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הפקולטה להנדסה  
ע"ש איבי ואלדור פליישימן  
אוניברסיטת תל אביב



# COMMUNITY DETECTION WITH APPLICATIONS TO MULTIREFERENCE ALIGNMENT

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Final report

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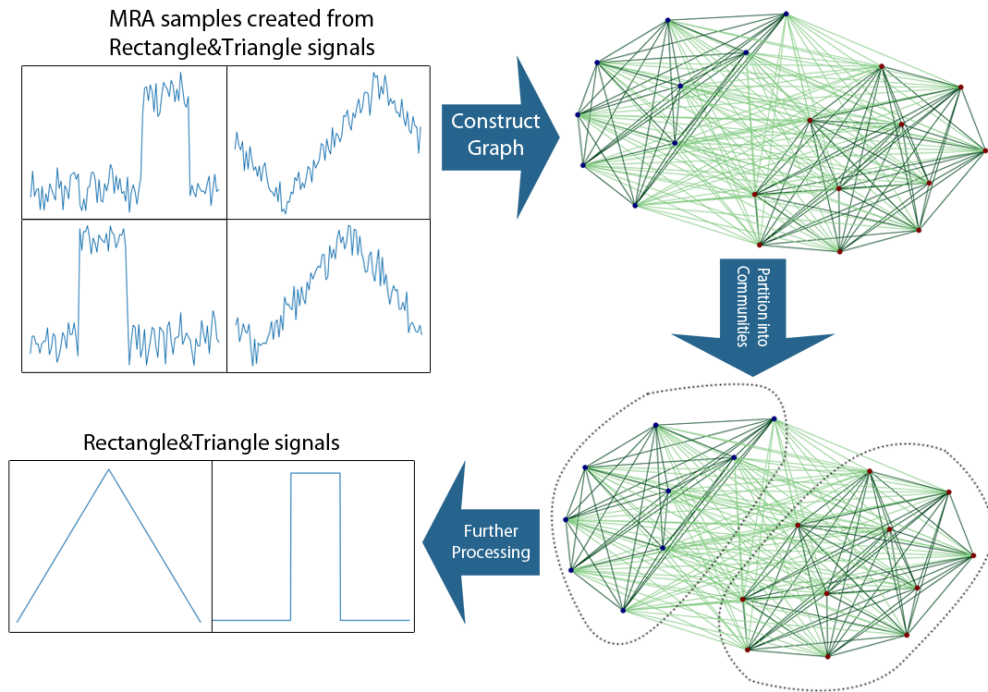
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## ABSTRACT

Single-particle reconstruction in Cryogenic Electron Microscopy (cryo-EM)[1] is a tool for constructing a 3D model of a biological macromolecule using 2D projections of the macromolecules taken by an electron microscope. An unsupervised classification of the 2D images is required in order to separate macromolecular projections of different conformations. Due to high noise levels and data heterogeneity, sophisticated clustering methods are needed.

In our project we will use Community Detection (CD) algorithms to cluster data generated from the Multireference Alignment (MRA) statistical model. The model abstracts away much of the intricacy of cryo-EM while retaining some of its essential features. **Conclusions should be added**



**Figure 1: Project process.** Further processing stage presents the idea behind clustering the data and is outside of the scope of the project.

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## **List of Abbreviations**

### **C**

**CD** Community Detection. 3, 7

**cryo-EM** Cryogenic Electron Microscopy. 3, 7, 8

### **F**

**FFT** Fast Fourier Transform. 8

### **M**

**MRA** Multireference Alignment. 1, 3, 4, 7, 8

### **S**

**SNR** Signal To Noise Ratio. 4, 7, 8

# 1 Introduction

Single-particle reconstruction in cryo-EM is a powerful image-processing tool used to determine the 3D structure of biological macromolecular complexes. 2D images (micrographs) of a macromolecule are taken by an electron microscope. Essentially, the set of all micrographs for a given macromolecule spans a 3D model of the macromolecule. Thus, single-particle reconstruction is using the micrographs to build a 3D model of the macromolecule.

Due to high sensitivity of the biological macromolecules to radiation damage, electron microscope provides limited electron doses when producing micrographs. This and the low contrast of micrographs result in cryo-EM data having very low Signal To Noise Ratio (SNR)[1].

cryo-EM technology has the potential to offer the ability to analyze different functional and conformational states of macromolecules, an important ability for the field of molecular biology. Practically, it entails the classification of heterogeneous cryo-EM data.

Many different approaches for cryo-EM data classification have been developed. Typically, likelihood optimization algorithms and Bayesian inference frameworks are used to deal with data heterogeneity[6, 5, 4, 7, 3].

In our project we propose a different approach to cryo-EM data classification using Community Detection (CD) algorithms from the field of complex networks. Namely, data will be classified following the steps:

- Converting data into a graph
- Applying Community Detection algorithms to partition the graph into distinct communities
- Each vertice in a graph that corresponds with a single sample will be given a label

For the sake of an abstraction of the cryo-EM data we will use the Heterogeneous Multireference Alignment (MRA) statistical model. Throughout our project we use the simplified 1D version of the model.



