

Biopolymer Networks: Image Analysis, Reconstruction and Modeling

Pablo Hernandez-Cerdan

Supervisor: Prof. M.A.K Williams

Co-Supervisor: Prof. Geoff Jameson

Doctoral Oral Examination – August 8, 2018

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Motivation

Sources of Strain-Stiffening

- [Storm et al., 2005]: strain stiffening arises from non linearity of single chains. Under the assumption that the network is isotropic and homogeneous.
- [Onck et al., 2005], at the same time an alternative explanation of strain stiffening arises exclusively from network connectivity and relative orientation of the fibers.

Strain-Stiffening: Validity of Affine Deformation approximation in semi-flexible polymers

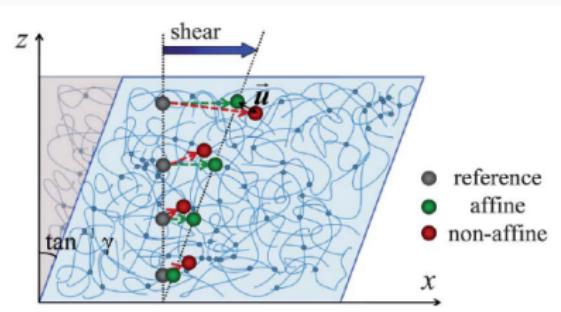
Affine transformations valid when:

- Isotropic and Homogeneous Network
- Stiff Chains
- Dense Networks

Non-Affine range when:

- Anisotropic Network
- Compliant Chains
- Coarse Networks

[Wilhelm and Frey, 2003]



Displacement of network points under affine and non-affine regimes. [Basu et al., 2011; Wen et al., 2012]

Goal of the thesis

Goals and research questions

- Going beyond the homogeneous and isotropic model of biopolymer networks: **Characterize the architecture** of connected filaments using images from different microscopy techniques depending on the size of the biopolymer.

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- How different architectures do influent the **mechanical properties**? Are completely different biopolymers sharing similar geometries?

Goals and research questions

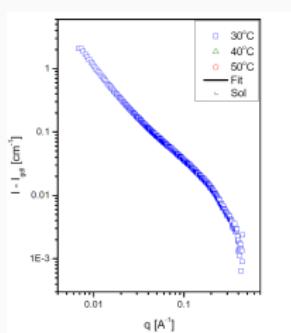
- Going beyond the homogeneous and isotropic model of biopolymer networks: **Characterize the architecture** of connected filaments using images from different microscopy techniques depending on the size of the biopolymer.
- How different architectures do influent the **mechanical properties**? Are completely different biopolymers sharing similar geometries?
- Develop an open-source, free, user friendly, tested, and well documented software for others to use with microscopy images.

Challenges

Gathering structure data:

Scattering: SAXS and SANS

- Study of peaks and fractality at different q values provides an **averaged** structural information (mesh size, width of single-chains)
- It does not require special sample preparation.
- Good statistics, fast, allow study of dynamics.
- **But**, it does not provide explicit 3D structure of exact connectivity.

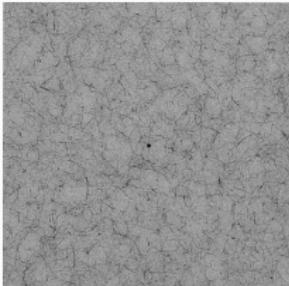


$I - I_0$ vs q Pectin from SAXS

To get detailed connectivity we need **3D microscopy**.

TEM tomography

- Necessary to reach polysaccharides scale.
- Sample preparation is hard.
Artifacts?
- **Working on validation method**
comparing it with scattering.



Confocal

- Suitable for most protein biopolymer networks.
- Sample preparation is more reliable.

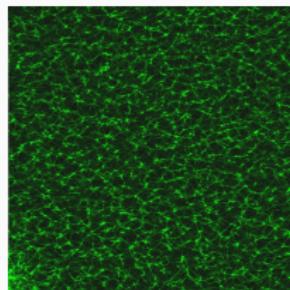


Image Analysis

Goal:

Process raw image data to get a spatial graph representation of the network.

Steps:

1. **Segmentation:** Extract object of interest from image. Binary image.
2. **Skeletonization:** Thin representation of the object.

The skeleton will then be adapted into a **Graph** for characterization.

Segmentation I

Goal: Extract feature or region of interest from the raw image.

Noise is the enemy. But also crowded environments from where only a specific feature is needed.

Main Segmentation Methods:

- **Threshold-Based:** Threshold at an intensity value. Entropy minimizing (Otsu) or other criteria.
- **Enhancement Filter:** Local-phase studies or eigenvalue analysis of Hessian matrix.
- **Deformable-Model:** Curve evolving under vector field to fit structure. LevelSet (closed curve) or Snakes (open).

Segmentation in Confocal and TEM images of biopolymers

Need of preprocessing steps to reduce noise and enhance features of interest.

