The Xeva user's guide

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Contents

1   Introduction

The Xeva package provides efficient and powerfull functions for patient drived xenograft (PDX) based pharmacogenomic data analysis.

2   Installation and Settings

Xeva requires that several packages are installed. However, all dependencies are available from CRAN or Bioconductor.

```
source('http://bioconductor.org/biocLite.R')
biocLite('Xeva')
```

Load Xeva into your current workspace:

```
library(Xeva)
```

Load PDXE breast cancer dataset:

```
data(brca)
print(brca)

## Xeva-set name: PDXE.BRCA
## Creation date: Fri Sep 14 11:41:33 2018
## Number of models: 849
## Number of drugs: 22
## Moleculer dataset: RNASeq, mutation, cnv
```

3   Definations

Before we further dive into the analysis and visualization, it is important to underastand terms used in the *Xeva* package. In a **Xeva** object, the **experiment** slot stores each individual PDX/mouse data. Other then the tumore growth data (time vs. tumor volume), for each individual PDX/mouse we can have meta data such as patient's age, sex, tissue histology, passage infromation etc. All this data is stored using the class **pdxModel** and a unique id called `model.id` is given to each PDX/mouse model. We will see later how to get data for an individual *model.id*.