

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)
df = getExperiment(pdx, experiment.id="X.1004.pael.paclitaxel")
head(df)
```

```
##      model.id drug.join.name time volume body.weight volume.change
## 1 X.1004.pael  paclitaxel    0  209.1      29.4      0.000000
## 2 X.1004.pael  paclitaxel    3  192.6      29.6     -7.890961
## 3 X.1004.pael  paclitaxel    6  134.5      29.5    -35.676710
## 4 X.1004.pael  paclitaxel   13  153.8      29.3   -26.446676
## 5 X.1004.pael  paclitaxel   17  189.0      28.8   -9.612626
## 6 X.1004.pael  paclitaxel   20  201.4      29.4   -3.682449
##      average.response body.weight.change drug.names.drug.1
## 1      0.000000      0.000000      paclitaxel
## 2     -3.945481      0.6802721      paclitaxel
## 3    -14.522557      0.3401361      paclitaxel
## 4    -17.503587     -0.3401361      paclitaxel
## 5    -15.925395     -2.0408163      paclitaxel
## 6    -13.884904      0.000000      paclitaxel
##      experiment.id best.response.time best.response.value
## 1 X.1004.pael.paclitaxel      13 -26.4466762314682
## 2 X.1004.pael.paclitaxel      13 -26.4466762314682
## 3 X.1004.pael.paclitaxel      13 -26.4466762314682
## 4 X.1004.pael.paclitaxel      13 -26.4466762314682
## 5 X.1004.pael.paclitaxel      13 -26.4466762314682
## 6 X.1004.pael.paclitaxel      13 -26.4466762314682
##      best.response.index best.average.response.time
## 1              4      13
## 2              4      13
## 3              4      13
## 4              4      13
## 5              4      13
## 6              4      13
##      best.average.response.value best.average.response.index mRECIST
```

```
## 1      -17.5035868005739      4      SD
## 2      -17.5035868005739      4      SD
## 3      -17.5035868005739      4      SD
## 4      -17.5035868005739      4      SD
## 5      -17.5035868005739      4      SD
## 6      -17.5035868005739      4      SD
```

To get the data for a model id

```
df = getExperiment(pdxe, experiment.id="X.1004.pael.paclitaxel")
head(df)
```

```
##      model.id drug.join.name time volume body.weight volume.change
## 1 X.1004.pael   paclitaxel    0  209.1      29.4      0.000000
## 2 X.1004.pael   paclitaxel    3  192.6      29.6     -7.890961
## 3 X.1004.pael   paclitaxel    6  134.5      29.5    -35.676710
## 4 X.1004.pael   paclitaxel   13  153.8      29.3    -26.446676
## 5 X.1004.pael   paclitaxel   17  189.0      28.8     -9.612626
## 6 X.1004.pael   paclitaxel   20  201.4      29.4     -3.682449
##      average.response body.weight.change drug.names.drug.1
## 1      0.000000      0.000000      paclitaxel
## 2     -3.945481      0.6802721      paclitaxel
## 3    -14.522557      0.3401361      paclitaxel
## 4    -17.503587     -0.3401361      paclitaxel
## 5    -15.925395     -2.0408163      paclitaxel
## 6    -13.884904      0.000000      paclitaxel
##      experiment.id best.response.time best.response.value
## 1 X.1004.pael.paclitaxel      13    -26.4466762314682
## 2 X.1004.pael.paclitaxel      13    -26.4466762314682
## 3 X.1004.pael.paclitaxel      13    -26.4466762314682
## 4 X.1004.pael.paclitaxel      13    -26.4466762314682
## 5 X.1004.pael.paclitaxel      13    -26.4466762314682
## 6 X.1004.pael.paclitaxel      13    -26.4466762314682
##      best.response.index best.average.response.time
## 1      4      13
## 2      4      13
## 3      4      13
## 4      4      13
## 5      4      13
## 6      4      13
##      best.average.response.value best.average.response.index mRECIST
## 1      -17.5035868005739      4      SD
## 2      -17.5035868005739      4      SD
## 3      -17.5035868005739      4      SD
## 4      -17.5035868005739      4      SD
## 5      -17.5035868005739      4      SD
## 6      -17.5035868005739      4      SD
```

To get all mode