Pre-processing pipeline:

- Multiscale characterization convolving image with gaussian operator of different sigmas/scales
- Denoise: Anisotropic edge-preserving filter.
- Enhancement Filter: Use a local-phase filter using a **monogenic-signal**, a N-D extension to the **analytic signal** used in modulation and demodulation of 1D communication signals.



Insight Toolkit: Registration and Segmentation

I am implementing a monogenic signal filter to ITK, the insight toolkit for image segmentation based on [Chenouard and Unser, 2011].

This filter applies operators in each direction of the FFT space, enhancing edge and line structures. It uses local phase information, and not absolute intensity, which helps detecting weak features.

It is almost finished. I have to do the eigenanalysis to the filter and contribute (again) to this open source library.

ITK is the main library for image analysis in C++, specially useful in segmentation of medical images and 3D stacks.

Segmentation after the enhancement of the monogenic filter

After enhancement with the monogenic filter two options:

- The monogenic signal phase can be used to detect lines and edges. Use this measure to detect edges (more reliable than gradient or Sobel). Then use a level-set method, where the edge-measure is used to set the external vector field constraining the evolution [Rajpoot et al., 2009].
- Exploit monogenic filter steering (rotation) properties. This allows to set an Eigensystem to find at each pixel the direction that maximizes the signal. Then threshold the enhanced image to get the segmentation [Chenouard and Unser, 2011].

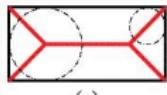
Skeletonization of segmented image

After segmentation, we have to thin the resulting binary object to a one-pixel wide representation that conserves topology.

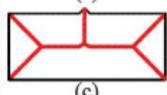
Skeletonization is really sensitive to noise in the borders, so a pruning is always required.

Global pruning:

- It applies after the skeleton has been extracted.
- Only takes into account length of branches removing short but thin branches that might be significant for the architecture.



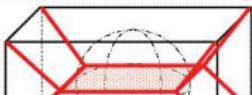
(a)



(c)

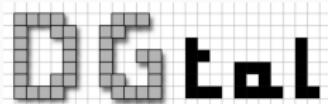
Local pruning:

- Novel method to pruning at the same time than skeleton is generated.
- The pruning is made locally, thanks to a measure of **length of branch versus thickness**.
- It conserves short branches that are locally thin, but deletes short branches that are thick (see figure)



(b)

Skeletonization: Cubical Complexes



DGTal:: Digital topology library

I have already contributed to DGtal the implementation of this local prune algorithm based on [Couprie and Bertrand, 2015].

And I am in the developing team!

VoxelComplex: CriticalKernels framework #1147

[Open](#) phcordan wants to merge 1 commit into 306d1-remaster from jscien:voxelcomplex-with-object-graph

Conversation 0 Commits 0 Files changed 37 +5,107 -321

phcordan commented on Mar 16

PR Description

Implementation of Critical Kernel framework based on M.Couprie and G.Bertrand articles:

- Asymmetric parallel 3D thinning scheme and algorithms based on isthmuses.
- Powerful Parallel and Symmetric 3D Thinning Schemes Based on Critical Kernels
- A 3D Sequential Thinning Scheme Based on Critical Kernels

Add general description of framework for docs.

Add LookUpTable Interface from #1155 (speeds an order of magnitude)

CLI script for testing in any image (future PR in DGtalTools)

Labels None yet

Milestone No milestone

Assignee No one assigned

Notifications

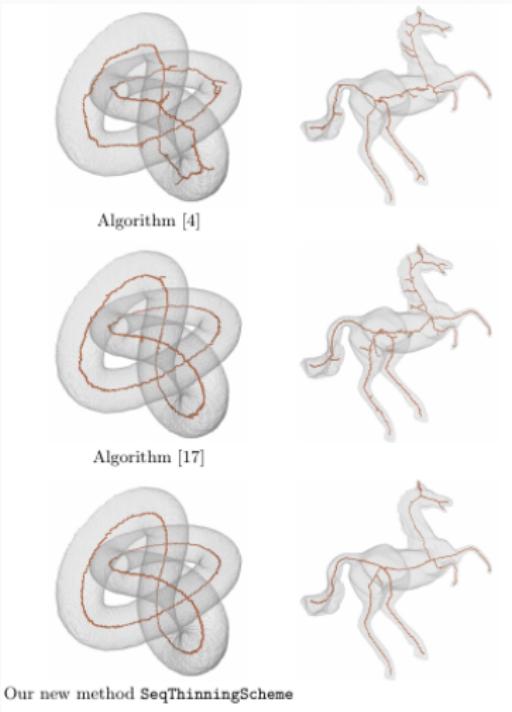
Unsubscribe You're receiving notifications because you authored the thread.

2 participants

Skeletonization: Cubical Complexes

Global pruning:

- Uses a framework called CubicalComplexes or VoxelComplexes, where a spel (voxel in 3D, pixel in 2D) is composed by points, lines and faces.
- This allow to define a topology property called Isthmus in all those components, that preserves topology in the skeletonization process.



Pipeline:

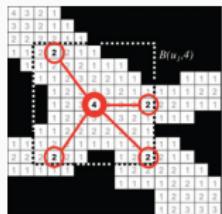
Multiscale analysis and denoise: Detect vessels of different radius.

