Xeva Tutorial

Arvind Mer

2017-01-13

Load Xeva

Load Xeva library and data.

```
library(Xeva)
data(lpdx)
head(modelInfo(lpdx))
```

```
##                                  model.id                      donor
## PHLC1106_P5.501.A1.1 PHLC1106_P5.501.A1.1 11101S-213RC-312S(F)-412S-
## PHLC1106_P5.504.A4.1 PHLC1106_P5.504.A4.1 11101S-213RC-312S(F)-412S-
## PHLC1106_P5.506.B1.1 PHLC1106_P5.506.B1.1 11101S-213RC-312S(F)-412S-
## PHLC1106_P5.507.B2.1 PHLC1106_P5.507.B2.1 11101S-213RC-312S(F)-412S-
## PHLC1106_P5.508.B3.1 PHLC1106_P5.508.B3.1 11101S-213RC-312S(F)-412S-
## PHLC1106_P5.511.C1.1 PHLC1106_P5.511.C1.1 11101S-213RC-312S(F)-412S-
##                           dob sex     PHLC biobase.id patient.id
## PHLC1106_P5.501.A1.1 Aug31.14   F PHLC1106   PHLC1106   PHLC1106
## PHLC1106_P5.504.A4.1 Aug31.14   F PHLC1106   PHLC1106   PHLC1106
## PHLC1106_P5.506.B1.1 Aug31.14   F PHLC1106   PHLC1106   PHLC1106
## PHLC1106_P5.507.B2.1 Aug31.14   F PHLC1106   PHLC1106   PHLC1106
## PHLC1106_P5.508.B3.1 Aug31.14   F PHLC1106   PHLC1106   PHLC1106
## PHLC1106_P5.511.C1.1 Sep14.14   F PHLC1106   PHLC1106   PHLC1106
```

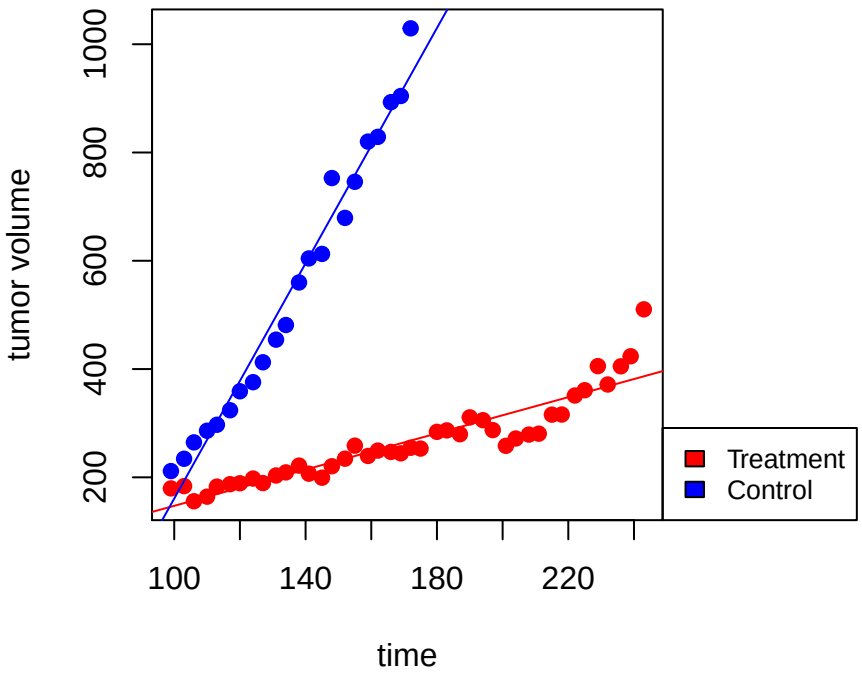
Models which belongs to same batch are in one list which is stored in expDesign slot. For example

```
print(batchNames(lpdx))
```

```
##   PHLC1106_P5    PHLC111_P7    PHLC119_P5    PHLC153_P6    PHLC181_P7
## "PHLC1106_P5"  "PHLC111_P7"  "PHLC119_P5"  "PHLC153_P6"  "PHLC181_P7"
##    PHLC189_P5    PHLC191_P5    PHLC191_P7    PHLC196_P5    PHLC215_P5
##  "PHLC189_P5"  "PHLC191_P5"  "PHLC191_P7"  "PHLC196_P5"  "PHLC215_P5"
##    PHLC229_P6    PHLC235_P4    PHLC655_P7     PHLC82_P5
##  "PHLC229_P6"  "PHLC235_P4"  "PHLC655_P7"   "PHLC82_P5"
```

To calculate angle between the treatment and control samples of this batch

```
batchNames <- batchNames(lpdx)
expDesign  <- expDesign(lpdx, batchNames[4])
ang <- calculateAngle(lpdx, expDesign, treatment.only = TRUE, plot=TRUE)
```




```
print(ang)
```

```
## $PHLC153_P6
## [1] 25.61293
```

Summarize Response of PDXs Get slop of each model and combine summarize all model slop which belongs to same patient by "mean"

```
lpdx_slop <- summarizeResponse(lpdx, response.measure = "slop",
                               group.by="patient.id", summary.stat = "mean")
```

Get angle between treatment and control model ids. For each batch it will give one angle value

```
lpdx_angle <- summarizeResponse(lpdx, response.measure = "angle")
```

Create mRECIST plot for PDXE Lung Cancer data

```
data(pdxe)
df <- getmRECIST(pdxe)
## add tumor.type information
dfMap <- mapModelSlotIds(object=pdxe, id=df$model.id, id.name="model.id",
                         map.to="tumor.type", unique = FALSE)
#dfx = merge(df, dfMap, by.x = "model.id", by.y = "model.id")
if(all(df$model.id==dfMap$model.id)) {df$tumor.type = dfMap$tumor.type}
lungDf = df[df$tumor.type=="NSCLC", ]
#pdf(file="DATA-raw/mRECIST_plot_NSCLC.pdf", width=12, height=10)
plotmRECIST(lungDf, groupBy = "biobase.id", control.name = "untreated")
```