

Computational Modelling and Simulations of Biomolecular Systems

Dr. Adolfo Poma

Assistant Professor at the Soft Matter and Biosystems Division, Warsaw, Poland



– Public Seminar for Habilitation –



Entirely supported by Polish National Science Centre (NCN) "Self-assembly and nanomechanical characterization of cellulose microfibril", 2018-2022. Grant No. 2017/26/D/N/Z1/00466



Fundacja na rzecz
Nauki Polskiej

Unia Europejska
Europejski Fundusz
Rozwoju Regionalnego



Main References for This Seminar

- A1 **Poma, A. B.**†, Chwastyk, M., Cieplak, M. (2015). Polysaccharide–protein complexes in a coarse-grained model. *J. Phys. Chem. B*, 119(36), 12028–12041.
- A2 **Poma, A. B.**†, Chwastyk, M., Cieplak, M. (2016). Coarse-grained model of the native cellulose I and the transformation pathways to the I allomorph. *Cellulose*, 23(3), 1573–159.
- A3 **Poma, A. B.**†, Chwastyk, M., Cieplak, M. (2017). Elastic moduli of biological fibers in a coarse-grained model: Crystalline cellulose and -amyloids. *Phys. Chem. Chem. Phys.*, 19(41), 28195–28206.
- A4 Thu, T. T. M.†, Moreira, R. A., Weber, S. A., **Poma, A. B.**† (2022). Molecular Insight into the Self-Assembly Process of Cellulose I Microfibril. *Int. J. Mol. Sci.*, 23(15), 8505
- A5 Moreira, R. A.†, Weber, S. A., **Poma, A. B.**† (2022). Martini 3 Model of cellulose microfibrils: on the route to capture large conformational changes of polysaccharides. *Molecules*, 27(3), 976.

Outline

1 Motivation

- From idea to realisation: The computational microscope
- Method Development
 - Gō-like Approach
 - GōMartini

2 Modelling and Simulation of Biomolecular Systems

- Cellulose fibrils: Structure and Dynamics
 - Biotechnological relevance of cellulose
 - Molecular Structure of Cellulose I
 - CG Model of Cellulose
 - Molecular Insights into Self-assembly Process of Cellulose
- Nanomechanics of biological fibrils through simulations
 - Continuum Mechanics at the Nanoscale
 - Nanomechanics of β -Amyloid Fibrils

3 Summary

Table of Contents

1 Motivation

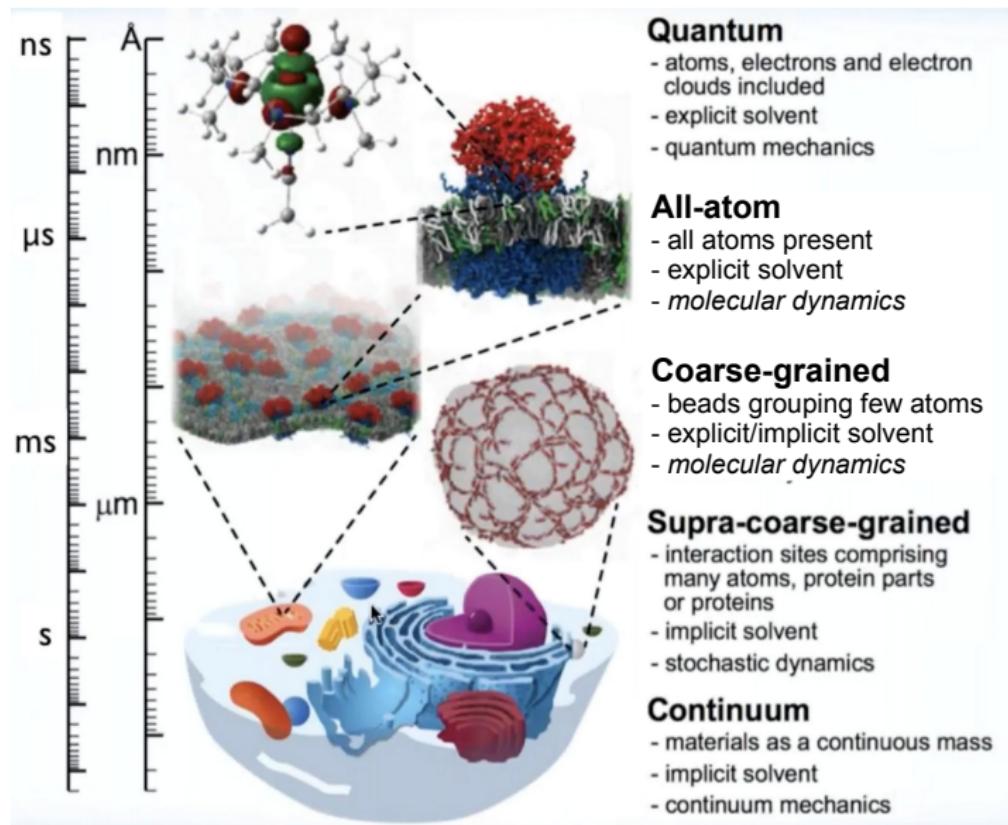
- From idea to realisation: The computational microscope
- Method Development
 - Gō-like Approach
 - GōMartini

2 Modelling and Simulation of Biomolecular Systems

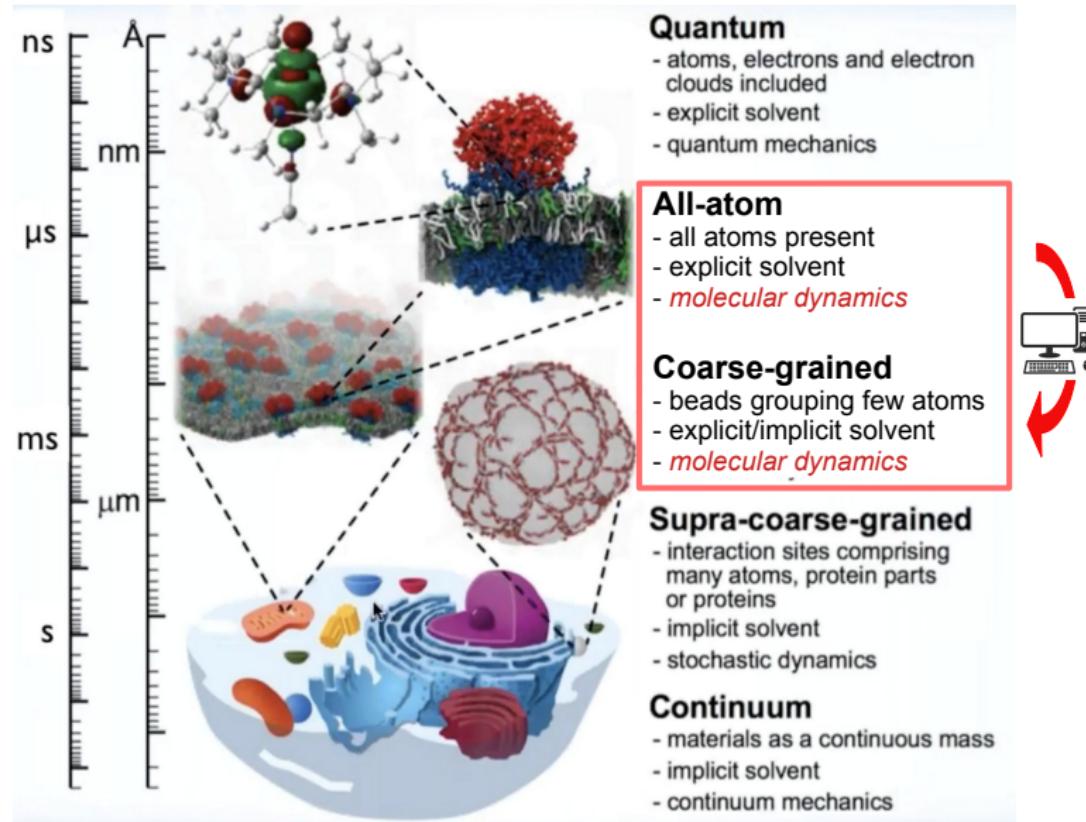
- Cellulose fibrils: Structure and Dynamics
 - Biotechnological relevance of cellulose
 - Molecular Structure of Cellulose I
 - CG Model of Cellulose
 - Molecular Insights into Self-assembly Process of Cellulose
- Nanomechanics of biological fibrils through simulations
 - Continuum Mechanics at the Nanoscale
 - Nanomechanics of β -Amyloid Fibrils

