IMAGE ANALYSIS ON BIOPOLYMER NETWORKS

Characterization using graphs

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MOTIVATION: ROLE OF NETWORK ARCHITECTURE

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

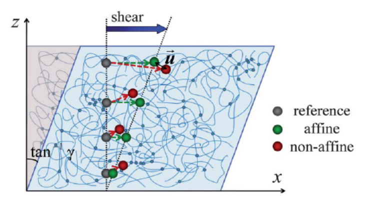
STRAIN-STIFFENING: VALIDITY OF AFFINE DEFORMATION APPROXIMATION IN SEMI-FLEXIBLE POLYMERS

Affine transformations valid when:

In Homogeneous and Isotropic Network

- Stiff Chains
- Dense Networks

[Wilhelm and Frey, 2003]



[Basu et al., 2011; Wen et al., 2012]

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Non-Affine range when:

In Homogeneous and Isotropic Network

- Compliant Chains
- Coarse Networks

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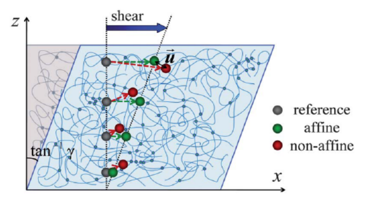

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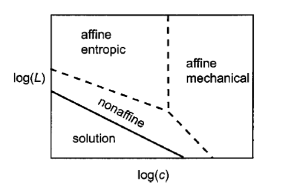

L: Molecular Weight, **c:** Concentration

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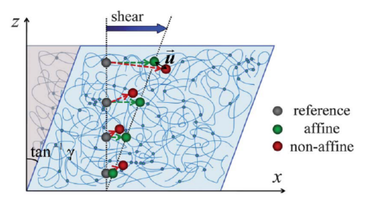

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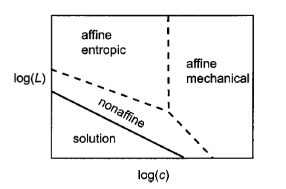

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Pre-stress and architecture role:

Affine approx. is valid at constrained networks

- Initial pre-stress constrains networks. [Cioroianu et al., 2015]

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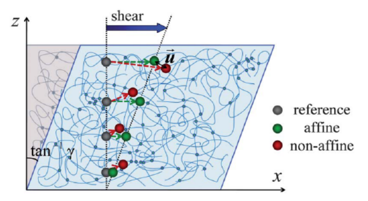

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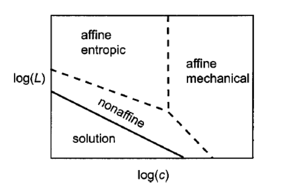

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Pre-stress and architecture role:

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- Role of **Anisotropy** or **Architecture**?

- 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

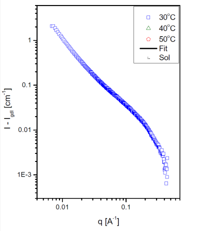
- Going beyond the homogeneous and isotropic model of biopolymer networks: **Characterize the architecture** of connected filaments using images from different microscopy techniques depending on the size of the biopolymer.
- How different architectures do influent the **mechanical properties**? Are completely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

STEPS TO CHARACTERIZE THE NETWORK

- Gathering the images. Microscopy.
- Image analysis. Skeletonization.
- Characterize the image with a graph representation.

GATHERING STRUCTURE DATA:

- 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.

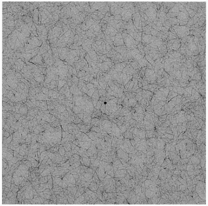


I vs q Pectin from SAXS

To get better architecture 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.

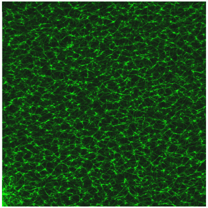


IMAGE ANALYSIS

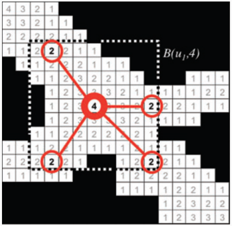
Goal:

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

Anisotropic denoise: Denoise conserving edges.

