

# Package ‘ProxSeek’

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**Title** ProxSeek priopritize eQTLs using Hi-C based promoter interactome

**Version** 1.0.0

**Description** What the package does (one paragraph).

**License** GPL (>=2)

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.2.0

**Imports** data.table,  
doSNOW,  
dplyr,  
foreach,  
plyr,  
stringr,  
MatrixEQTL

## R topics documented:

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ProxSeek_runProxeQTL	<i>Run Proximity-based eQTL Analysis</i>
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## Description

This function performs proximity-based eQTL analysis using SNP and gene expression data, integrating cell type-specific physical interaction regions (P-PIRs). It outputs significant Prox-eQTLs, considering cellular context.

**Usage**

```
ProxSeek_runProxeQTL(SNP_file_name, expression_file_name, snps_location_file_name,
  gene_location_file_name, covariates_file_name, cell.type = NA, chr = NA,
  output.file = "./test/ciseqtl.tsv", n.cluster = 4)
```

**Arguments**

SNP_file_name	Path to the SNP genotype file.
expression_file_name	Path to the gene expression file.
snps_location_file_name	Path to the file with SNP locations.
gene_location_file_name	Path to the file with gene locations.
covariates_file_name	Path to the covariates file.
cell.type	Specific cell type to analyze.
chr	integer. Chromosome to analyze.
output.file	Output file path for the results.
n.cluster	Number of clusters for analysis.
P_PIR_folder	The folder where P-PIR dataset were downloaded.

**Details**

This function integrates MatriceQTL pipeline and P-PIR information to identify prox-eQTLs.

**Value**

A data frame with the results of the proximity-based eQTL analysis.

**Examples**

```
# Example usage of ProxSeek_runProxeQTL
## Not run:
result <- ProxSeek_runProxeQTL("path/to/SNP_file.txt", "path/to/expression_file.txt",
  "path/to/snps_location_file.txt", "path/to/gene_location_file.txt",
  "path/to/covariates_file.txt", cell.type = "monocyte", chr = "X")

## End(Not run)
```

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ProxSeek\_selectProxCis

*ProxSeek\_selectProxCis*


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## Description

This function select cis-eQTLs that lie within promoter and promoter interaction region (P-PIR) based on tissue/cell type Hi-C data. It reads cis-eQTL and cell type P-PIR files, performs filtering and annotation, and returns an annotated data frame.

## Usage

```
ProxSeek_selectProxCis(
  ciseqtl.file = NA,
  P_PIR_folder = NA,
  cell.type = NA,
  n.cluster = 4
)
```

## Arguments

<code>ciseqtl.file</code>	A string specifying the path to the cis-eQTL file. Default value is NA. It's recommended to provide the actual file path for specific analyses.
<code>cell.type</code>	A string specifying the cell type. This is used to construct the file name of the cell type-specific P-PIR file.
<code>n.cluster</code>	An integer specifying the number of clusters to use in parallel processing. Default is 4. This should be set according to the hardware capabilities of the system.

## Value

An annotated data frame with the results of the cis-eQTL and Hi-C interaction processing.

## Examples

```
# Example usage:
## Not run:
demo.ciseqtl.file<-system.file("data", "ciseqtl.csv", package = "ProxSeek")
result <- ProxSeek_selectProxCis(ciseqtl.file = demo.ciseqtl.file, P_PIR_folder = /path/to/downloaded/PIRfiles/,
cell.type = "monocyte", n.cluster =4)

## End(Not run)
```

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