

Xeva Tutorial

Arvind Mer

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Load Xeva library and KRAS/P53 PDX data

```
library(Xeva)
data(lpdx)
```

To see all the model.id

```
lpdx.mod = modelInfo(lpdx)
head(lpdx.mod$model.id)
```

```
## [1] "PHLC1106_P5.501.A1" "PHLC1106_P5.504.A4" "PHLC1106_P5.506.B1"
## [4] "PHLC1106_P5.507.B2" "PHLC1106_P5.508.B3" "PHLC1106_P5.511.C1"
```

To get the data for one model.id

```
modId = lpdx.mod$model.id[82]
df = getExperiment(lpdx, model.id = modId)
head(df)
```

```
##           model.id      drug.join.name time    volume width length
## 1 PHLC191_P5.503.A3 Vinorelbine+ Cisplatin    0  81.20558  5.18  5.82
## 2 PHLC191_P5.503.A3 Vinorelbine+ Cisplatin    8  93.24844  5.57  5.78
## 3 PHLC191_P5.503.A3 Vinorelbine+ Cisplatin   15  90.13298  5.16  6.51
## 4 PHLC191_P5.503.A3 Vinorelbine+ Cisplatin   19 213.92906  6.99  8.42
## 5 PHLC191_P5.503.A3 Vinorelbine+ Cisplatin   22 252.04349  7.43  8.78
## 6 PHLC191_P5.503.A3 Vinorelbine+ Cisplatin   26 375.84838  8.65  9.66
##   dose body.weight      date      comment volume.change
## 1  0.0      19.762 2014-09-25          <NA>      0.00000
## 2  0.0      20.424 2014-10-03    clip removed      14.83010
## 3  0.0      21.130 2014-10-10          <NA>      10.99359
## 4 75.4      21.103 2014-10-14 Start Treatment      163.44135
## 5 74.1      20.761 2014-10-17          <NA>      210.37708
## 6 72.1      20.178 2014-10-21          <NA>      362.83569
##   average.response
## 1      0.000000
## 2      7.415048
## 3      8.607894
## 4     47.316257
## 5     79.928421
## 6    127.079632
```

In the data.frame df you will see that for first 3 time points dose is 0, which indicate no treatment is given during this time. If you want the data only during the treatment periode specify treatment.only = TRUE

```
df = getExperiment(lpdx, modId, treatment.only = TRUE)
head(df)
```

```
##           model.id           drug.join.name time  volume width length dose
## 4 PHLC191_P5.503.A3 Vinorelbine+ Cisplatin   19 213.9291  6.99   8.42 75.4
## 5 PHLC191_P5.503.A3 Vinorelbine+ Cisplatin   22 252.0435  7.43   8.78 74.1
## 6 PHLC191_P5.503.A3 Vinorelbine+ Cisplatin   26 375.8484  8.65   9.66 72.1
## 7 PHLC191_P5.503.A3 Vinorelbine+ Cisplatin   29 526.0954  9.40  11.45 73.3
## 8 PHLC191_P5.503.A3 Vinorelbine+ Cisplatin   33 683.3432 10.43  12.08 73.3
## 9 PHLC191_P5.503.A3 Vinorelbine+ Cisplatin   36 807.8725 10.97  12.91 75.9
##   body.weight      date      comment volume.change average.response
## 4      21.103 2014-10-14 Start Treatment      163.4413           47.31626
## 5      20.761 2014-10-17              <NA>      210.3771           79.92842
## 6      20.178 2014-10-21              <NA>      362.8357          127.07963
## 7      20.528 2014-10-24              <NA>      547.8563          187.19059
## 8      20.534 2014-10-28              <NA>      741.4979          256.47900
## 9      21.257 2014-10-31              <NA>      894.8486          327.40896
```

Models which are replicates are stored together in expDesign slot. To get the data for all the replicates pass the 'batch.name' in the getExperiment function.