3 Summary

From idea to realisation: A computational microscope



From idea to realisation: A computational microscope



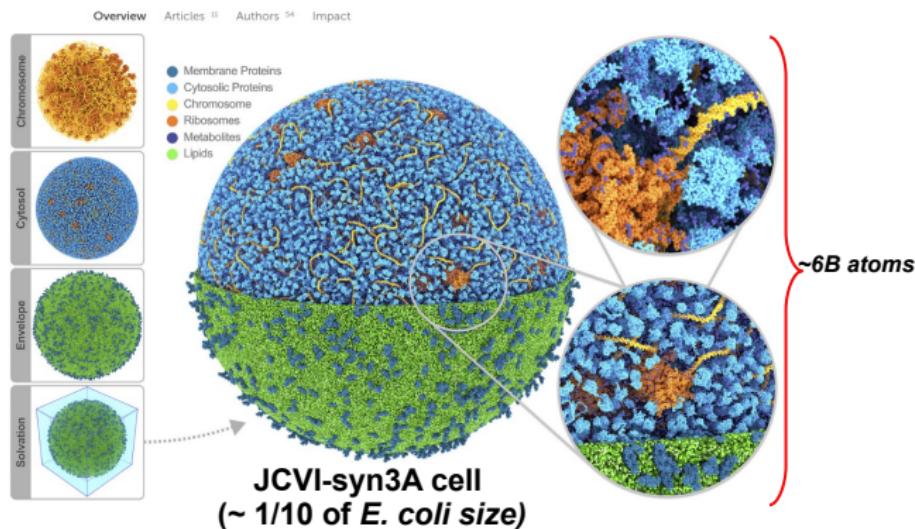
From idea to realisation: A computational microscope

Frontiers in Chemistry > Theoretical and Computational ... > Research Topics > Recent Advances in Computation...

Recent Advances in Computational Modelling of Biomolecular Complexes

Poblete S, Pantano S, Okazaki K-i, Liang Z, Kremer K and Poma AB* (2023), Editorial: Recent advances in computational modelling of biomolecular complexes. *Front. Chem.* 11:1200409.

1,350 Total Downloads 16k Views Download PDF → Download EPUB →



Stevens JA et al. (2023), Molecular dynamics simulation of an entire cell. *Front. Chem.* 11:1106495.

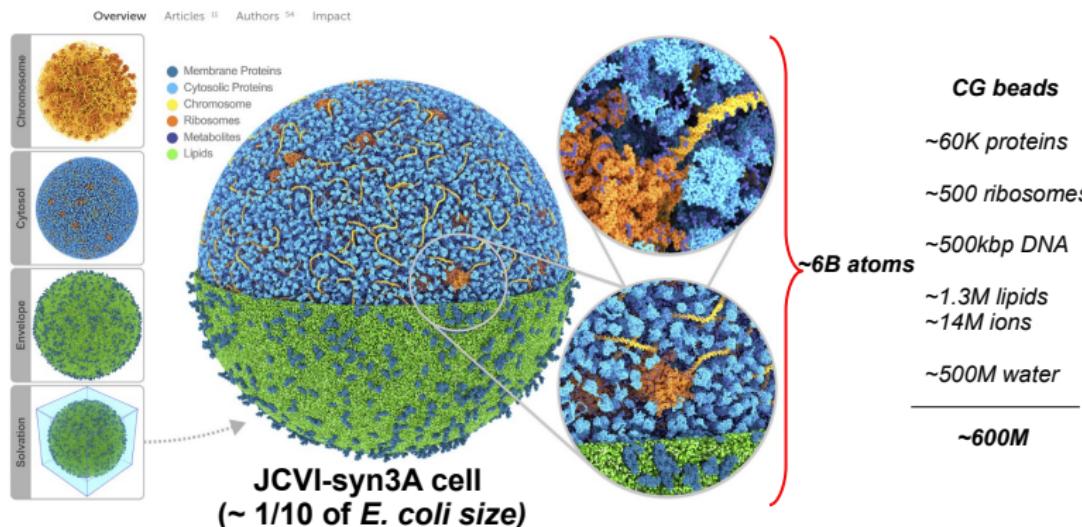
From idea to realisation: A computational microscope

Frontiers in Chemistry > Theoretical and Computational ... > Research Topics > Recent Advances in Computatio...

Recent Advances in Computational Modelling of Biomolecular Complexes

Poblete S, Pantano S, Okazaki K-i, Liang Z, Kremer K and Poma AB* (2023), Editorial: Recent advances in computational modelling of biomolecular complexes. *Front. Chem.* 11:1200409.

1,350 Total Downloads 16k Views Download PDF → Download EPUB →



Stevens JA et al. (2023), Molecular dynamics simulation of an entire cell. *Front. Chem.* 11:1106495.

