*APRES* ChIP-Seq User Manual

The **A**nalysis **P**ipeline for **R**eplicate **E**xperiments across **S**pecies.

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# Introduction

Chromatin immunoprecipitation followed by DNA sequencing, also known as ChIP-seq, is a popular experimental technique to determine genomic locations that are enriched for binding by a particular DNA-binding protein. ChIP-seq is typically used to study DNA-binding transcription regulator proteins. A common experimental approach is to perform ChIP-seq in different conditions – perhaps different cells strains, species, or environmental conditions – and then compare the effects on DNA-binding of a particular protein.

ChIP-seq methods have become well established for mapping sequenced reads to their reference genome [cite XX], and finding “peaks” with significantly enriched binding [cite XX]. However, it remains less established how binding data should be compare between replicates, across different conditions, and across species.

**APRES** ChIP-Seq is an **A**nalysis **P**ipeline for **R**eplicate **E**xperiments across **S**pecies. APRES maps ChIP-seq binding events to their putative target gene, and then compares these maps between replicates in the same conditions, across replicates in different conditions, and between species.

APRES takes as input (1) the output of a peak-calling software, such as MACS, (2) a genome features file that defines the genomic location of genes, and (3) an APRES configuration file that specifies replicates, groups of replicates, and species.

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# Download and Install

APRES is available for download from it’s Github repository:

XX insert github URL XXX

APRES is written in **Python** and **R**. It uses a few commonly-used Python libraries: **scipy**, **numpy**, and **matplotlib**. You made need to install these libraries separately.

# Input Files

asdfadsf

# Usage

APRES is a Python script that is run from the command-line. APRES may require several hours to finish, depending on the size of your ChIP-seq project. During its run, APRES will print useful updates to the terminal.

# Output Files

Asdfadsf

# Troubleshooting

asdfasdf