## 2 Background

### 2.1 Heterogeneous 1D Multireference Alignment model

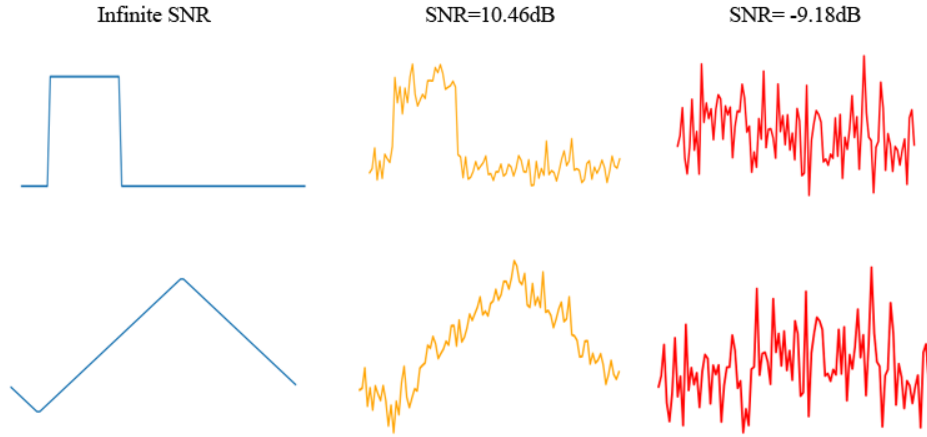
In our project we will use the Heterogeneous 1D Multireference Alignment statistical model[2] (MRA shortly) for the sake of cryo-EM data abstraction. Bellow is the definition of the model.

Let  $x_1, \dots, x_K \in \mathbb{R}^L$  be  $K$  unknown normalized signals (distinct even up to shift) and let  $R_s$  be the cyclic shift operator:  $(R_s x)[n] = x[(n - s)_L]$ . We are given  $N$  observations:

$$y_j = R_{s_j} x_{k_j} + \varepsilon_j, \quad j = 1, \dots, N \quad (1)$$

where  $s_j \sim U[0, L - 1]$ ,  $k_j \sim U[0, K - 1]$  and  $\varepsilon_j \sim \mathcal{N}(0, \sigma^2 I)$  is i.i.d white Gaussian noise. Our goal is to estimate the signals  $x_1, \dots, x_K$  from the observations.

Simply speaking, MRA observation is a randomly chosen signal  $x_{k_j}$ , shifted randomly by  $s_j$  and distorted using white noise. **Figure 2** shows an example of two MRA observations at different noise levels.



**Figure 2: Example of MRA observations at different SNR levels.** Each column shows a shifted distinct signal at different noise level. We can see that for low SNR the task of signal estimation is quite challenging.

In order to build a graph from MRA observations, a similarity measure between observations must be defined. We will use the cross-correlation, as its invariance to shift holds great value.

$$(x \star y)_n \triangleq \sum_{l=-\infty}^{\infty} x_l^* (y)_{n+l} \quad (2)$$

The convolution theorem states that the convolution of two signals equals to the inverse Fourier transform of the product of the Fourier transforms of each signal. Thus we can write the equation above in terms of Fourier transforms and later exploit FFT in our simulations.

$$(x \star y)_n = \mathcal{F}^{-1}\{X^* \cdot Y\}_n \quad (3)$$

In order to obtain normalized cross-correlation MRA samples must first be normalized.

### 2.2 Introduction to graphs

### **3 Aim 1 Title**

#### **3.1 Introduction to Aim 1**

An introduction to Aim 1.

#### **3.2 Background to Aim 1**

This section will include the most relevant literature addressing this aim.

#### **3.3 Methods**

Maybe you'll discuss some methods.

##### **3.3.1 Some crucial details about the method**

It'll probably have a sub(sub)heading.

##### **3.3.2 Conceptual model, research questions and hypotheses**

Blah blah blah.

#### **3.4 Results of Aim 1**

Blah blah blah.

#### **3.5 Discussion of Aim 1**

Blah blah blah.

#### **3.6 Conclusion of Aim 1**

Blah blah blah.

## **4 Aim 2 Title**

### **4.1 Introduction to Aim 2**

An introduction to Aim 2.

### **4.2 Background to Aim 2**

This section will include the most relevant literature addressing this aim.

### **4.3 Methods**

Maybe you'll discuss some methods.

#### **4.3.1 Some crucial details about the method**

It'll probably have a sub(sub)heading.

#### **4.3.2 Conceptual model, research questions and hypotheses**

Blah blah blah.

### **4.4 Results of Aim 2**

Blah blah blah.

### **4.5 Discussion of Aim 2**

Blah blah blah.

### **4.6 Conclusion of Aim 2**

Blah blah blah.

## **5 Aim 3 Title**

### **5.1 Introduction to Aim 3**

An introduction to Aim 3.

### **5.2 Background to Aim 3**

This section will include the most relevant literature addressing this aim.

### **5.3 Methods**

Maybe you'll discuss some methods.

#### **5.3.1 Some crucial details about the method**

It'll probably have a sub(sub)heading.

#### **5.3.2 Conceptual model, research questions and hypotheses**

Blah blah blah.

### **5.4 Results of Aim 3**

Blah blah blah.

### **5.5 Discussion of Aim 3**

Blah blah blah.

### **5.6 Conclusion of Aim 3**

Blah blah blah.

## **6 Discussion**

Some detailed discussion.

### **6.1 A subheading**

Blah blah blah

## 7 Conclusion

This section would contain the conclusions drawn from the entire body of work.

### 7.1 A subheading

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## 9 Appendix

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