Table of Contents

1 Motivation

- From idea to realisation: The computational microscope

● Method Development

- Gō-like Approach
- GōMartini

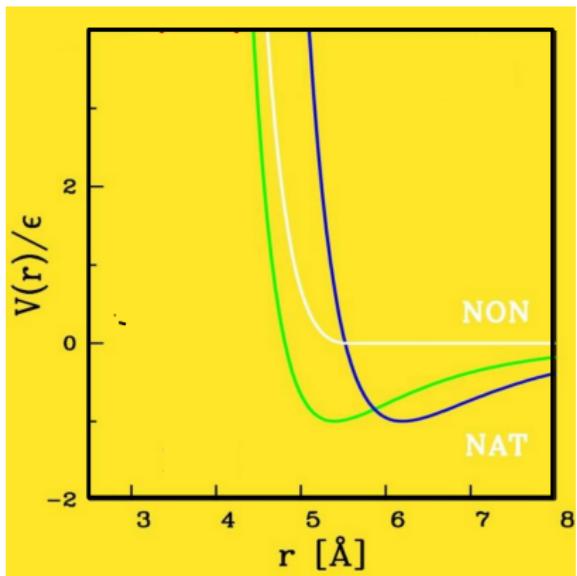
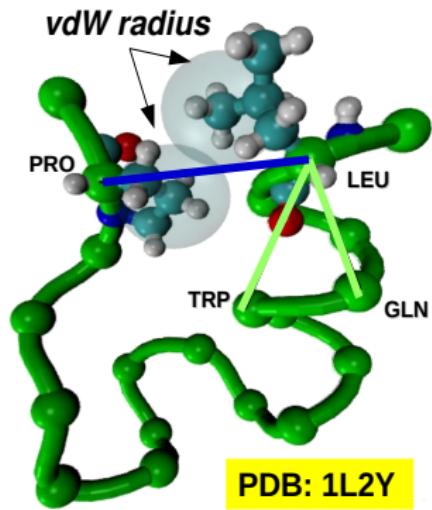
2 Modelling and Simulation of Biomolecular Systems

- Cellulose fibrils: Structure and Dynamics
 - Biotechnological relevance of cellulose
 - Molecular Structure of Cellulose I
 - CG Model of Cellulose
 - Molecular Insights into Self-assembly Process of Cellulose
- Nanomechanics of biological fibrils through simulations
 - Continuum Mechanics at the Nanoscale
 - Nanomechanics of β -Amyloid Fibrils

3 Summary

Gō-like Approach

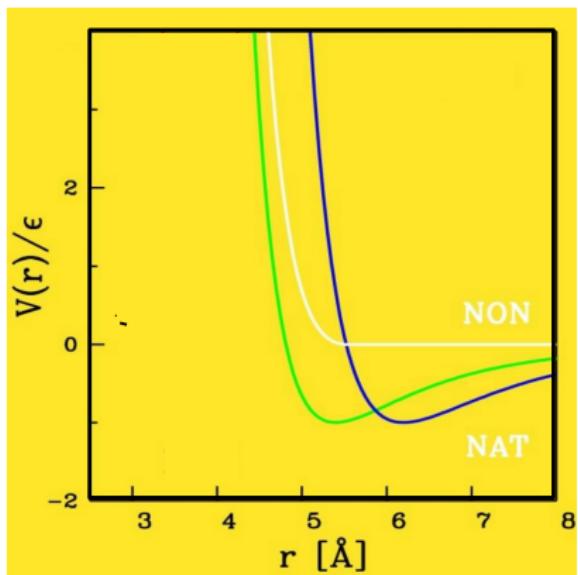
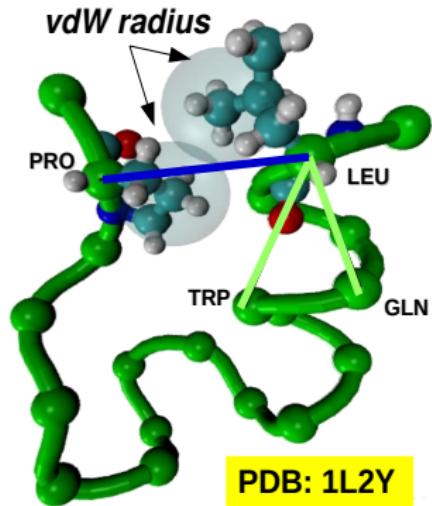
Developed in collaboration with Prof. M. Cieplak (1950-2021) and Dr. M. Chwastyk at IFPAN.



- Calculate atomic overlap between N,C and O atoms
- σ_{ij} calculated based on $r_{\min} = d(|C_i^\alpha - C_j^\alpha|)$ such $\sigma_{ij} = r_{\min}/2^{1/6}$
$$U_{\text{native}} = U_{\text{bonded}}^{\text{NAT}}(k_r, k_\theta, k_\phi) + \sum_{i < j}^{\text{NAT}} 4e' \left[\left(\frac{\sigma_{ij}}{r_{ij}} \right)^{12} - \left(\frac{\sigma_{ij}}{r_{ij}} \right)^6 \right] \text{ and } U_{\text{non-native}} = \sum_{i < j}^{\text{NON}} 4e' \left(\frac{r_{\text{cut}}}{r_{ij}} \right)$$
- Determine contacts using OV and rCSU (See <http://pomalab.ippt.pan.pl/GoContactMap>).

Gō-like Approach

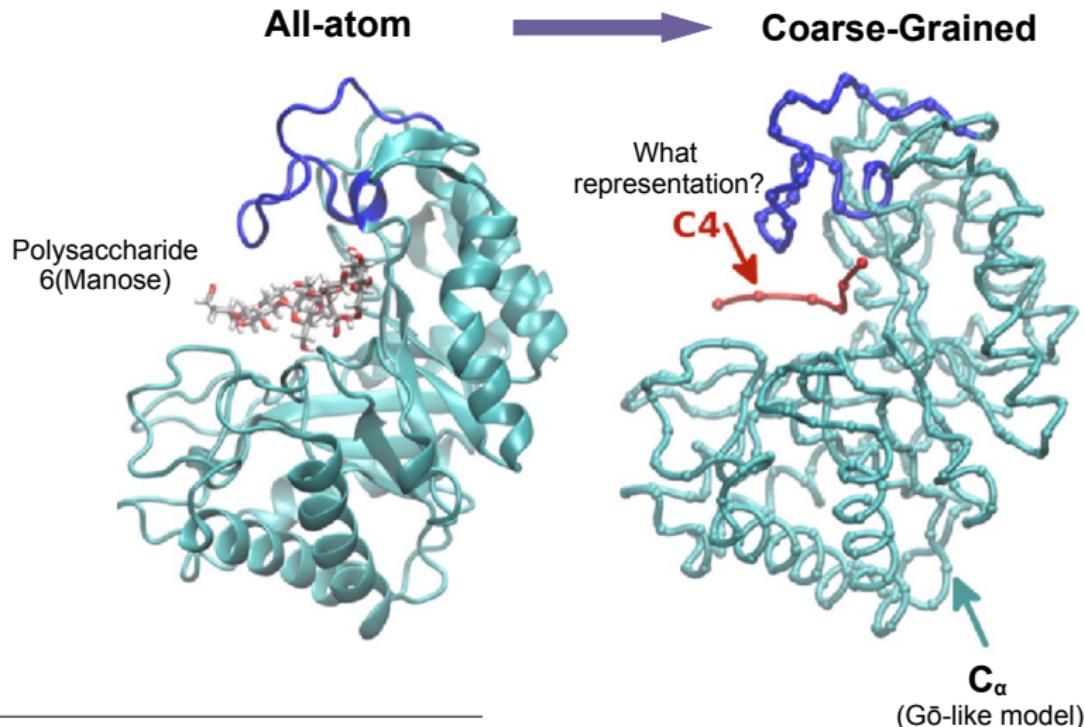
Developed in collaboration with Prof. M. Cieplak (1950-2021) and Dr. M. Chwastyk at IFPAN.



