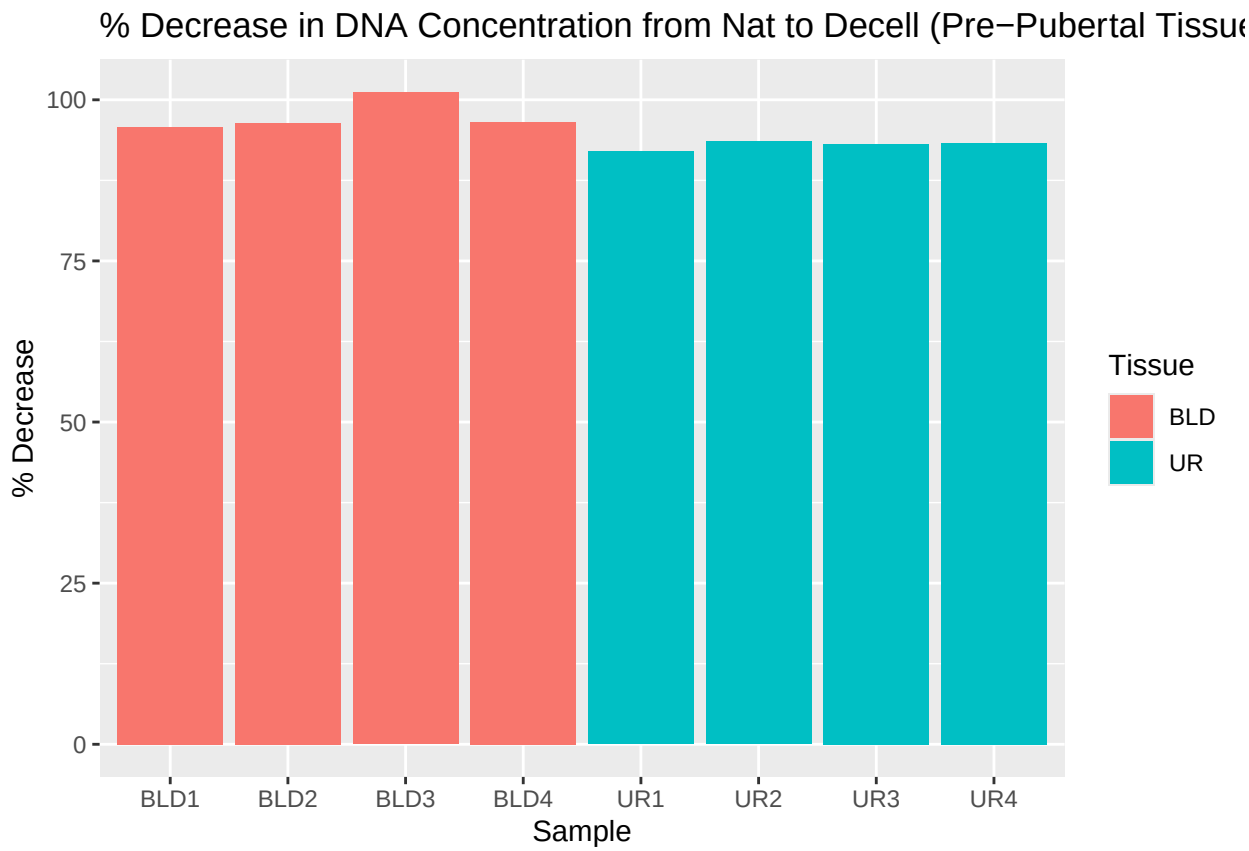
```
## [1] 2.863799e-05
```

```
cr8_stats$bld$p
```

```
## [1] 7.977792e-09
```

```
# barplot of percent dec
cr8_df <- cbind("Sample" = c(paste("UR", 1:nrow(cr8), sep = ""),
                             paste("BLD", 1:nrow(cr8), sep = "")),
                cr8_df)

ggplot(cr8_df, aes(x = Sample, y = percent_dec, fill = Tissue)) +
  geom_bar(stat = "identity") +
  labs(title = "% Decrease in DNA Concentration from Nat to Decell (Pre-Pubertal Tissues)", x = "Sample
```



CR9 Post-Pubertal

```
#getting figures
cr9_stats <- list(
  #ur = get_stats(cr9$ur_native, cr9$ur_dcdet),
  bld = get_stats(cr9$bld_native, cr9$bld_dcdet)
)

cr9_df <- data.frame(cr9_stats$bld[-3])
cr9_df <- cbind("Tissue" = rep("BLD", nrow(cr9)),
                cr9_df)

# summary
knitr::kable(cr9_df, caption = "CR9 Post-Pubertal Summary")
```

