

Getting Started with 4DNvestigator

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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. This document outlines each of the core functions of the 4DNvestigator which can be run using **ExampleScript.m**.

Initial Setup of 4DNvestigator Environment

The 4DNvestigator requires the following MATLAB Toolboxes:

- Statistics and Machine Learning Toolbox
- Computer Vision Toolbox
- Bioinformatics Toolbox
- Image Processing Toolbox

In **ExampleScript.m**, we first prepare the MATLAB environment:

```
close all, clear %% Close figures and reset variables
restoredefaultpath %% Ensure no other folders on current path
addpath(genpath(pwd)) %% Add all 4DNvestigator folders and files to path
```

Loading Processed Hi-C and RNA-seq Data

The 4DNvestigator accepts Hi-C data from Juicer (.hic) and RNA-seq data from RSEM (.genes.results). To input these data into MATLAB, the 4DNvestigator requires a metadata table, referred to as an “Index File”, to describe the data. Rows correspond to sequencing data samples (RNA-seq or Hi-C), and the columns correspond to data descriptors. The Index File must have 5 columns with the following headers:

- "path" defines the computer path to the sequencing data
- "dataType" defines the type of sequencing data, either "hic" or "rnaseq"
- "sample" defines the sample, (e.g. "treatment" or "control")
- "timePoint" defines the time point of sample, (e.g. 0 or 24)
- "refGenome" defines the reference genome for the sample (e.g. "hg19")

All example data and the example index file should be downloaded to the directory **data\exampleData** from Google Drive: [4DNvestigator Example Data](#). This data can be loaded using 4DNvestigator as shown below. Pre-processed Hi-C contacts can also be loaded from comma separated files (loc1, loc2, score) using **fdnLoadGenericHic**.

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

[dataInfo] = fdnLoadUserInput(Index_Loc); %%% Load index file
[H] = fdnLoadHic(Data_Loc,dataInfo,'single'); %%% Load Hi-C data
[R] = fdnLoadRnaseq(Data_Loc,dataInfo,H); %%% Load RNA-seq data
```

Example Usage of the 4DNvestigator Tools

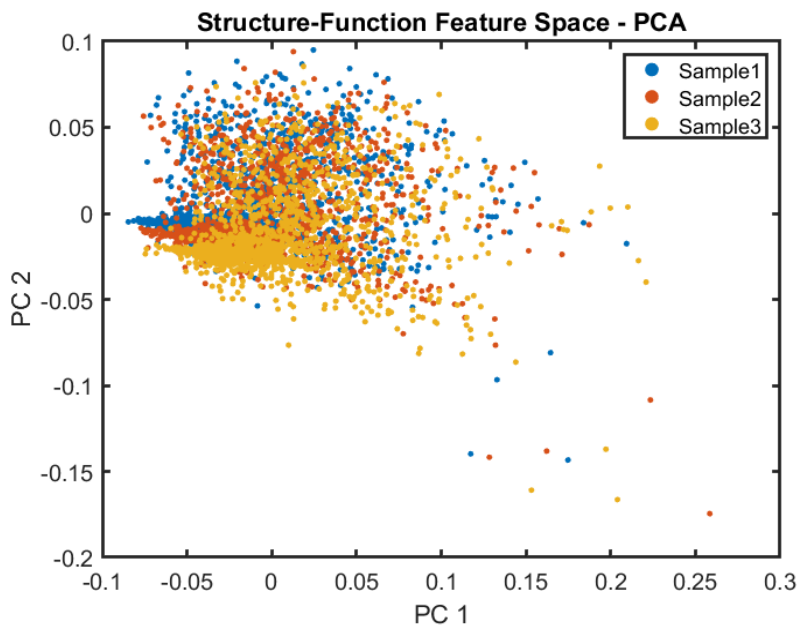
Feature Analyzer

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 [1].

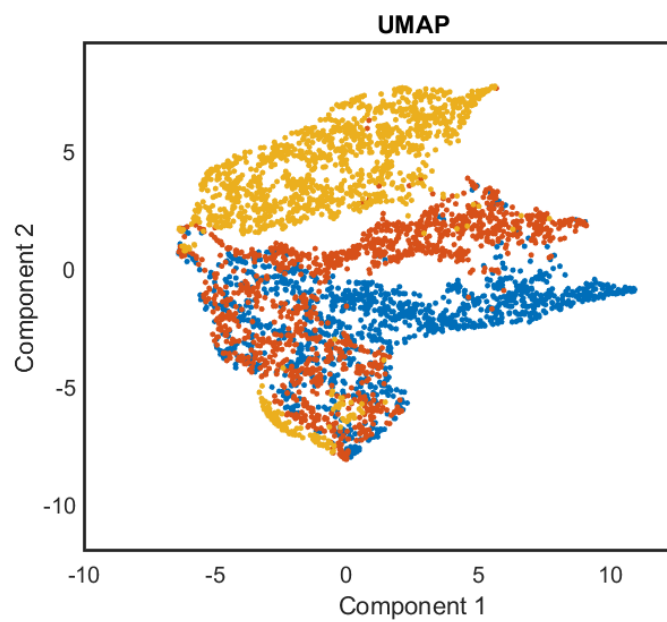
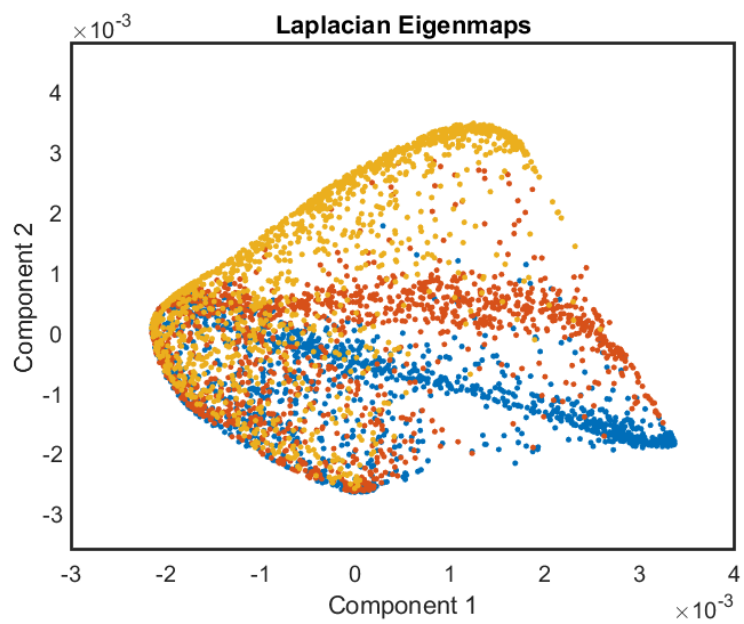
The function **featureAnalyzerExample** requires the parameters **Data_Loc** and **Folder_Result** which denote the locations where the data can be accessed and the output figure is stored, respectively. The remaining parameters, **chrSelect**, **dimReduc**, **binSize**, and **sfType** correspond to the chromosome used for analysis, the method of dimension reduction used for visualization (PCA = 'pca', Laplacian Eigenmaps = 'lapeigen', or t-SNE = 'tsne'), the desired resolution of the data, and whether the structure-function feature will be constructed/visualized using dimension reduction or if structure and function are used directly in a phase plane. 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;
sfType = 'sfmatrix';
featureAnalyzerExample(Data_Loc, Folder_Result, chrSelect, dimReduc, binSize, sfType)
```