- Calculate atomic overlap between N,C and O atoms
- σ_{ij} calculated based on $r_{\min} = d(|C_i^\alpha - C_j^\alpha|)$ such $\sigma_{ij} = r_{\min}/2^{1/6}$
$$U_{\text{native}} = U_{\text{bonded}}^{NAT}(k_r, k_\theta, k_\phi) + \sum_{i < j}^{NAT} 4\epsilon' \left[\left(\frac{\sigma_{ij}}{r_{ij}} \right)^{12} - \left(\frac{\sigma_{ij}}{r_{ij}} \right)^6 \right] \text{ and } U_{\text{non-native}} = \sum_{i < j}^{NON} 4\epsilon' \left(\frac{r_{cut}}{r_{ij}} \right)$$
- Determine contacts using OV and rCSU (See <http://pomalab.ippt.pan.pl/GoContactMap>).

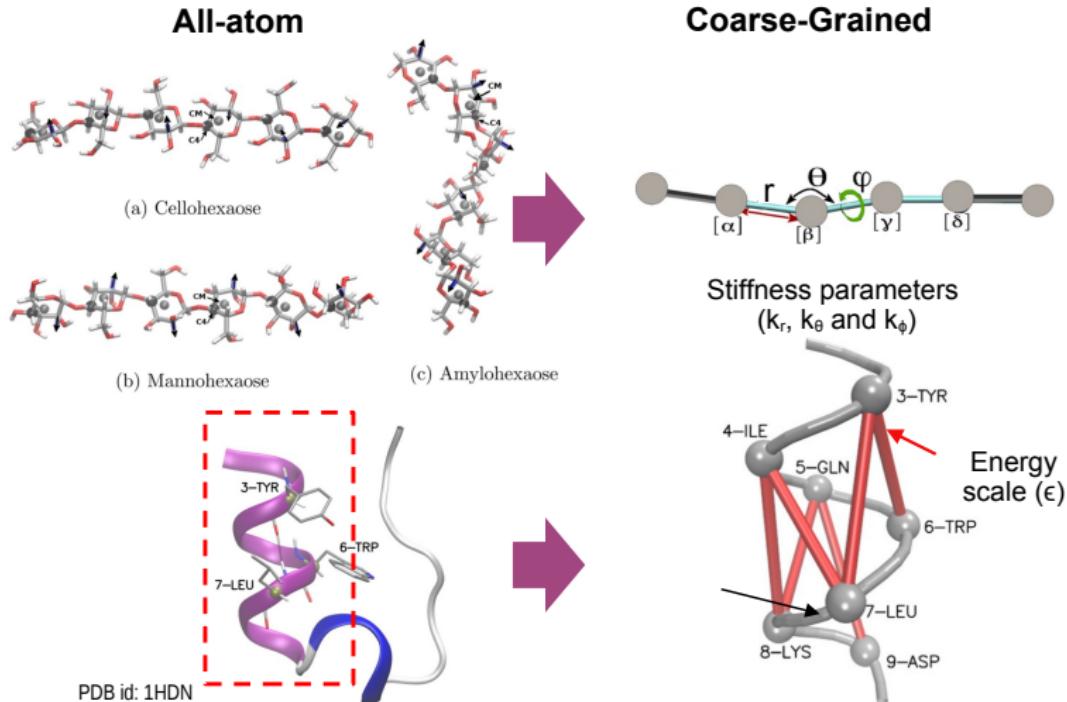
Gō-like Approach

Reparametrizing ϵ and stiffness constants (i.e. k_r , k_θ and k_ϕ) for protein-sugar complex [A1].



Gō-like Approach

Reparametrizing ϵ and stiffness constants (i.e. k_r , k_θ and k_ϕ) for protein-sugar complex [A1].



Gō-like Approach

Results

[1] Define, $V_{CG}(q) = k_q(q - q_0)^2$ and perform CG-MD

[2] Employ iterative Boltzmann Inversion method (Moore et al 2014)

$$V^{i+1}_{CG} = V^i + k_B T \ln[P_{CG}(q)/P_{ref}(q)], \quad P_{ref}(q) \text{ is the atomistic distribution}$$

[3] Get $P_{CG}(q)$ and improve the form of $V_{CG}(q) \rightarrow$ finally get a converged k_q

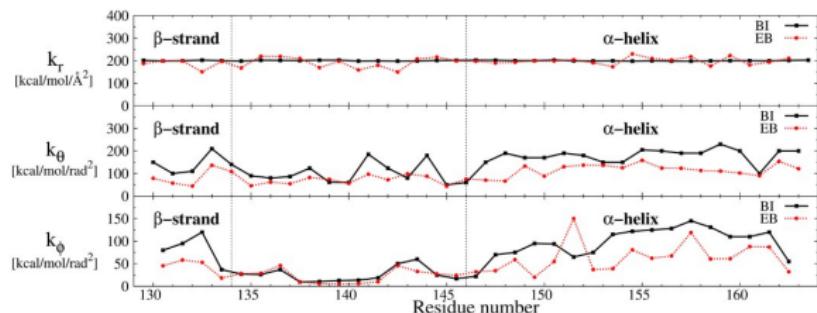
Molecular Stiffness

Sugar

	BI
r	$k_r [\text{kcal/mol}/\text{\AA}^2]$
cellohexaose	41.0 \pm 2.4
mannohexaose	29.0 \pm 2.2
amylohexaose	23.4 \pm 1.8
cellohexaose ^{HB}	100.8 \pm 3.2
AM cellulose	115.68
OR cellulose	219.31
CE cellulose	368.10
cellulose	179.92
	BI
θ	$k_\theta [\text{kcal/mol}/\text{rad}^2]$
cellohexaose	40.1 \pm 3.4
mannohexaose	27.9 \pm 4.4
amylohexaose	17.1 \pm 3.1
cellohexaose ^{HB}	40.5 \pm 3.1
AM cellulose	127.53
OR cellulose	401.52
CE cellulose	516.25
cellulose	212.00

~1/5

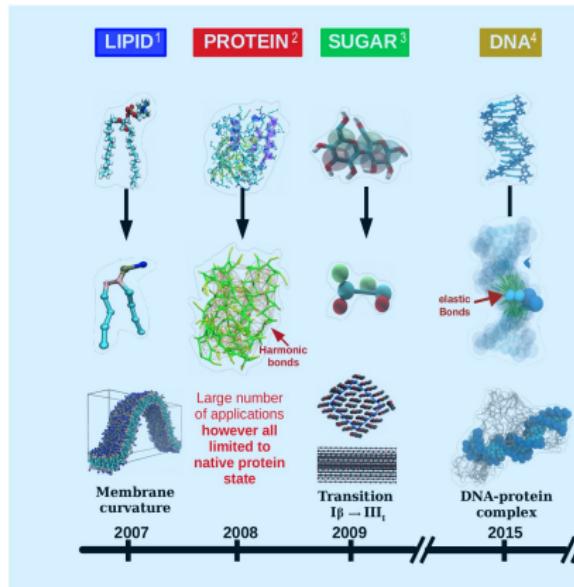
Protein



Moore, T. C., et al. (2014). J. Chem. Phys. 140(22), 06B606_1

GōMartini Approach

Biomolecular simulation is challenging because of the different biomolecules and multitude of spatial and temporal scales involved. CG models replace atomistic detail with lower resolution models and allow to reach large length and time scales.



