

Xeva Tutorial

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Load Xeva

Load Xeva library and data

```
library(Xeva)
data(pdx)
```

Access experiment slot

Get all model.id for which drug “paclitaxel” was used and tumor.type is “BRCA”

```
modelIds = getModelIds(pdx, drug="paclitaxel", drug.match.exact=TRUE, tumor.type="BRCA")
print(modelIds)
```

```
## [1] "X.1004.pael" "X.1008.pael" "X.1286.pael" "X.1298.pael" "X.1371.pael"
## [6] "X.1383.pael" "X.1407.pael" "X.1468.pael" "X.1600.pael" "X.1631.pael"
## [11] "X.1828.pael" "X.1832.pael" "X.1916.pael" "X.1921.pael" "X.2195.pael"
## [16] "X.2344.pael" "X.2353.pael" "X.2487.pael" "X.2524.pael" "X.2640.pael"
## [21] "X.2780.pael" "X.3077.pael" "X.3078.pael" "X.3201.pael" "X.3298.pael"
## [26] "X.3450.pael" "X.3468.pael" "X.3697.pael" "X.3873.pael" "X.4347.pael"
## [31] "X.4567.pael" "X.4824.pael" "X.4888.pael" "X.4949.pael" "X.5249.pael"
## [36] "X.5355.pael" "X.5502.pael" "X.5975.pael" "X.6047.pael"
```

To get the data for a model id

```
df = getExperiment(pdx, model.id="X.1655.LE11.biib")
head(df)
```

```
##           model.id      drug.join.name time volume body.weight
## 1 X.1655.LE11.biib LEE011 + binimetinib    0 200.93      24.1
## 2 X.1655.LE11.biib LEE011 + binimetinib    3 203.64      24.8
## 3 X.1655.LE11.biib LEE011 + binimetinib    7 220.28      24.5
## 4 X.1655.LE11.biib LEE011 + binimetinib   10 212.34      25.6
## 5 X.1655.LE11.biib LEE011 + binimetinib   14 207.00      25.3
## 6 X.1655.LE11.biib LEE011 + binimetinib   20 158.37      25.5
## volume.change average.response body.weight.change drug.names.drug.1
## 1      0.000000      0.0000000      0.000000      LEE011
## 2      1.348728      0.6743642      2.904564      LEE011
## 3      9.630219      3.6596493      1.659751      LEE011
## 4      5.678595      4.1643856      6.224066      LEE011
## 5      3.020953      3.9356990      4.979253      LEE011
## 6     -21.181506     -0.2505018      5.809129      LEE011
## drug.names.drug.2      experiment.id
## 1      binimetinib X.1655.LE11.biib.LEE011 + binimetinib
```

```
## 2      binimetinib X.1655.LE11.biib.LEE011 + binimetinib
## 3      binimetinib X.1655.LE11.biib.LEE011 + binimetinib
## 4      binimetinib X.1655.LE11.biib.LEE011 + binimetinib
## 5      binimetinib X.1655.LE11.biib.LEE011 + binimetinib
## 6      binimetinib X.1655.LE11.biib.LEE011 + binimetinib
## best.response.time best.response.value best.response.index
## 1              65    -47.5140596227542              17
## 2              65    -47.5140596227542              17
## 3              65    -47.5140596227542              17
## 4              65    -47.5140596227542              17
## 5              65    -47.5140596227542              17
## 6              65    -47.5140596227542              17
## best.average.response.time best.average.response.value
## 1              84      -18.9353715748087
## 2              84      -18.9353715748087
## 3              84      -18.9353715748087
## 4              84      -18.9353715748087
## 5              84      -18.9353715748087
## 6              84      -18.9353715748087
## best.average.response.index mRECIST
## 1              19      SD
## 2              19      SD
## 3              19      SD
## 4              19      SD
## 5              19      SD
## 6              19      SD
```

To get all mode

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When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
summary(cars)
```

```
##      speed      dist
## Min.   : 4.0    Min.   :  2.00
## 1st Qu.:12.0    1st Qu.: 26.00
## Median :15.0    Median : 36.00
## Mean   :15.4    Mean   : 42.98
## 3rd Qu.:19.0    3rd Qu.: 56.00
## Max.   :25.0    Max.   :120.00
```

Including Plots

You can also embed plots, for example:



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.