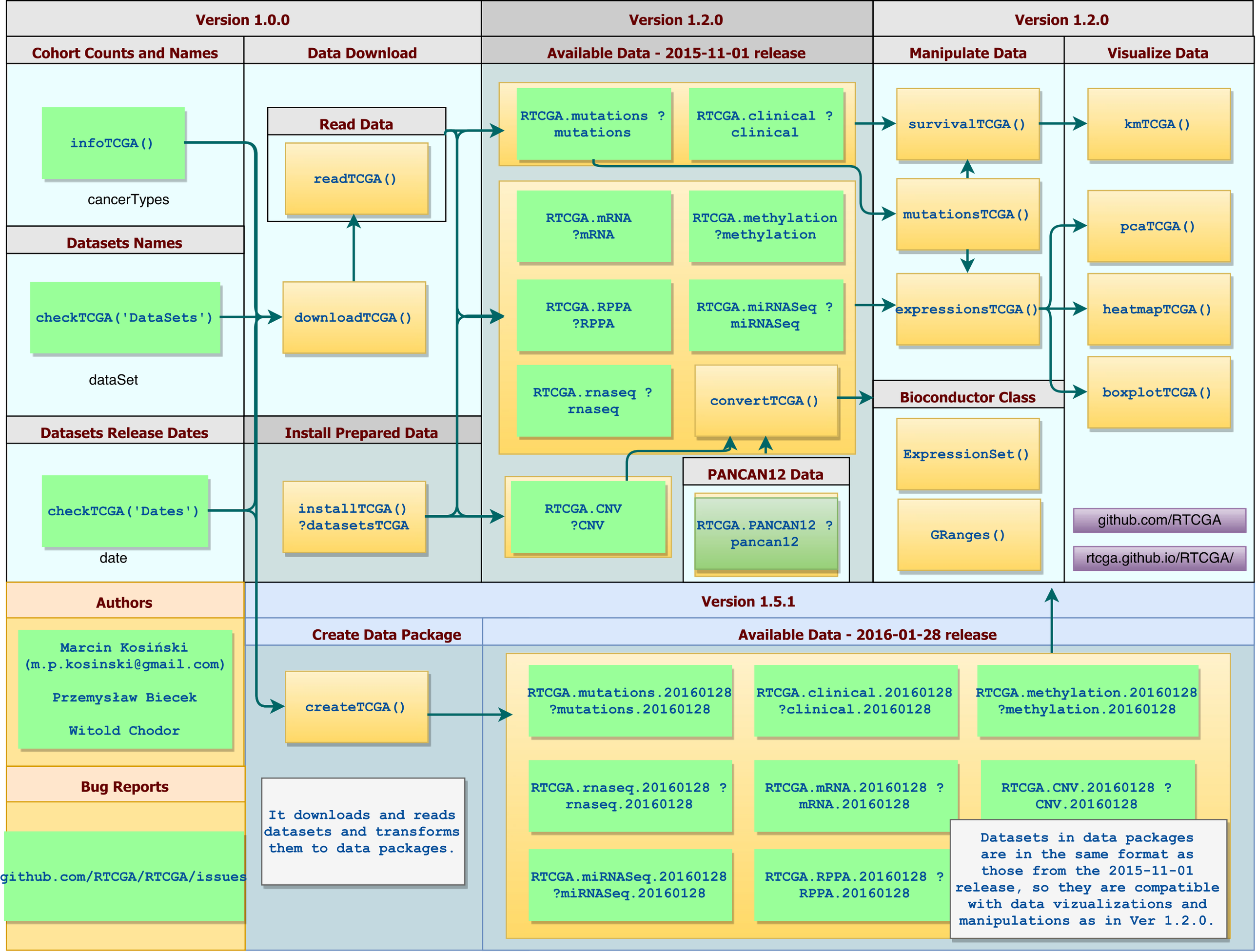
Version 1.0.0
Version 1.2.0
Version 1.2.0
Cohort Counts and Names
Data Download
Available Data - 2015-11-01 release
Manipulate Data
Visualize Data
infoTCGA()
cancerTypes
Read Data
readTCGA()
Datasets Names
checkTCGA('DataSets')
dataSet
downloadTCGA()
Datasets Release Dates
checkTCGA('Dates')
date
Install Prepared Data
installTCGA()
?datasetsTCGA
RTCGA.mutations ?
mutations
RTCGA.clinical ?
clinical
RTCGA.mRNA
?mRNA
RTCGA.methylation
?methylation
RTCGA.RPPA
?RPPA
RTCGA.miRNASeq ?
miRNASeq
RTCGA.rnaseq ?
rnaseq
convertTCGA()
RTCGA.CNV
?CNV
PANCAN12 Data
RTCGA.PANCAN12 ?
pancan12
survivalTCGA()
mutationsTCGA()
expressionsTCGA()
Bioconductor Class
ExpressionSet()
GRanges()
kmTCGA()
pcaTCGA()
heatmapTCGA()
boxplotTCGA()
github.com/RTCGA
rtcga.github.io/RTCGA/
Version 1.5.1
Authors
Marcin Kosiński
(m.p.kosinski@gmail.com)
Przemysław Biecek
Witold Chodor
Bug Reports
github.com/RTCGA/RTCGA/issues
Create Data Package
createTCGA()
It downloads and reads datasets and transforms them to data packages.
Available Data - 2016-01-28 release
RTCGA.mutations.20160128
?mutations.20160128
RTCGA.clinical.20160128
?clinical.20160128
RTCGA.methylation.20160128
?methylation.20160128
RTCGA.rnaseq.20160128 ?
rnaseq.20160128
RTCGA.mRNA.20160128 ?
mRNA.20160128
RTCGA.CNV.20160128 ?
CNV.20160128
RTCGA.miRNASeq.20160128
?miRNASeq.20160128
RTCGA.RPPA.20160128 ?
RPPA.20160128
Datasets in data packages are in the same format as those from the 2015-11-01 release, so they are compatible with data vizualizations and manipulations as in Ver 1.2.0.