MARTINI 1.0

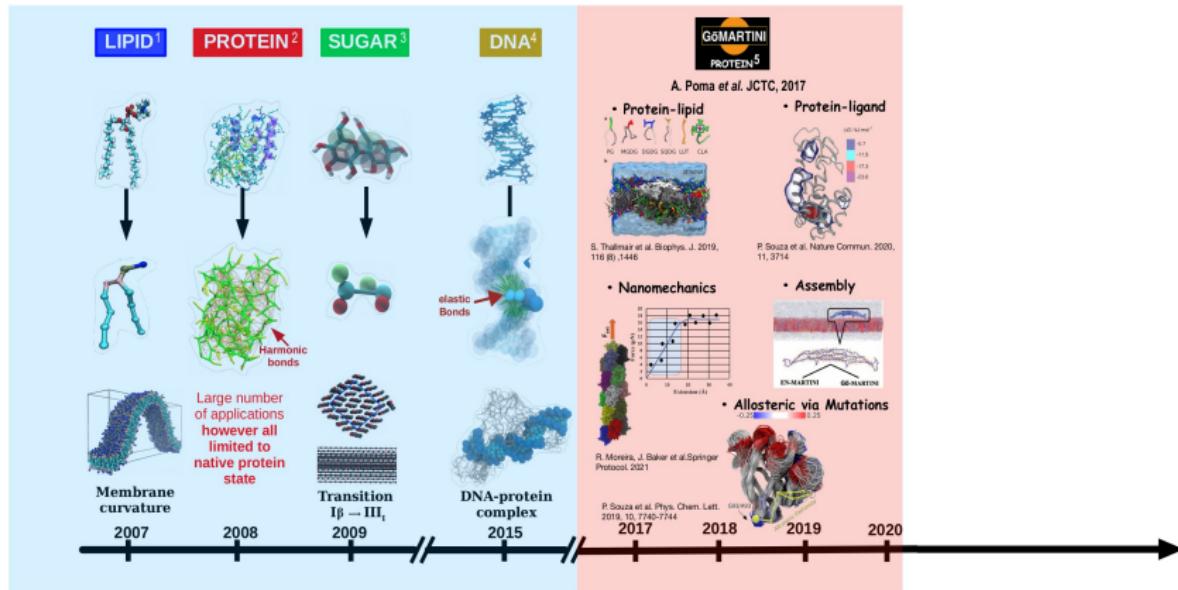
- [1] S.J. Marrink et al. JPCB 111, 7812 (2007)
- [2] L. Monticelli et al. JCTC 4, 819 (2008)

MARTINI 2.0

- [3] C.A. Lopez et al. JCTC 5, 3195 (2009)
- [4] J.J. Uusitalo et al. JCTC 11, 3932 (2015)

GōMartini Approach

Biomolecular simulation is challenging because of the different biomolecules and multitude of spatial and temporal scales involved. CG models replace atomistic detail with lower resolution models and allow to reach large length and time scales.



MARTINI 1.0

- [1] S.J. Marrink et al. JPCB 111, 7812 (2007)
- [2] L. Monticelli et al. JCTC 4, 819 (2008)

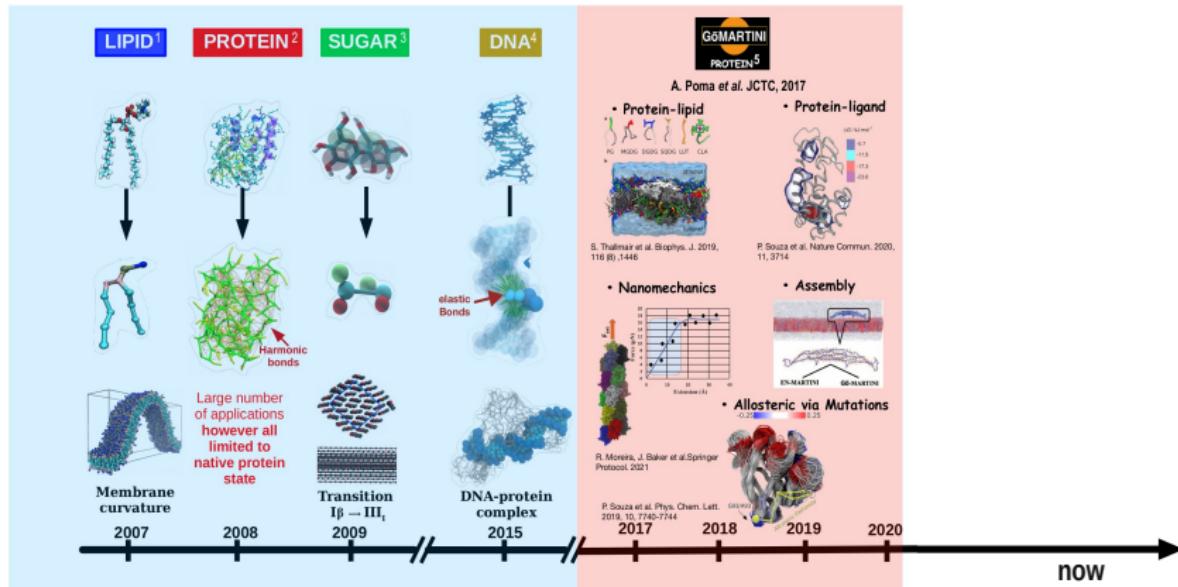
MARTINI 2.0

- [3] C.A. Lopez et al. JCTC 5, 3195 (2009)
- [4] J.J. Uusitalo et al. JCTC 11, 3932 (2015)

- [5] A.B Poma et al. JCTC 13, 1366 (2017)

GōMartini Approach

Biomolecular simulation is challenging because of the different biomolecules and multitude of spatial and temporal scales involved. CG models replace atomistic detail with lower resolution models and allow to reach large length and time scales.



MARTINI 1.0

- [1] S.J. Marrink et al. JPCB 111, 7812 (2007)
- [2] L. Monticelli et al. JCTC 4, 819 (2008)