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

```
## [1] "PHLC1106_P5" "PHLC111_P7" "PHLC119_P5" "PHLC153_P6" "PHLC181_P7"
## [6] "PHLC189_P5" "PHLC191_P5" "PHLC191_P7" "PHLC196_P5" "PHLC215_P5"
## [11] "PHLC229_P6" "PHLC235_P4" "PHLC655_P7" "PHLC82_P5"
```

```
df = getExperiment(lpdx, batch.name = batchNames(lpdx)[1], treatment.only = TRUE)
head(df)
```

```
##           model.id           drug.join.name time  volume width length
## 8 PHLC1106_P5.502.A2 Vinorelbine+ Cisplatin   39 167.5273  6.46   7.72
## 9 PHLC1106_P5.502.A2 Vinorelbine+ Cisplatin   40 172.7149  6.48   7.91
## 10 PHLC1106_P5.502.A2 Vinorelbine+ Cisplatin   43 164.4621  6.38   7.77
## 11 PHLC1106_P5.502.A2 Vinorelbine+ Cisplatin   47 187.4881  6.76   7.89
## 12 PHLC1106_P5.502.A2 Vinorelbine+ Cisplatin   50 264.0641  7.64   8.70
## 13 PHLC1106_P5.502.A2 Vinorelbine+ Cisplatin   54 174.6014  6.66   7.57
##   dose body.weight      date      comment volume.change
## 8  79.2      22.182 2014-12-08 Start Treatment      126.5905
## 9  78.8      22.051 2014-12-09              <NA>      133.6070
## 10 78.6      21.995 2014-12-12              <NA>      122.4445
## 11 78.0      21.827 2014-12-16              <NA>      153.5886
## 12 80.2      22.467 2014-12-19              <NA>      257.1621
## 13 79.2      22.185 2014-12-23              <NA>      136.1586
##   average.response exp.type
## 8      47.16826 treatment
## 9      56.77256 treatment
## 10     63.33976 treatment
## 11     71.54420 treatment
## 12     87.01235 treatment
## 13     90.79283 treatment
```

Here the data.frame contains an extra column 'exp.type'. This indicates if this is treatment or control.

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

```
batchNames <- batchNames(lpdx)
expDesign <- expDesign(lpdx, batchNames[1])
ang <- calculateAngle(lpdx, expDesign, treatment.only = TRUE, plot=TRUE)
#print(ang)

for(I in batchNames)
{
  expDesign <- expDesign(lpdx, I)
  ang <- calculateAngle(lpdx, expDesign, treatment.only = TRUE, plot=TRUE)
  #print(ang)
}
```

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")
```

```
## Warning in .summarizePerBatchResponse(object, response.measure = "angle", : 'patient.id' mapped to m
## batch.name patient.id
## 1 PHLC191_P5 PHLC191
## 2 PHLC191_P7 PHLC191
```

Get mutation expression profile

```
ldxe_mut <- getMolecularProfiles(lpdx, data.type="mutation")
print(ldxe_mut)
```

```
## ExpressionSet (storageMode: lockedEnvironment)
## assayData: 16116 features, 12 samples
## element names: exprs
## protocolData: none
## phenoData
## sampleNames: PHLC1106 PHLC111 ... PHLC82 (12 total)
## varLabels: PHLC.ID X.ID
## varMetadata: labelDescription
## featureData
## featureNames: NOC2L ISG15 ... RNF128 (16116 total)
## fvarLabels: probe.Id
## fvarMetadata: labelDescription
## experimentData: use 'experimentData(object)'
## Annotation: MUT
```

The sample names in expression set are called biobase.id in model slot. Sample names from the expression set can be mapped to individual PDX model.ids as

```
# get sample names
library(Biobase)
```

```
## Loading required package: BiocGenerics
```

```
## Loading required package: parallel
```

```
##
```

```
## Attaching package: 'BiocGenerics'
```

```
## The following objects are masked from 'package:parallel':
```

```
##
```

```
##   clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,
##   clusterExport, clusterMap, parApply, parCapply, parLapply,
##   parLapplyLB, parRapply, parSapply, parSapplyLB
```

