# 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.
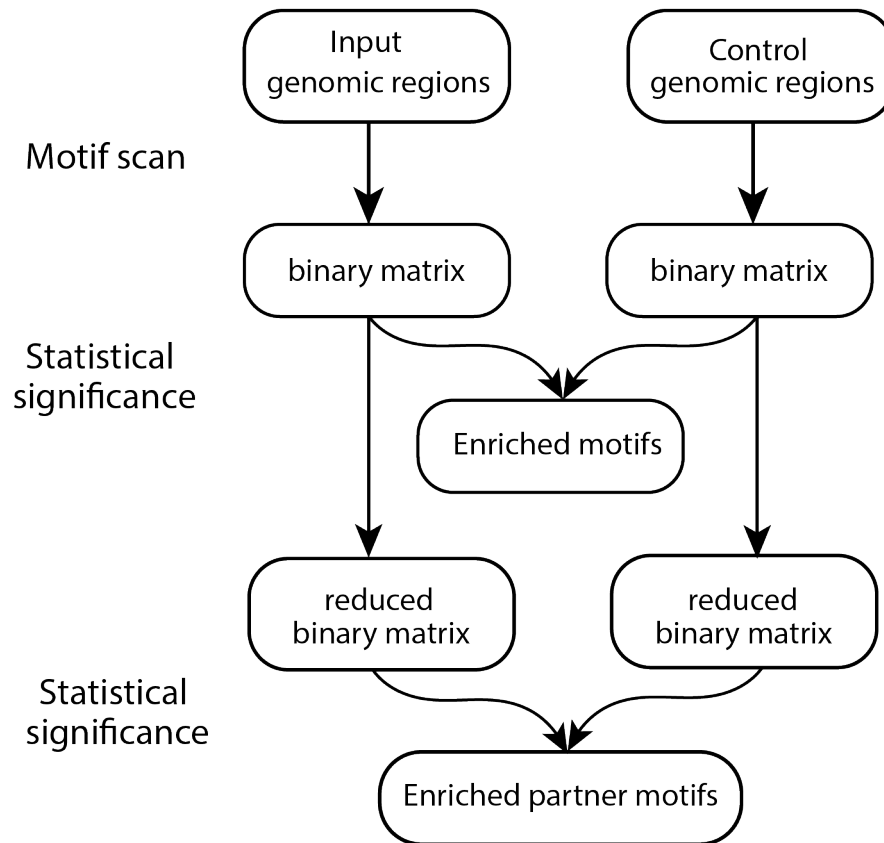
Supplementary Figure S1: Schematic of enrichmotifpairR package pipeline

Figure 1: enrichmotifpairR framework