Points in the figure below correspond to genomic loci (100 kb). Here we use the linear dimension reduction method PCA to visualize the structure-function feature matrix.



The structure-function feature matrix can also be visualized using non-linear dimension reduction techniques:



Von Neumann Graph Entropy

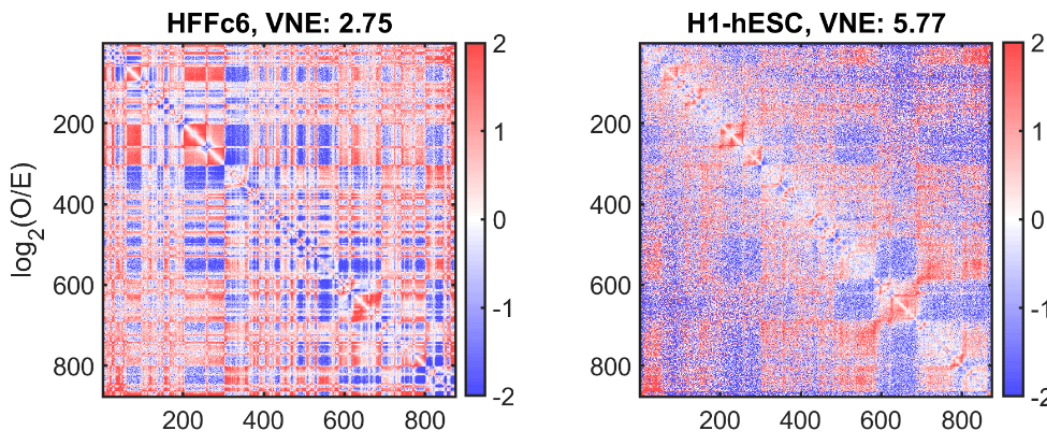
Two Cell Types

Von Neumann Graph Entropy (VNE) 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 to highlight the differences in chromatin organization and their entropy [2, 3, 4].