```
## The following object is masked from 'package:BBmisc':
```

```
##
```

```
##   normalize
```

```
## The following objects are masked from 'package:stats':
```

```
##
```

```
##   IQR, mad, xtabs
```

```
## The following objects are masked from 'package:base':
```

```
##
```

```
##   Filter, Find, Map, Position, Reduce, anyDuplicated, append,
##   as.data.frame, cbind, colnames, do.call, duplicated, eval,
##   evalq, get, grep, grepl, intersect, is.unsorted, lapply,
##   lengths, mapply, match, mget, order, paste, pmax, pmax.int,
##   pmin, pmin.int, rank, rbind, rownames, sapply, setdiff, sort,
##   table, tapply, union, unique, unsplit, which, which.max,
##   which.min
```

```
## Welcome to Bioconductor
```

```
##
```

```
##   Vignettes contain introductory material; view with
```

```
##   'browseVignettes()'. To cite Bioconductor, see
```

```
##   'citation("Biobase)"', and for packages 'citation("pkgname)"'.
```

```
sn <- Biobase::sampleNames(ldxe_mut)
```

```
smap <- mapModelSlotIds(lpdx, id=sn, id.name = "biobase.id", map.to = "model.id")
```

```
head(smap)
```

```
##               biobase.id          model.id
## PHLC1106_P5.501.A1  PHLC1106 PHLC1106_P5.501.A1
## PHLC1106_P5.504.A4  PHLC1106 PHLC1106_P5.504.A4
## PHLC1106_P5.506.B1  PHLC1106 PHLC1106_P5.506.B1
## PHLC1106_P5.507.B2  PHLC1106 PHLC1106_P5.507.B2
## PHLC1106_P5.508.B3  PHLC1106 PHLC1106_P5.508.B3
## PHLC1106_P5.511.C1  PHLC1106 PHLC1106_P5.511.C1
```

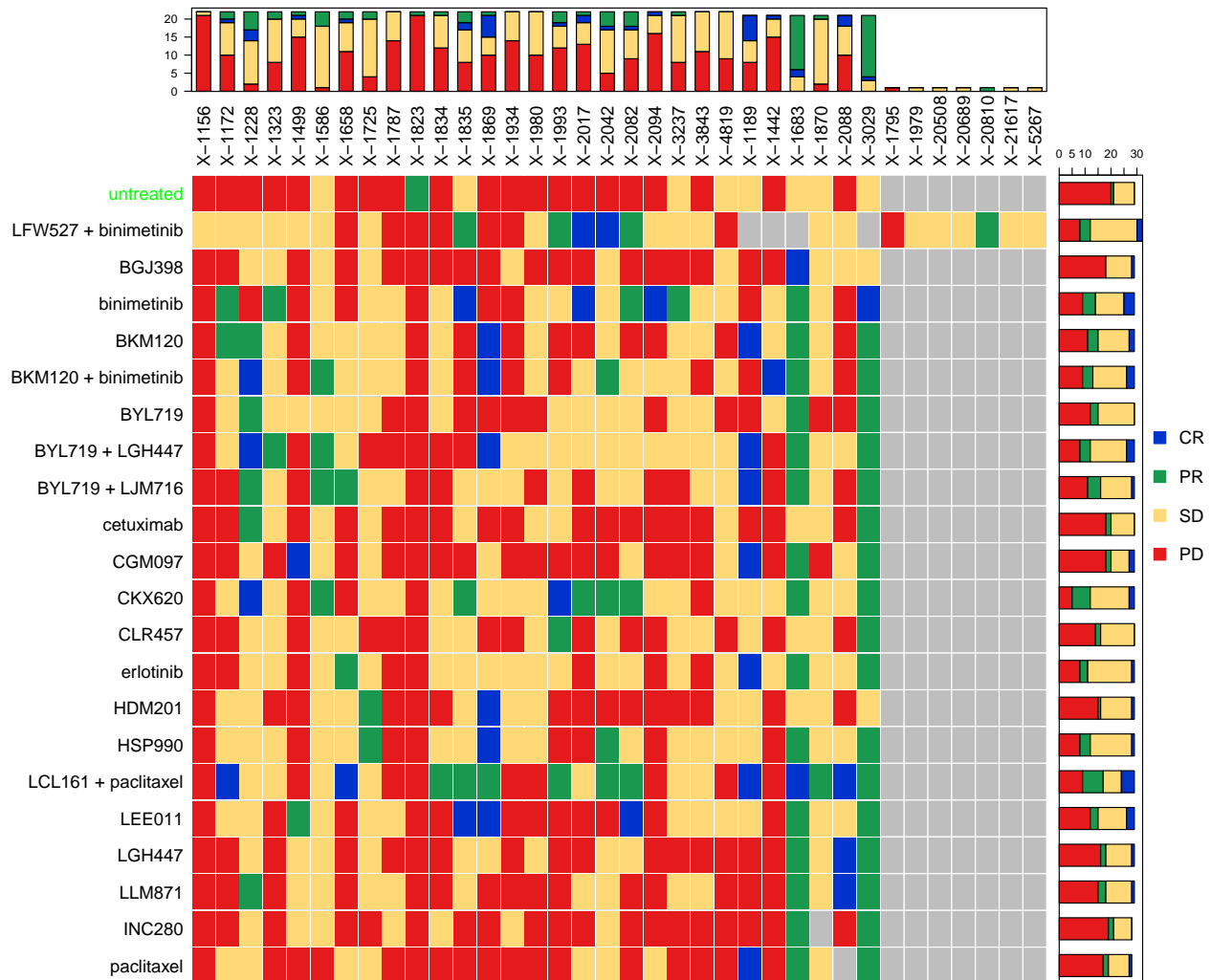
What should we do here

