**Tutorial for installing L1KProcs package**

1. **Description**

L1Procs is a parallel R package for L1000 data processing and analyzing. Major function of L1KProcs includes (a) l1kpreprocs, which preprocesses raw data, and generates normalized gene expression data; (b) egem, which provides some interesting genes as target related genes, and potential transcription factors involved in the function of the compounds; (c) csNMF, which can detect compound signatures, and provide interesting compounds as drug candidates.

1. **Details**

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| biocViews | Bioinformatics, Software |
| Version | 0.9.9 |
| Name | L1KProcs |
| Title | Pipeline for L1000 data processing and analyzing |
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| License | GPL-3 |
| Depends | R(>3.0), preprocessCore, stats, prada, SeqGSEA, methods |
| Enhances | doParallel (>= 1.0.1) |

1. **How to install**

Before installing L1KProcs, the system must meet the package requirements. (Please refer to Details: Depends). L1KProcs requires R (>3.0). To install R, please go to <http://cran.us.r-project.org/> for details. Packages preprocessCore, prada, SeqGSEA are available in bioconductor. Packages stats, doParallel are available in CRAN.

To install these packages, start R and enter:

source("http://bioconductor.org/biocLite.R")

biocLite("preprocessCore ")

biocLite(“prada”)

bioCLite(“SeqGSEA”)

install.packages(“stats”)

install.packages(“doParallel”)

install.package(“gplots”)

install.packages([path/to/L1KProcs.tar.gz],repos=NULL,type=”source”)

The package “doParallel” is optional.

To install L1KProcs using source code, in the R session, enter:

install.packages([path/to/L1KProcs.tar.gz],repos=NULL,type=”source”)