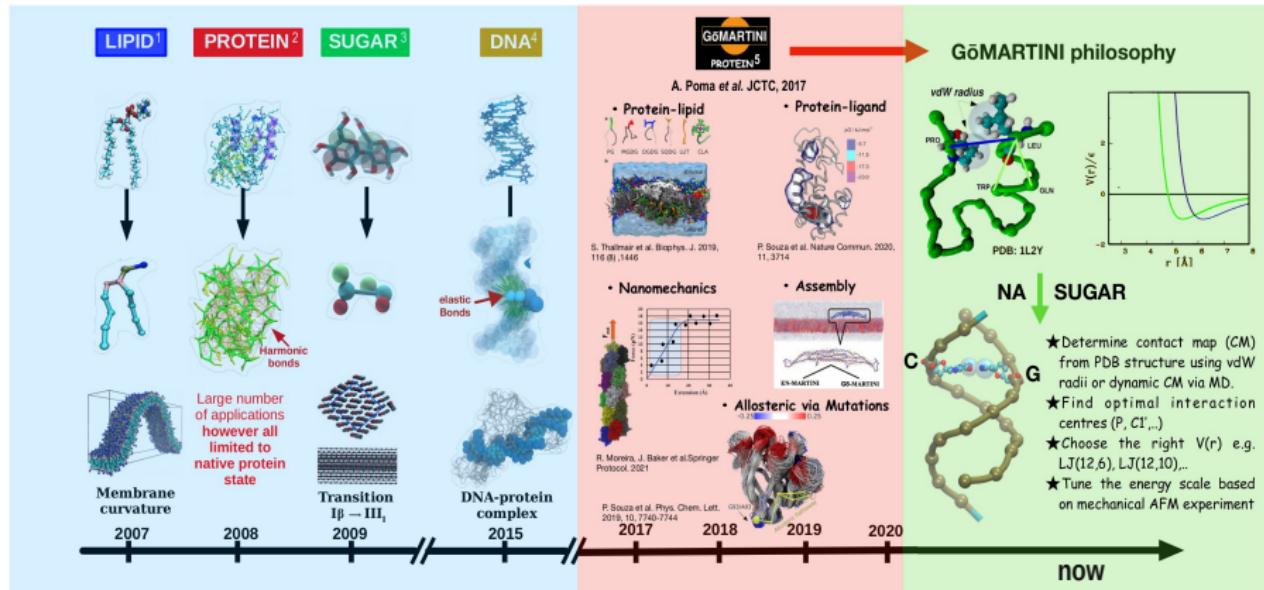
MARTINI 2.0

- [3] C.A. Lopez et al. JCTC 5, 3195 (2009)
- [4] J.J. Uusitalo et al. JCTC 11, 3932 (2015)

- [5] A.B Poma et al. JCTC 13, 1366 (2017)

GōMartini Approach

Biomolecular simulation is challenging because of the different biomolecules and multitude of spatial and temporal scales involved. CG models replace atomistic detail with lower resolution models and allow to reach large length and time scales.



MARTINI 1.0

- [1] S.J. Marrink et al. JPCB 111, 7812 (2007)
- [2] L. Monticelli et al. JCTC 4, 819 (2008)

MARTINI 2.0

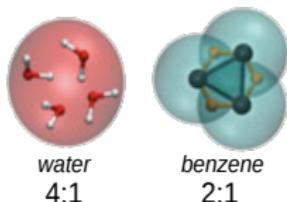
- [3] C.A. Lopez et al. JCTC 5, 3195 (2009)
- [4] J.J. Uusitalo et al. JCTC 11, 3932 (2015)

MARTINI 3.0⁶

- [5] A.B. Poma et al. JCTC 13, 1366 (2017)
- [6] P. Souza et al. Nature Methods 18, 382 (2021)
- [A5] R. Moreira, S.A. Weber, A.B. Poma. Molecules, 27(3), 976 (2022)

GōMartini Approach

Mapping Scheme



Type of CG particles

Types

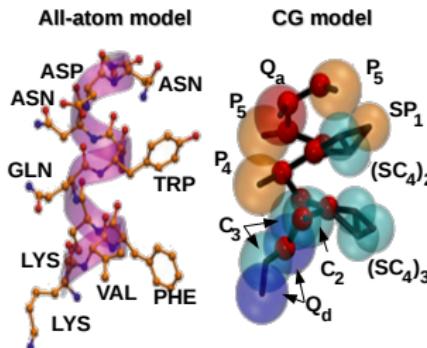
Polar (P)
Non Polar (N)
Apolar (C)
Charged (Q)

Subtypes (HB)

d = donor
a = acceptor
da = both
0 = none

Degree of Polarity
1 (low) to 5 (high)

Note: for ring-like structure is defined a new type called "S".



Martini Force-Field

$$\mathcal{U} = U_{\text{bonded}} +$$

$$\sum_{i < j} \sum_j \frac{q_i q_j}{4\pi\epsilon_0\epsilon_{\text{rel}} r_{ij}} + \sum_{i < j} \sum_j 4\epsilon_{ij} \left[\left(\frac{\sigma_{ij}}{r_{ij}} \right)^{12} - \left(\frac{\sigma_{ij}}{r_{ij}} \right)^6 \right] + \sum_{i < j}^{NAT} 4\epsilon' \left[\left(\frac{\sigma_{ij}}{r_{ij}} \right)^{12} - \left(\frac{\sigma_{ij}}{r_{ij}} \right)^6 \right]$$

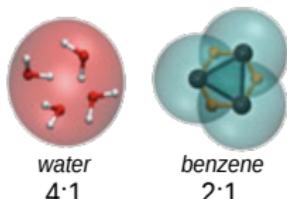
Electrostatics between charged (Q) particles is mediated by Coulomb interaction with explicit screening

Typical effective size of particle $\sigma \sim 0.47\text{nm}$ (rings bead 4.3\AA) and the energy strength ranges from $\epsilon = 2 - 5.6 \text{ kJ/mol}$.

Gō-like model defined between C_α atoms.

GōMartini Approach

Mapping Scheme



Type of CG particles

Types

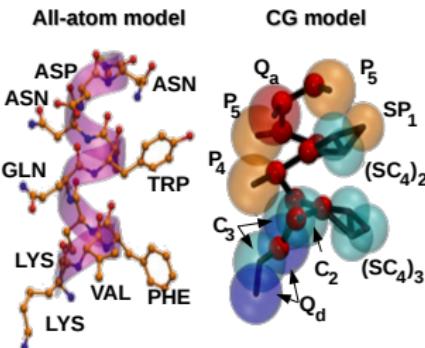
Polar (P)
Non Polar (N)
Apolar (C)
Charged (Q)

Subtypes (HB)

d = donor
a = acceptor
da = both
0 = none

Degree of Polarity
1 (low) to 5 (high)

Note: for ring-like structure is defined a new type called "S".



Martini Force-Field

$$\mathcal{U} = U_{\text{bonded}} +$$

$$\sum_{i < j} \sum_j \frac{q_i q_j}{4\pi\epsilon_0\epsilon_{\text{rel}} r_{ij}} + \sum_{i < j} \sum_j 4\epsilon_{ij} \left[\left(\frac{\sigma_{ij}}{r_{ij}} \right)^{12} - \left(\frac{\sigma_{ij}}{r_{ij}} \right)^6 \right] + \sum_{i < j}^{NAT} 4\epsilon' \left[\left(\frac{\sigma_{ij}}{r_{ij}} \right)^{12} - \left(\frac{\sigma_{ij}}{r_{ij}} \right)^6 \right]$$

Electrostatics between charged (Q) particles is mediated by Coulomb interaction with explicit screening

Typical effective size of particle $\sigma \sim 0.47\text{nm}$ (rings bead 4.3\AA) and the energy strength ranges from $\epsilon = 2 - 5.6 \text{ kJ/mol}$.

Gō-like model defined between C_α atoms.

