



# COMMUNITY DETECTION WITH APPLICATIONS TO MULTIREFERENCE ALIGNMENT

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Final report

by

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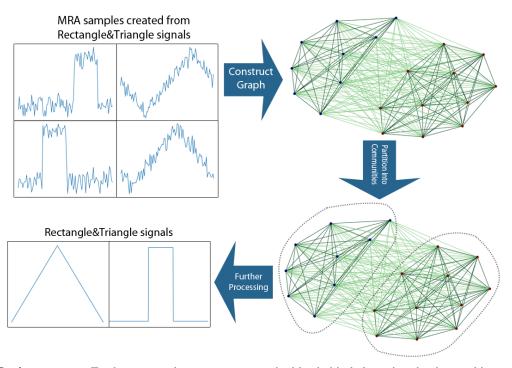
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#### **ABSTRACT**

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**

 $\mathbf{C}$ 

**CD** Community Detection. 3, 7

cryo-EM Cryogenic Electron Microscopy. 3, 7

 $\mathbf{M}$ 

**MRA** Multireference Alignment. 3, 7

 $\mathbf{S}$ 

**SNR** Signal To Noise. 7

#### 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, and 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 (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, 2]. In our project we will use Community Detection (CD) from the field of complex networks by converting cryo-EM data into a graph and applying CD on it to obtain classification of the heterogeneous cryo-EM data.

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

#### 1.1 Some subsection

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# 2 Background

This section should include a comprehensive review of prior work across the stated aims. It also provides a summary of the gaps in the current literature and is will be substantially longer than a background section in a manuscript.

# 2.1 Referencing Citations

Citations are straight forward and will be automatically sorted on rendering. Include your citations in the *references.bib* file. For examples, see this *handy citation guide*. Here's an example usage where I cite this project [3]. Boom!

# 2.2 Including figures

You might include a figure here...

...and reference it like so: Figure 2.

# 2.3 Making tables

Or maybe you'll make a table...

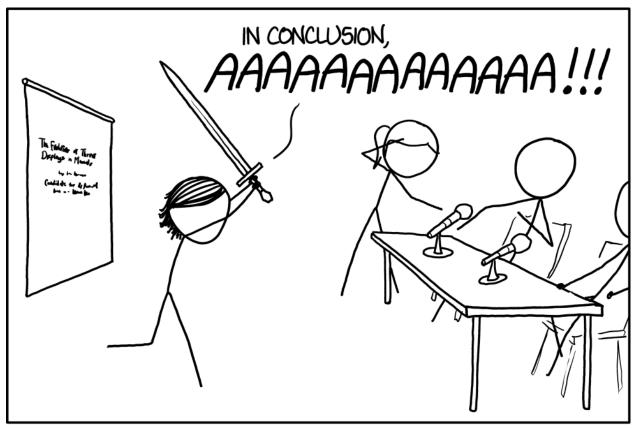
**Table 1:** Your first table.

Value 1	Value 2	Value 3
$\alpha$	$\beta$	$\gamma$
1	1110.1	a
2	10.1	b
3	23.113231	c

...an reference it too: Table 1

#### 2.4 Using Abbreviations

You may also use abbreviations like



THE BEST THESIS DEFENSE IS A GOOD THESIS OFFENSE.

**Figure 2: The best thesis defense is a good thesis offense.** A conceptual illustration of the celebrated thesis *offense*, an ambitious but often effective tactical maneuver.

# 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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