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)
```

The VNE for an undifferentiated cell type (embryonic stem cell, H1-hESC) is much higher than the more differentiated cell type (fibroblast, HFFc6). Intra-chromosome log₂(A) Hi-C matrices are shown at 100 kb resolution for chromosome 14.



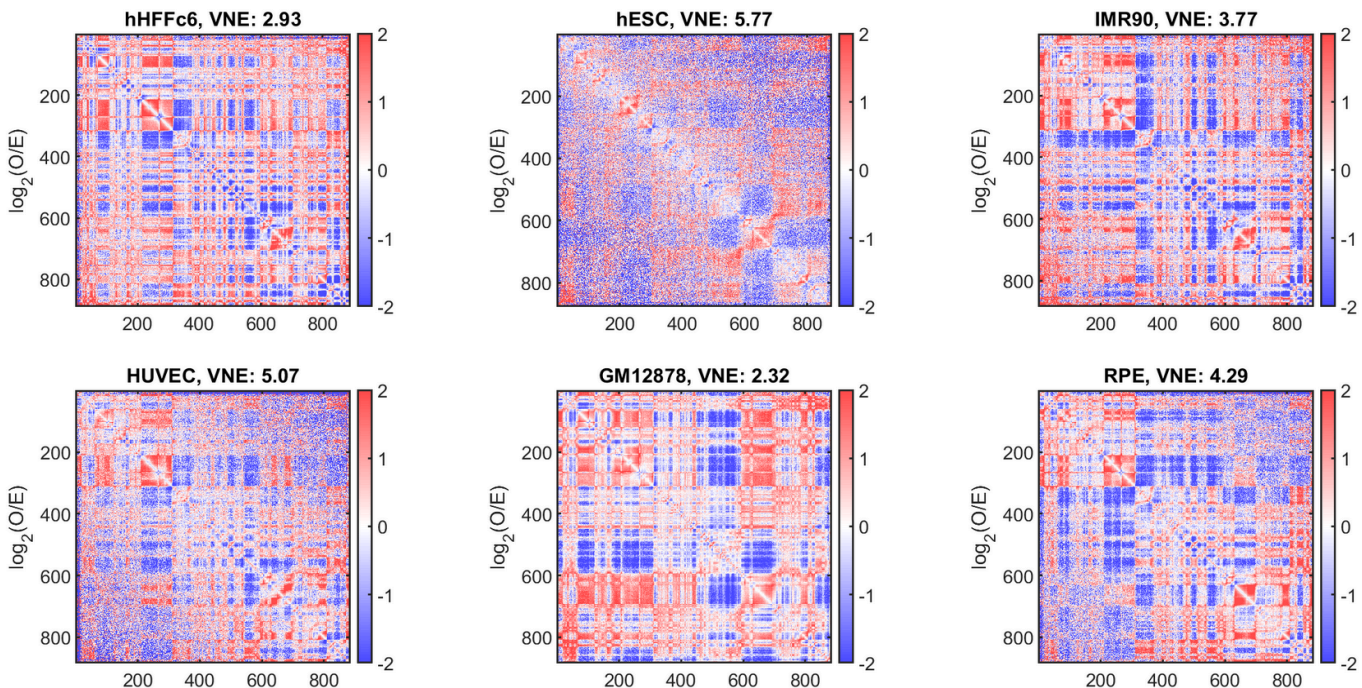
Many Cell Types

The function **vneExampleExpanded** is similar to the standard 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)
```

Hi-C matrices from six cell types and their respective VNE. The more pluripotent cell lines (hESC, HUVEC) have a much higher VNE than the more differentiated cell lines (IMR90, hHFF6c, GM12878). Intra-chromosome $\log_2(A)$ Hi-C matrices are shown at 100 kb resolution for chromosome 14.



