

# Getting Started with 4DNvestigator

## Table of Contents

4DNvestigator Overview.....	1
What is the 4DNvestigator.....	1
Initial setup of 4DNvestigator Environment.....	1
Loading Processed Hi-C and RNA-seq Data.....	1
Example Usage of the 4DNvestigator Tools.....	1
Feature Analyzer.....	1
Von Neumann Entropy.....	2
Simple Von Neumann Entropy - Two Cell Types.....	2
Expanded Von Neumann Entropy - Many Cell Types.....	3
Larntz-Perlman.....	4
Network Analysis.....	4

## 4DNvestigator Overview

### What is the 4DNvestigator

The 4DNvestigator is a toolbox for analyzing time-series genome-wide chromosome conformation capture (Hi-C) and gene expression (RNA-seq) data.

### Initial setup of 4DNvestigator Environment

```
close all, clear all
restoredefaultpath
addpath(genpath(pwd))
```

### Loading Processed Hi-C and RNA-seq Data

```
Index_Loc = 'data\exampleData\myodData\sampleMyodDataIndexTp-48_8_80.xlsx'; %% index file
Data_Loc = 'data\exampleData\myodData\'; %% data input

if exist('sampleMyodDataIndexTp-48_8_80.xlsx','file')==2
    [dataInfo] = fdnLoadUserInput(Index_Loc);
    [H] = fdnLoadHic(Data_Loc,dataInfo,'single');
    [R] = fdnLoadRnaseq(Data_Loc,dataInfo,H);
end
```

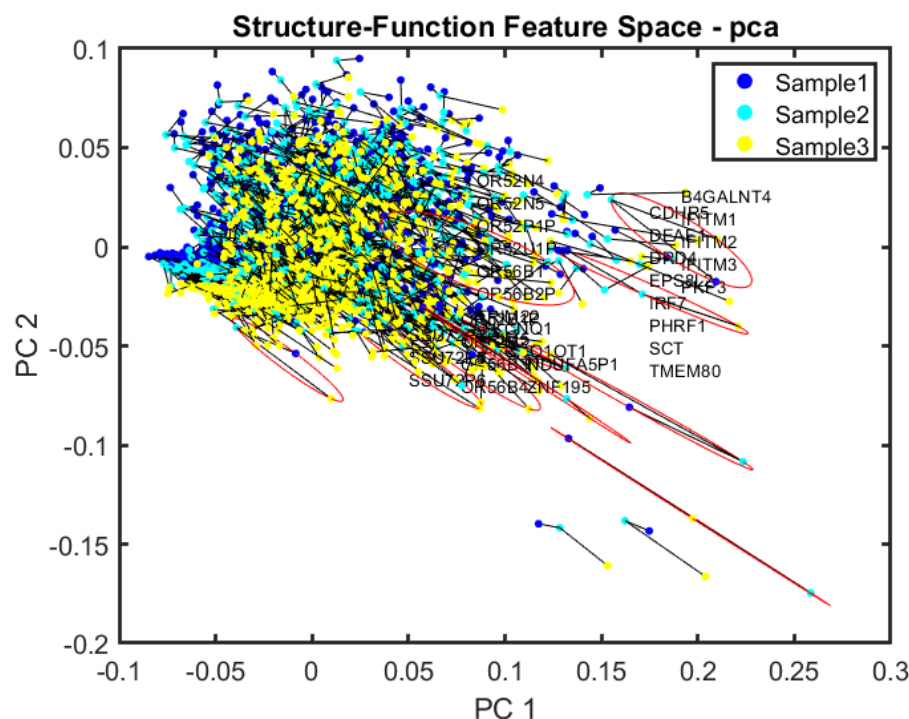
## Example Usage of the 4DNvestigator Tools

### Feature Analyzer

The Feature Analyzer takes in Hi-C and RNA-seq data (formatted as shown above) and computes the changes in structure and function between samples. For ease of use, a pre-formatted dataset from a cellular reprogramming experiment is used as an example.

