DESeq2Design

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```
library(DESeq2)
```

Upload the dds object and do your own design experiment

```
dds <- readRDS("Analysis/dds.rds")
```

Two types of design

1. with intercept where you can contrast individual

```
design(dds) <- ~  class
dds0 <- DESeq(dds)
resultsNames(dds0)
results(dds0, contrast = c("class", "CHLA01_211", "CHLA01_vo"))
```

Limit of this you can not compare one group vs another directly

2. For contrast between groups you need to remove intercept

```
design(dds) <- ~ 0 +  class
dds1 <- DESeq(dds)
resultsNames(dds1)
results(dds1, contrast = c("class", "CHLA01_211", "CHLA01_vo"))
```

It is same as:

```
results(dds1, contrast = list( "classCHLA01_211", "classCHLA01_vo"), listValues = c(1,-1))
```

listValues is optional in above case (1 vs 1)

You can list from available names in resultsNames(dds1)

One vs many

```
results(dds1, contrast = list( c("classCHLA01_211"),
                               c("classCHLA01_vo", "classD425_211")),
                               listValues = c(1,-1/2))
```

Many vs Many

```
res <- results(dds1, contrast = list( c("classCHLA01_211", "classD425_211", "classDAOY_211"),
                                c("classCHLA01_vo", "classD425_vo", "classDAOY_vo" )),
                                listValues = c(1/3, -1/3))
```