Binarization: Choose threshold that best conserves architecture.

Distance Map: Distance to the background for each pixel.



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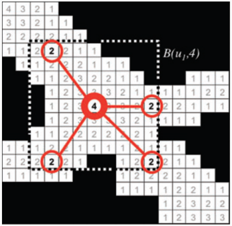

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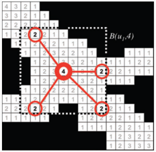
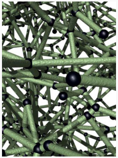
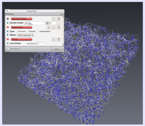
Branch Merging and Pruning: Fill gaps and remove short branches.







Network / Spatial Graph

Pre-processing techniques

1. Hessian Matrix: Eigenvalues to detect vesselness.
2. Anisotropic Difussion: Denoise, keeping edges information.
3. Multiscale characterization with gaussian operator.

Other Skeleton Methods

1. Open Contours: Snakes
2. Template Matching
3. Morphology Operators

GRAPH CHARACTERIZATION

GRAPHS: A LINK TO COMPLEX SYSTEMS

We can now link our spatial graph to standard complex network libraries.

IGraph C, R, Python (GPL licence)

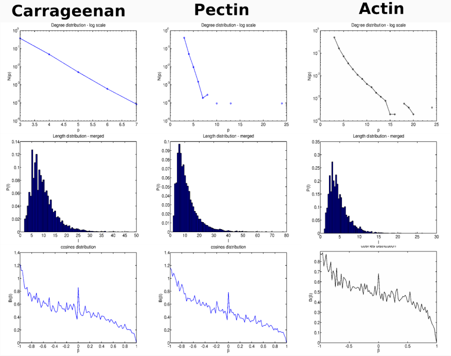
Boost: Graph and GraphParallel C++ (MIT licence)

NetworkX Python (MIT licence)

RESULTS: PROOF OF CONCEPT

Three Networks analyzed:

- Polysaccharides using TEM: Pectin, Carrageenan
- Proteins using Confocal: Actin (Collagen from literature [Lindström et al., 2013]).



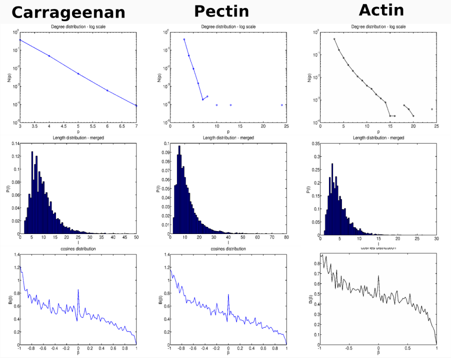
Degree: Geometrical distribution
$N(p) = q(1-q)^{p-3}$
where $q = 1/(Z-2)$, and Z is the average node degree.

Node-to-node dist.: Log-normal
$P(\ell) = \frac{1}{\ell s\sqrt{2\pi}} \exp\left(-\frac{(\mu - \ln \ell)^2}{2s^2}\right)$

Edge relative orientation: Power-Series
$B(\beta) = \sum_{k=1}^{m} b_k (1-\beta)^{2k-1}$

RESULTS: PROOF OF CONCEPT

Statistical distributions of local graph properties: Showing same functional forms



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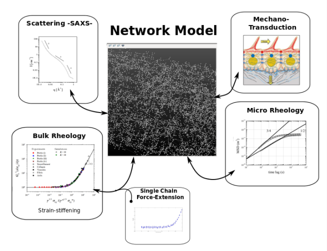
Digging up the network geometry

- 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 input force-extension curve of single chains + network architecture to get bulk rheology. But initial configuration setup and pre-stress play a role in simulations.



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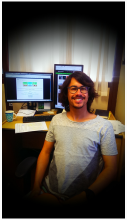

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- Leif Lundin. SP Food and Bioscience. Sweden.

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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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