The function **featureAnalyzerExample** requires the parameters **Data\_Loc** and **Folder\_Result** which denote the locations where the data can be accessed and the output figure is stored, respectively. The remaining parameters, **chrSelect**, **dimReduc**, and **binSize**, correspond to the chromosome used for analysis, the method of dimension reduction used for visualization, and the desired resolution of the data. The values assigned to these parameters shown below are the default if none are specified.

```
Data_Loc = 'data\exampleData\myodData\myodData.mat'; %% data input
Folder_Result = 'results\featureAnalyzerResults'; %% output folder
chrSelect = 11;
dimReduc = 'pca';
binSize = 1E5;
featureAnalyzerExample(Data_Loc, Folder_Result, chrSelect, dimReduc, binSize)
```



## Von Neumann Entropy

### Simple Von Neumann Entropy - Two Cell Types

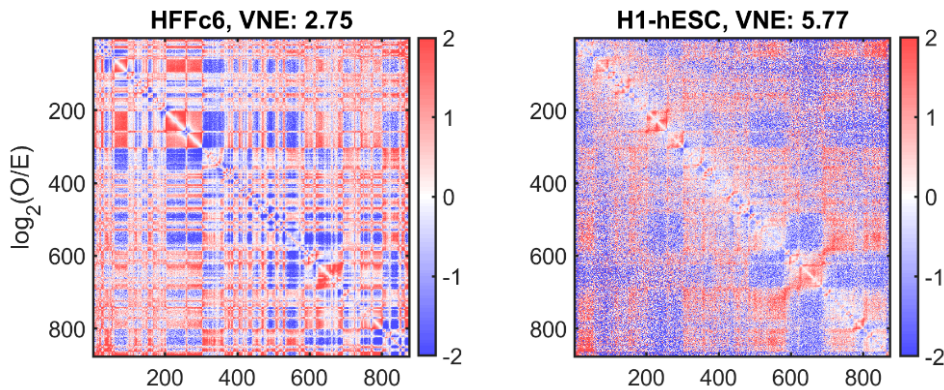
Von Neumann Entropy is calculated for Hi-C data (formatted as shown above) and can be used to compare the entropy of multiple cell types. In this example, we show two cell types, fibroblast and stem cell, to highlight the differences in chromatin organization.

The function **vneExample** requires the parameters **Data\_Loc** and **Folder\_Result** which denote the locations where the data can be accessed and the output figure is stored, respectively. The remaining parameters, **chrSelect**, **bpFrag**, and **binSize**, correspond to the chromosome used for analysis, the choice of coordinates (base pair = BP or fragment = FRAG), and the desired resolution of the data. The values assigned to these parameters shown below are the default if none are specified.

```
Data_Loc = {'data\exampleData\4DNFIFLJLIS5.hic', ...
            'data\exampleData\4DNFIOX3BGNE.hic'}; %% data input
Folder_Result = 'results\vneExampleResults'; %% output folder
```

```
chrSelect = 14;
bpFrag = 'BP';
binSize = 1E5;

vneExample(Data_Loc, Folder_Result, chrSelect, bpFrag, binSize)
```