```
df = getExperiment(lidx, "PHLC119_P5.506.B1")  
#print(df[df$time>85 & df$time<109, c("time", "width", "length", "volume", "comment", "dose")])
```

Create mRECIST plot for PDXE Lung Cancer data

```
data(pdx)
#select lung cancer PDXE data
pdx.lung <- summarizeResponse(pdx, response.measure = "mRECIST_recomputed",
                              group.by="patient.id", tumor.type="NSCLC")

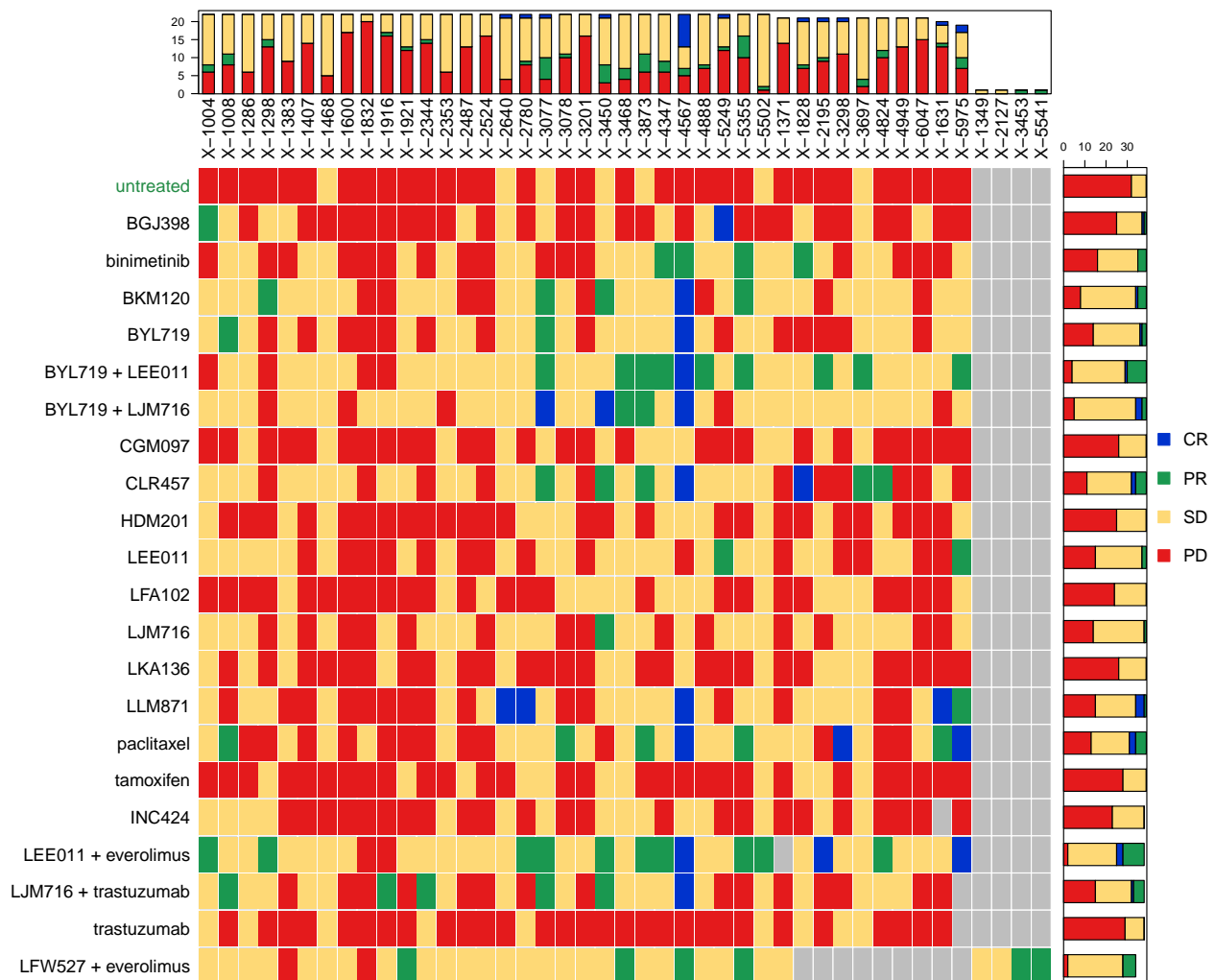
## plot matrix
plotmRECIST(pdx.lung, control.name = "untreated")
```



Create mRECIST plot for PDXE Breast Cancer data

```
data(pdx)
#select lung cancer PDXE data
pdx.brca <- summarizeResponse(pdx, response.measure = "mRECIST",
                              group.by="patient.id", tumor.type="BRCA")

## plot matrix
plotmRECIST(pdx.brca, control.name = "untreated", control.col = "#238b45")
```



Creat mR vs slop bar-plot

```
data(pdx)

lung_pdx_slope <- summarizeResponse(pdx, response.measure = "slop", group.by="patient.id",
                                   summary.stat = "mean", tumor.type = "NSCLC")

lung_pdx_mR <- summarizeResponse(pdx, response.measure = "mRECIST_recomputed",
                                 group.by="patient.id", tumor.type="NSCLC")

slope=c(); mR=c()
for(dn in rownames(lung_pdx_slope))
{
  for(pi in colnames(lung_pdx_slope))
  {
    v = c(lung_pdx_slope[dn,pi], lung_pdx_mR[dn,pi])
    if(!is.na(v[1]) & !is.na(v[2]))
    { slope = c(slope,v[1]); mR=c(mR,v[2]) }
  }
}
```

```
df = data.frame(mR= mR, slope= as.numeric(slope), stringsAsFactors = FALSE)
df$mR= factor(df$mR, c("CR", "PR", "SD", "PD"))

colPalette = c("#377eb8", "#4daf4a", "#fec44f", "#e41a1c")
boxplot(slope~mR, data=df, col=colPalette, main="mRECIST vs slope",
        xlab="mRECIST", ylab="slope")
```