Summary of image analysis

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Segmentation: Get a binary object that conserves features.



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Multiscale analysis and denoise: Detect vessels of different radius.

Segmentation: Get a binary object that conserves features.

Skeletonization: One-pixel wide (thin) representation of binary object, conserving topology.

Graph adaptor: Transform skeleton to a graph, to connect with ComplexSystems tools for characterization.



Graph Characterization

A graph is a representation of connected components in terms of nodes and edges/links.

Spatial Network of biopolymers:

- A node corresponds to a junction/crosslink of biopolymers.
- An edge represents the polymer-chain itself.

Graphs are a powerful tool connecting to the field of **Complex Systems**.

We want to take advantage of all those existing algorithms for **characterization** of soft materials.

Graphs: A Link to Complex Systems

With a graph representation of the system we can now link our spatial graph to standard complex network libraries.

IGraph C, R, Python (GPL licence)

Boost: Graph and GraphParallel C++ (MIT licence)

NetworkX Python (MIT licence)

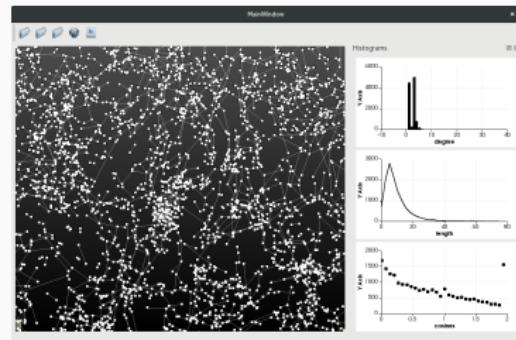


Generating Software Tools



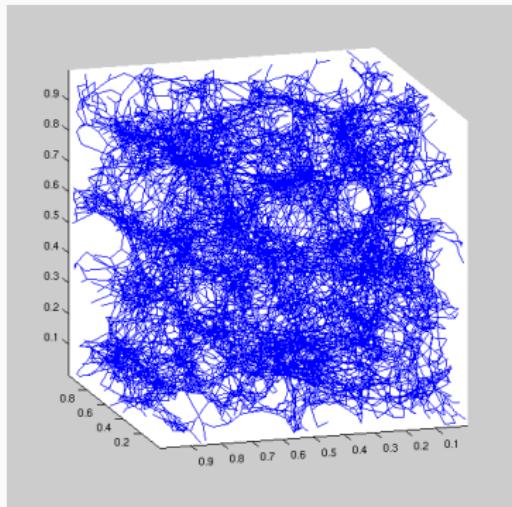
Radial FFT analysis to compare

images and SAXS:

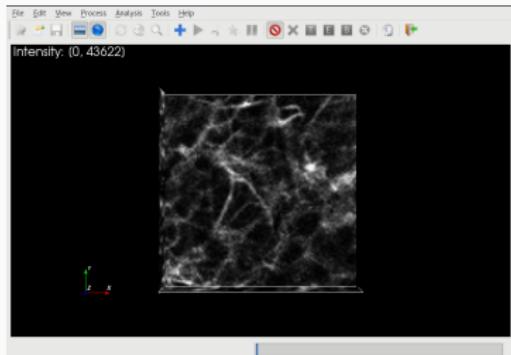


Compute statistical distributions from

graph.



Reconstruct in-silico network from
graph statistical distributions

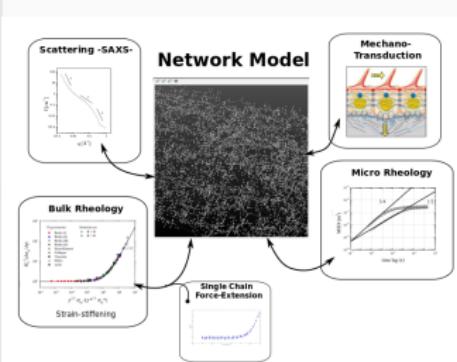


Not revealed yet (sorry!): Merge of

software when segmentation is ready.
SGEXT: Spatial Graph Extractor.
Name suggestions welcome!
(MAIDEN?)

Exploring network geometries:

- When does architecture matter? What is its role at lower scales?
- Gather best image analysis techniques for biopolymers.
- Link to complex network libraries for graph analysis. **Reconstruct in-silico networks from it**
- **The dream** would be to provide soft-matter scientists with a reliable tool to **characterize** their materials, linking to the field of ComplexSystems.



Acknowledgments



**The MacDiarmid
Institute**
*for Advanced Materials
and Nanotechnology*



Main Supervisor: **Prof. M.A.K Williams**

- Andrew Leis. CSIRO Animal Health. Australia.
- Leif Lundin. SP Food and Bioscience. Sweden.



Dr. Brad Mansel, New Zealand

Visit us in NZ or online at:
www.biophysics.ac.nz

Thanks for your attention!

Follow development live in github

Keep up to date with further development at my github page:

github.com/phcerdan

Get this beamer theme from:

github.com/matze/mtheme



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