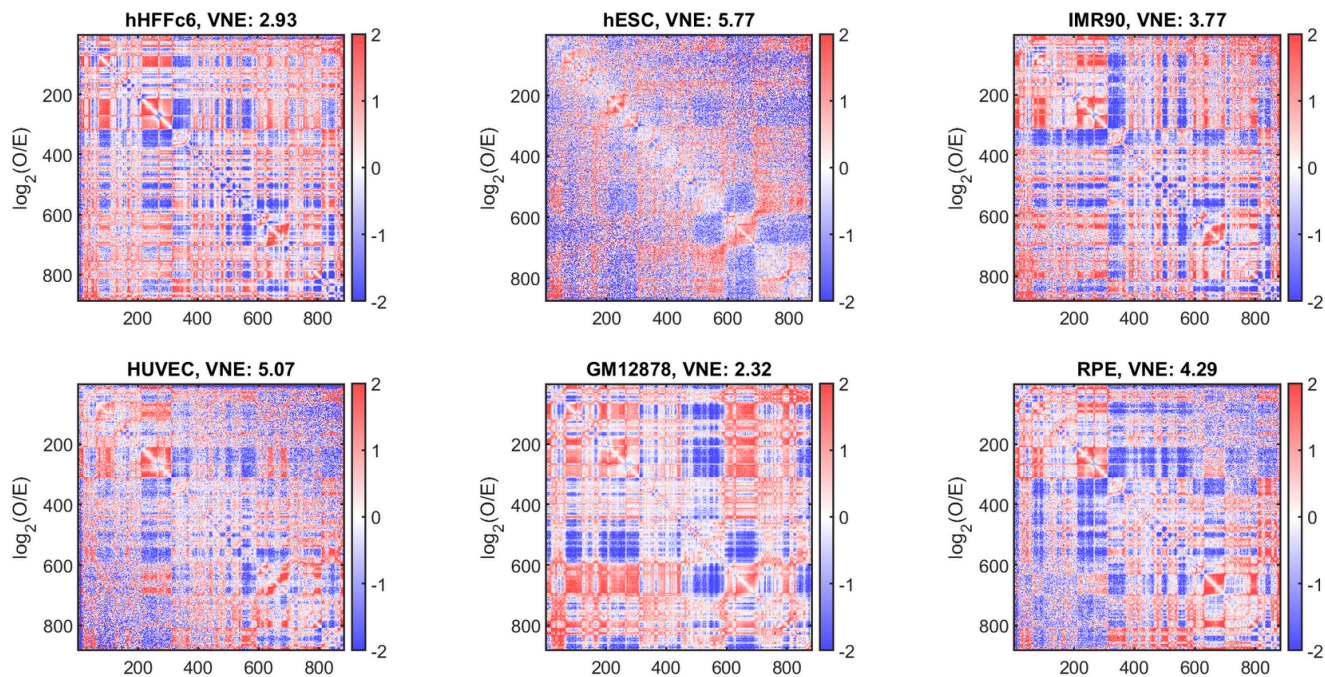


### Expanded Von Neumann Entropy - Many Cell Types

The function **vneExampleExpanded** is similar to the simple VNE function above but highlights that more than two cell types can be calculated at once.

```
Data_Loc = { 'data\exampleData\4DNFIFLJLIS5.hic';... %% data input
             'data\exampleData\4DNFIOX3BGNE.hic';...
             'https://hicfiles.s3.amazonaws.com/hiseq/imr90/in-situ/combined.hic';...
             'https://hicfiles.s3.amazonaws.com/hiseq/huvec/in-situ/combined.hic';...
             'https://hicfiles.s3.amazonaws.com/hiseq/gm12878/in-situ/combined.hic';...
             'http://hicfiles.s3.amazonaws.com/hiseq/rpe1/DarrowHuntley-2015/WT-combined.hic'};
Folder_Result = 'results\vneExampleExpandedResults'; %% output folder
chrSelect = 14;
bpFrag = 'BP';
binSize = 1E5;

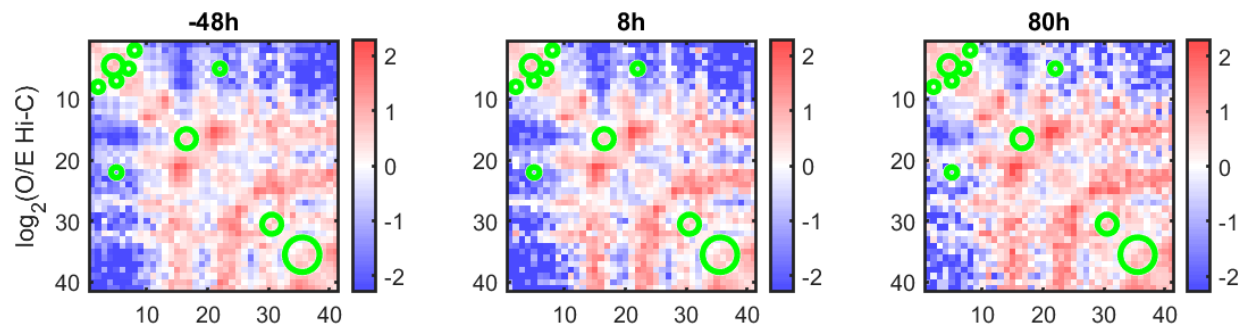
vneExampleExpanded(Data_Loc, Folder_Result, chrSelect, bpFrag, binSize)
```



## Larntz-Perlman

```
close all
Data_Loc = 'data\exampleData\myodData\myodData.mat'; %% data input
Folder_Result = 'results\lpExampleResults'; %% output folder

lpExample(Data_Loc, Folder_Result);
```



## Network Analysis

```
Data_Loc = 'data\exampleData\networkData\'; %% data input folder
Folder_Result = 'results\networkExamplesResults'; %% output folder

networkExamples(Data_Loc, Folder_Result);
```