Larntz-Perlman Method

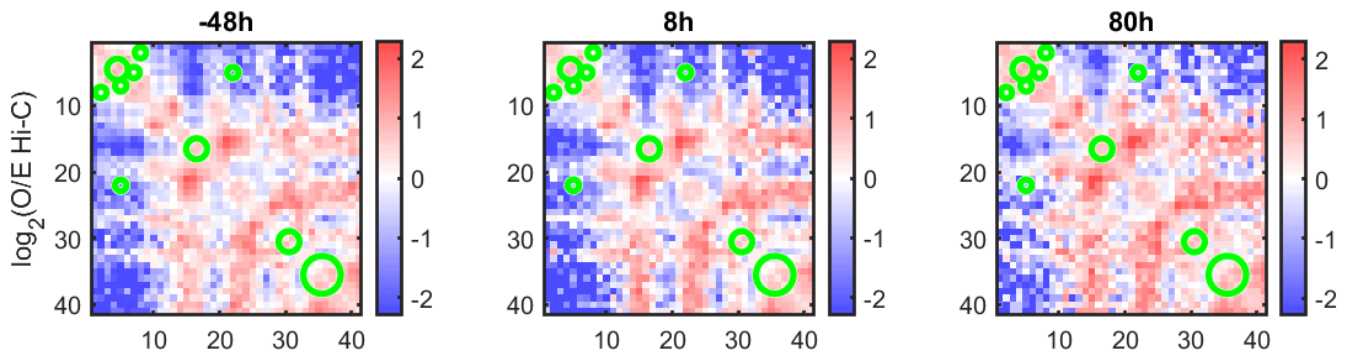
The Larntz-Perlman (LP) method is used to compare Hi-C matrices from different cell types or time points. This is done by testing the equality of the Hi-C correlation matrices after a log2 transformation [5]. In this example, we show where a region of interest differs between three time points {-48, 8, 80 hours}. We recommend that the LP method is performed at Hi-C resolutions ≤ 100 kb and that regions do not extend > 5 Mb. The LP method calculates a P -value for the equality of Hi-C matrices and a matrix S , where the largest values in S correspond to genomic regions that are most different between samples.

The function **lpExample** 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. Within the function **lpExample**, the specific region of interest can be modified by the user.

```
Data_Loc = 'data\exampleData\myodData\myodData.mat'; %% Data input
Folder_Result = 'results\lpExampleResults'; %% Output folder

lpExample(Data_Loc, Folder_Result);
```

The LP method highlights where samples are most significantly different within a region of interest.



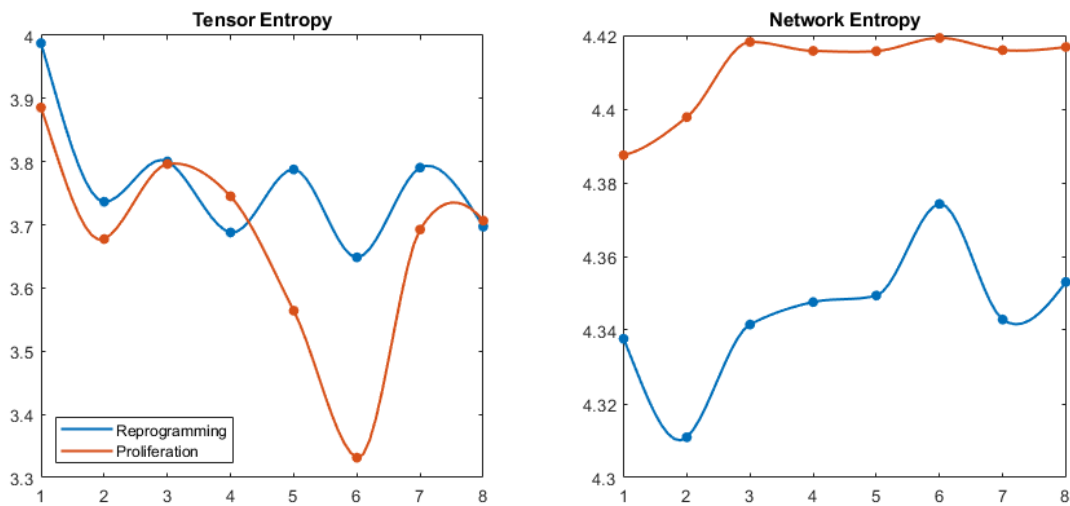
Tensor Entropy

The function **tensorEntropyExample** 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.

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

tensorEntropyExample(Data_Loc, Folder_Result);
```

The example outputs of **tensorEntropyExample** are two figures depicting the tensor entropy and network entropy of Hi-C data over 8 time points of a cellular reprogramming experiment. This figure highlights the bifurcation between the proliferating fibroblasts and reprogrammed fibroblasts at the 32 hr time point (time point 6).



Summary

The core functions of the 4DNvestigator offer multiple ways to study both gene expression and chromosome conformation over time. These functions can be easily adapted for other applications by changing their data input location. Through small modifications within each function, the 4DNvestigator can be used to study the genome as a whole, chromosomes, particular regions within chromosomes, or genes of interest. In addition, the 4DNvestigator contains many functions for more simple analyses including differential expression of genes and chromatin partitioning.

References

1. Liu, S., Chen, H., Ronquist, S., Seaman, L., Ceglia, N., Meixner, W., Chen, P.-Y., Higgins, G., Baldi, P., Smale, S., et al. (2018) Genome Architecture Mediates Transcriptional Control of Human Myogenic Reprogramming. *iScience*, 6

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4. Meshorer, E. and Misteli, T. (2006) Chromatin in pluripotent embryonic stem cells and differentiation. *Nature reviews Molecular cell biology*, 7 (7), 540.
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