Table 2: CR9 Post-Pubertal Summary

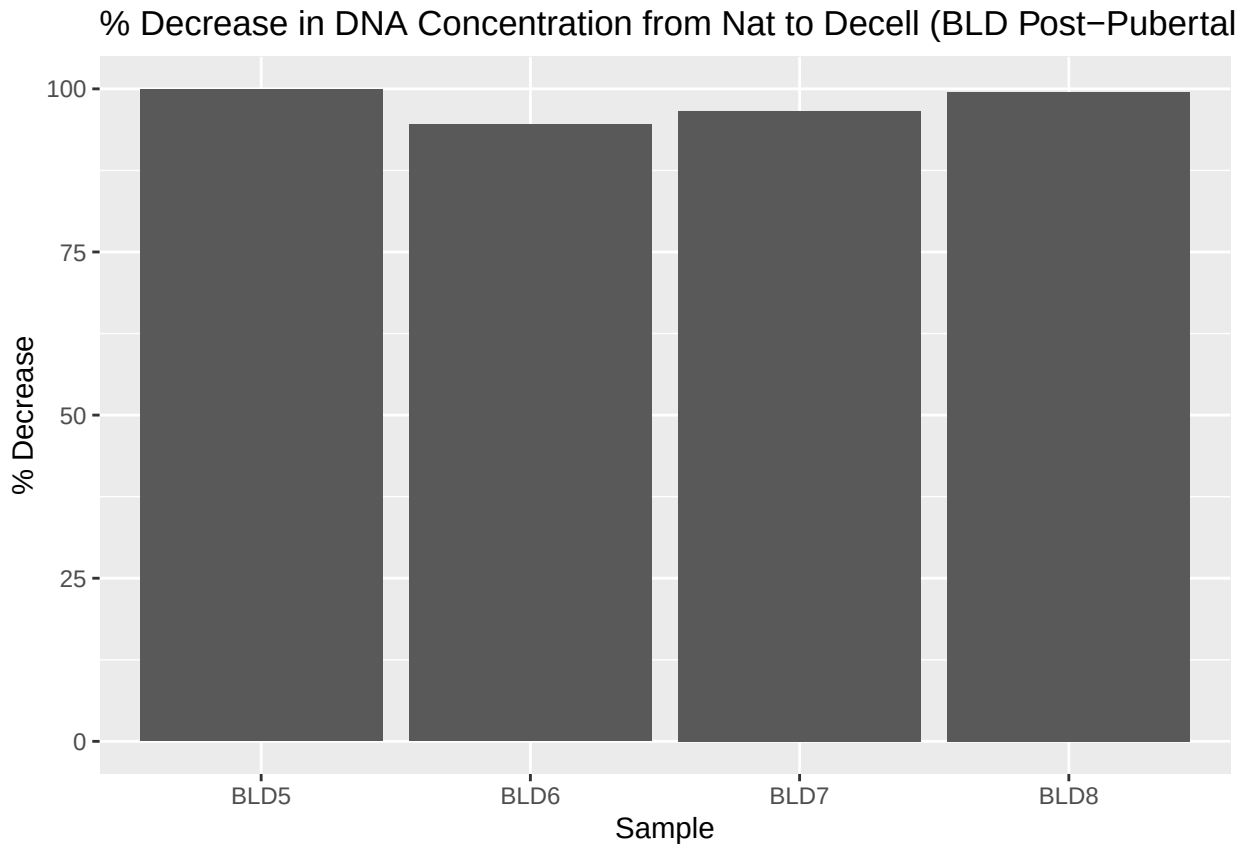
Tissue	nat	decell	foldchange	percent_dec
BLD	8.020000	0.0064160	0.0008000	99.92000
BLD	9.541667	0.5205660	0.0545571	94.54429
BLD	9.641667	0.3322642	0.0344613	96.55387
BLD	9.975000	0.0480755	0.0048196	99.51804

```r
# p values
cr9_stats$bld$p
```

```
## [1] 0.0001033993
```

```r
# barplot of percent dec
cr9_df <- cbind("Sample" = paste("BLD", (nrow(cr8)+1):(nrow(cr8)+nrow(cr9)), sep = ""),
                cr9_df)

ggplot(cr9_df, aes(x = Sample, y = percent_dec)) +
  geom_bar(stat = "identity") +
  labs(title = "% Decrease in DNA Concentration from Nat to Decell (BLD Post-Pubertal Tissues)", x = "Sa
```



CR8/CR9 PRE-PUBERTAL / POST-PUBERTAL COMPARATIVE ANALYSIS

```r
#setting up the df
comparison_df <- rbind(cr8_df, cr9_df)
comparison_df <- add_column(comparison_df,
           Dataset = c(rep("Pre-Pubertal", nrow(cr8_df)), rep("Post-Pubertal", nrow(cr9_df))),
           .before = "Tissue")
```

```r
comparison_df$Sample <- factor(comparison_df$Sample, levels = unique(comparison_df$Sample))

#barplot
ggplot(comparison_df, aes(x = Sample, y = percent_dec, fill = Tissue)) +
  geom_bar(stat = "identity") +
  geom_bracket(data = comparison_df, xmin = "UR1", xmax = "BLD4", y.position = 103, label =
                "Pre-Pubertal") +
  geom_bracket(data = comparison_df, xmin = "BLD5", xmax = "BLD8", y.position = 103,
               label = "Post-Pubertal") +
  labs(title = "% Decrease in DNA Concentration from Nat to Decell", x = "Sample", y = "% Decrease")
```