```
library(Xeva)
data("celineData")
head(ModelInfo(lpdX))
```

```
##                                     model.id
## PHLC1106_P5.501.A1.1.Control        PHLC1106_P5.501.A1.1
## PHLC1106_P5.502.A2.1.vincristine + cisplatin PHLC1106_P5.502.A2.1
## PHLC1106_P5.503.A3.1.vincristine + cisplatin PHLC1106_P5.503.A3.1
## PHLC1106_P5.504.A4.1.Control        PHLC1106_P5.504.A4.1
## PHLC1106_P5.505.A5.1.vincristine + cisplatin PHLC1106_P5.505.A5.1
## PHLC1106_P5.506.B1.1.Control        PHLC1106_P5.506.B1.1
##                                     experiment.id
## PHLC1106_P5.501.A1.1.Control        PHLC1106_P5.501.A1.1.Control
## PHLC1106_P5.502.A2.1.vincristine + cisplatin PHLC1106_P5.502.A2.1.vincristine + cisplatin
## PHLC1106_P5.503.A3.1.vincristine + cisplatin PHLC1106_P5.503.A3.1.vincristine + cisplatin
## PHLC1106_P5.504.A4.1.Control        PHLC1106_P5.504.A4.1.Control
## PHLC1106_P5.505.A5.1.vincristine + cisplatin PHLC1106_P5.505.A5.1.vincristine + cisplatin
## PHLC1106_P5.506.B1.1.Control        PHLC1106_P5.506.B1.1.Control
##                                     donor
## PHLC1106_P5.501.A1.1.Control        11101S-213RC-312S(F)-412S-
## PHLC1106_P5.502.A2.1.vincristine + cisplatin 11101S-213RC-312S(F)-412S-
## PHLC1106_P5.503.A3.1.vincristine + cisplatin 11101S-213RC-312S(F)-412S-
## PHLC1106_P5.504.A4.1.Control        11101S-213RC-312S(F)-412S-
## PHLC1106_P5.505.A5.1.vincristine + cisplatin 11101S-213RC-312S(F)-412S-
## PHLC1106_P5.506.B1.1.Control        11101S-213RC-312S(F)-412S-
##                                     dob sex
## PHLC1106_P5.501.A1.1.Control        Aug31.14  F
## PHLC1106_P5.502.A2.1.vincristine + cisplatin Aug31.14  F
## PHLC1106_P5.503.A3.1.vincristine + cisplatin Aug31.14  F
## PHLC1106_P5.504.A4.1.Control        Aug31.14  F
## PHLC1106_P5.505.A5.1.vincristine + cisplatin Aug31.14  F
## PHLC1106_P5.506.B1.1.Control        Aug31.14  F
##                                     PHLC biobase.id
## PHLC1106_P5.501.A1.1.Control        PHLC1106      <NA>
## PHLC1106_P5.502.A2.1.vincristine + cisplatin PHLC1106      <NA>
## PHLC1106_P5.503.A3.1.vincristine + cisplatin PHLC1106      <NA>
## PHLC1106_P5.504.A4.1.Control        PHLC1106      <NA>
## PHLC1106_P5.505.A5.1.vincristine + cisplatin PHLC1106      <NA>
## PHLC1106_P5.506.B1.1.Control        PHLC1106      <NA>
##                                     patient.id
## PHLC1106_P5.501.A1.1.Control        <NA>
## PHLC1106_P5.502.A2.1.vincristine + cisplatin <NA>
## PHLC1106_P5.503.A3.1.vincristine + cisplatin <NA>
## PHLC1106_P5.504.A4.1.Control        <NA>
## PHLC1106_P5.505.A5.1.vincristine + cisplatin <NA>
## PHLC1106_P5.506.B1.1.Control        <NA>
```

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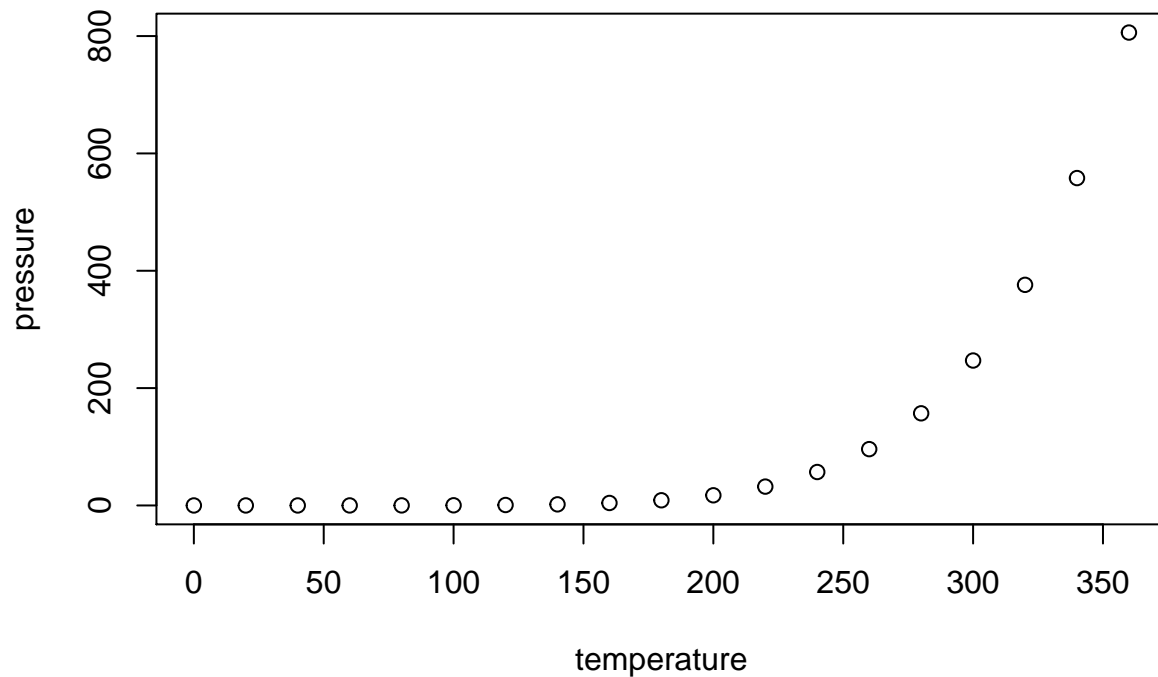
When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
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.