Table of Contents

1 Motivation

- From idea to realisation: The computational microscope
- Method Development
 - Gō-like Approach
 - GōMartini

2 Modelling and Simulation of Biomolecular Systems

● Cellulose fibrils: Structure and Dynamics

- Biotechnological relevance of cellulose
- Molecular Structure of Cellulose I
- CG Model of Cellulose
- Molecular Insights into Self-assembly Process of Cellulose

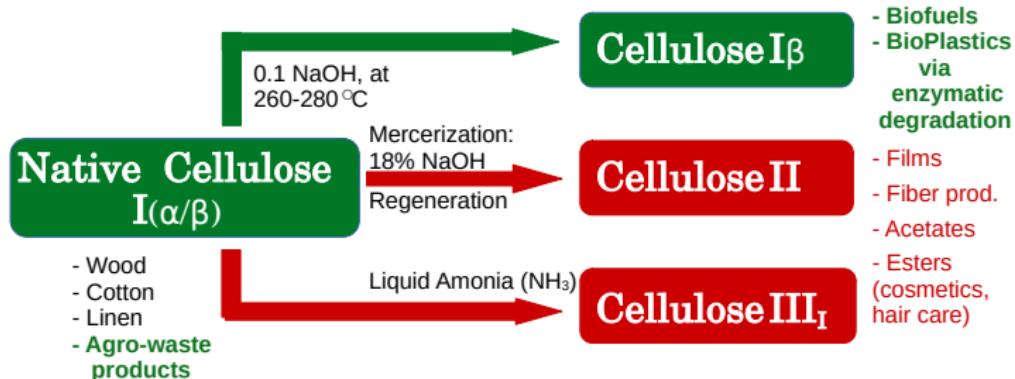
● Nanomechanics of biological fibrils through simulations

- Continuum Mechanics at the Nanoscale
- Nanomechanics of β -Amyloid Fibrils

3 Summary

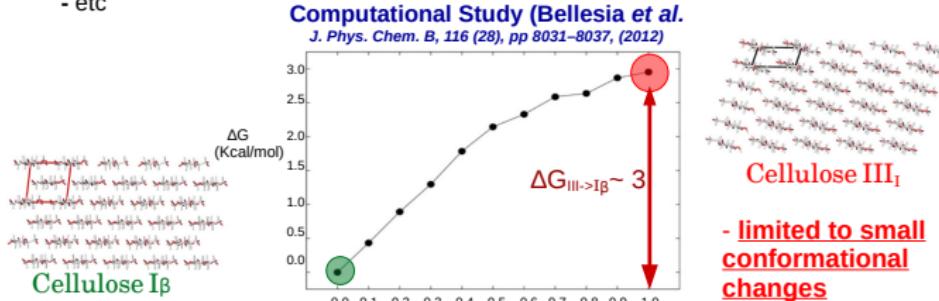
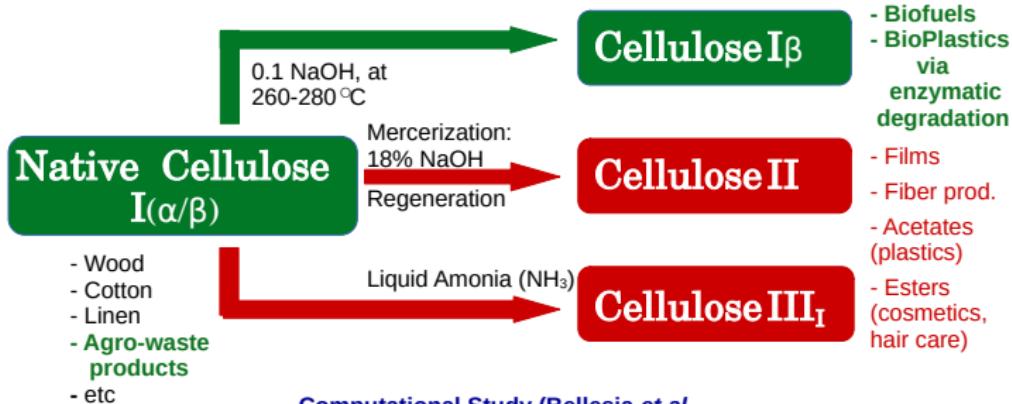
Biotechnological relevance of cellulose

Interconversion of Native Cellulose I



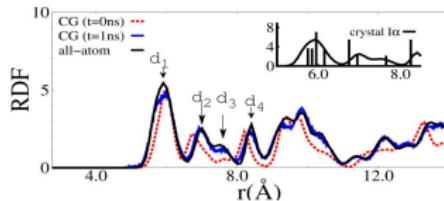
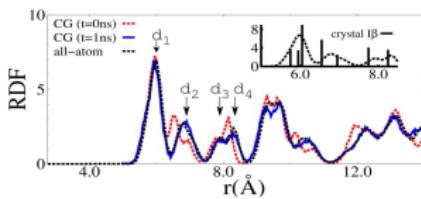
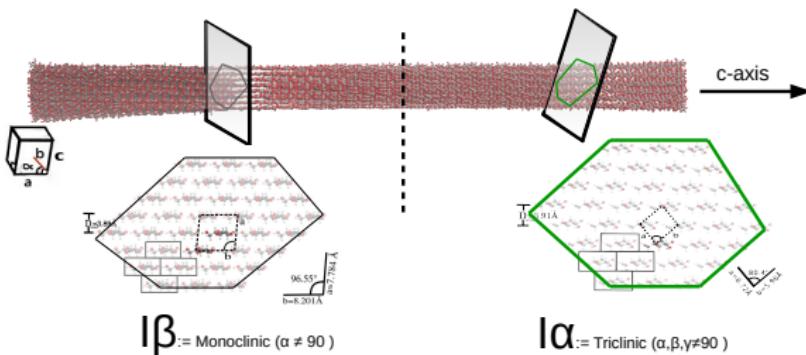
Biotechnological relevance of cellulose

Interconversion of Native Cellulose I



Molecular Structure of Cellulose I

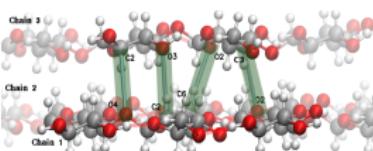
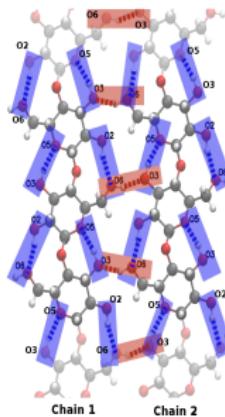
Energetic and Structural Stability [A2]



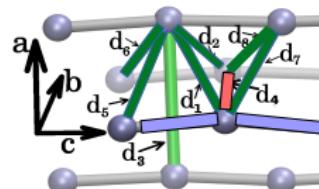
CG Model of Cellulose

Energetic and Structural Stability [A2]

Explicit: all-atom



CG: I β with C4



Effective Lennard-Jones coupling (ϵ [kcal/mol])

Intrachain HB	
O3-H \cdots O5	43%
O2-H \cdots O6	46%
Interchain HB	
O6-H \cdots O3	14%

