# README

Introduction

The identification and differential enrichment of transcription factor (TF) motifs in a given set of genomic regions relative to control regions is a common task in regulatory genomics. Here, we present enrichmotifpairR, an R package for identification of differentially enriched TF motifs and their binding partner motifs, or enriched motif pairs, in a given set of genomic regions relative to a control set of genomic regions.
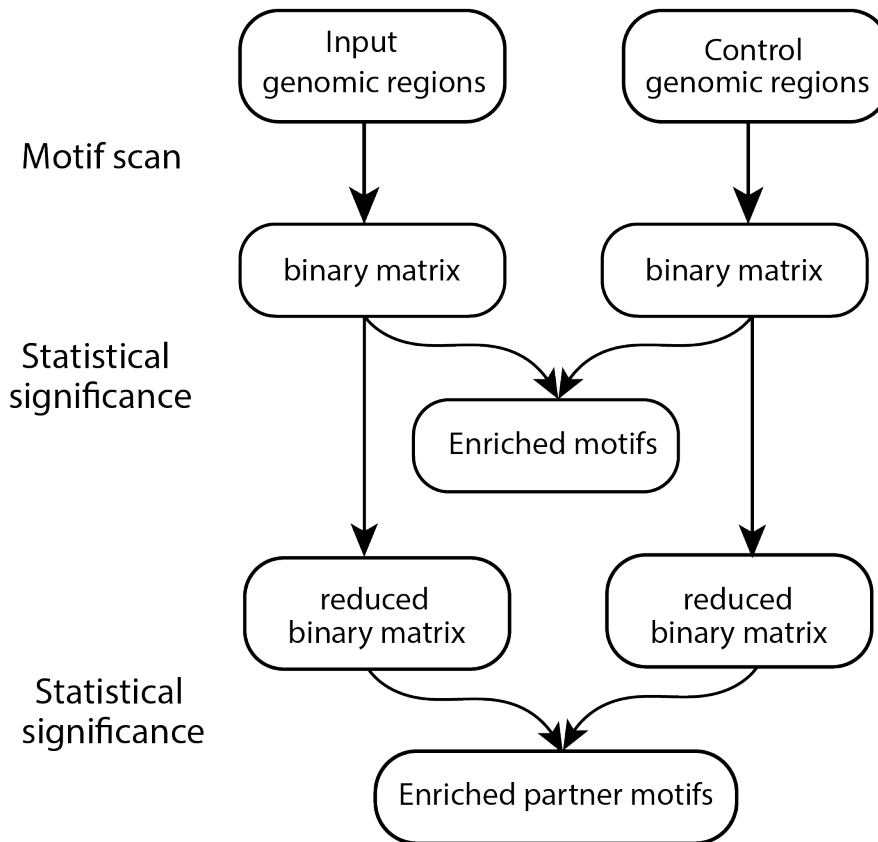
Supplementary Figure S1: Schematic of enrichmotifpairR package pipeline

Installation

First install the dependency packages.

```r
# install devtools and biocmanager if necessary
if (!requireNamespace("BiocManager", quietly = TRUE))
    install.packages(c("BiocManager", "devtools"))

# other dependency packages
BiocManager::install(c("GenomicRanges", "SummarizedExperiment", "motifmatchr",
                       "BiocGenerics", "Biostrings", "GenomeInfoDb", "IRanges",
                       "TFBSTools", "S4Vectors", ""))

# genome annotations
BiocManager::install(c("BSgenome.Hsapiens.UCSC.hg19", "BSgenome.Hsapiens.UCSC.hg38"))

# other packages
install.packages(c("dplyr", "assertthat", "Matrix", "rlang"))
```

Next install the enrichmotifpairR package

```r
# installation
devtools::install_github("nashchem/enrichmotifpairR")

# load
library(enrichmotifpairR)
```

Use case examples

See the vignettes directory for several use case examples.