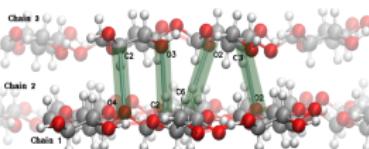
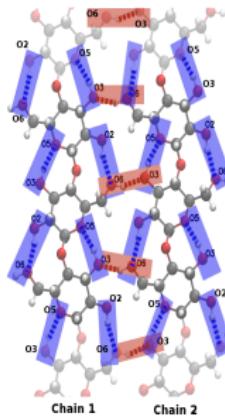
Intersheet HB	
C2-H \cdots O3	4%
C3-H \cdots O2	2%
C1-H \cdots O6	3%
C5-H \cdots O1	2%

kr(intrachain)	103
k θ	364
k ρ	4
Interchain	7.4
Intersheet	2.3
Intersheet	3.0

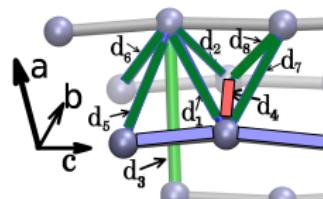
CG Model of Cellulose

Energetic and Structural Stability [A2]

Explicit: all-atom



CG: α with C4



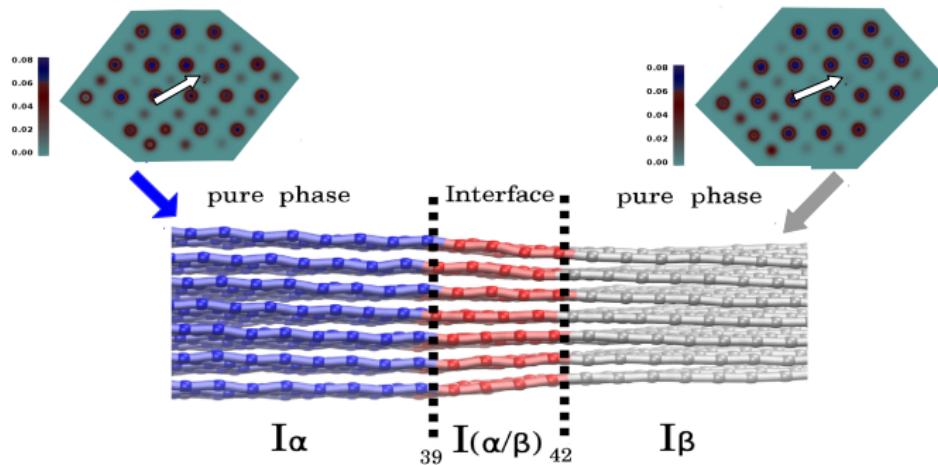
Effective Lennard-Jones coupling (ϵ [kcal/mol])

Intrachain HB	Intersheet HB
O3-H \cdots O5 40%	C2-H \cdots O3 3%
O2-H \cdots O6 43%	C3-H \cdots O2 1%
Interchain HB	
O6-H \cdots O3 12%	C1-H \cdots O6 2%
	C5-H \cdots O1 1%

k_r (intrachain)	102
$k\theta$	360
$k\phi$	4
Interchain	7.3
Intersheet	1.9
Intersheet	2.5

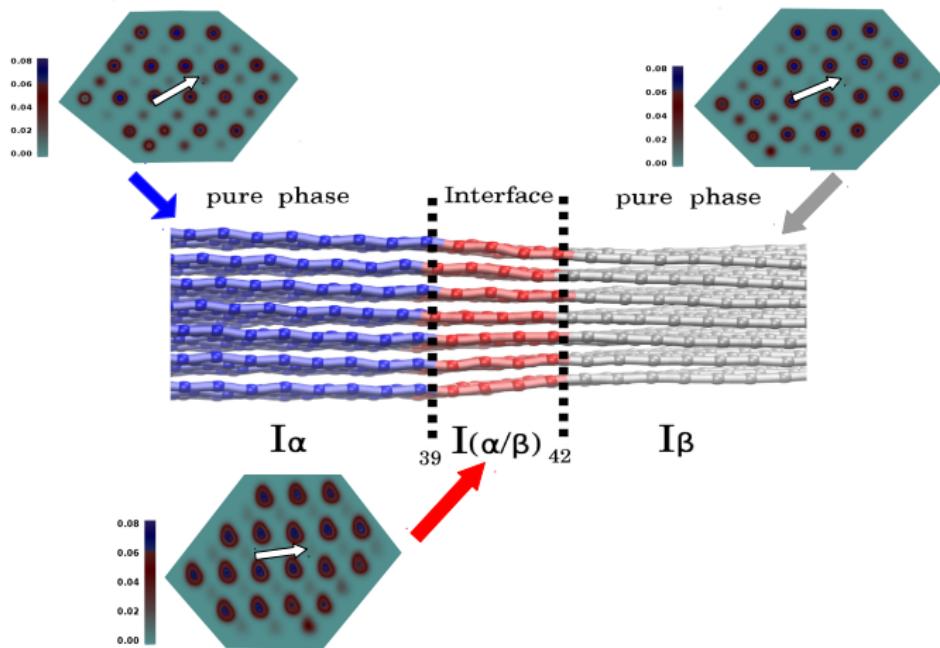
CG Model of Cellulose

Coexisting $I(\alpha/\beta)$ crystalline phases [A2]



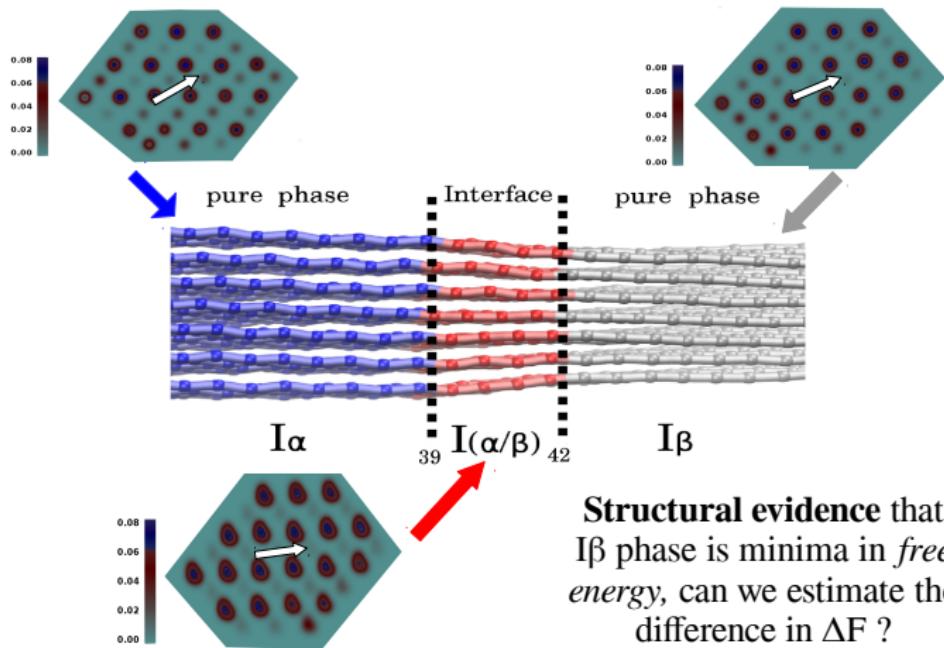
CG Model of Cellulose

Coexisting $I(\alpha/\beta)$ crystalline phases [A2]



CG Model of Cellulose

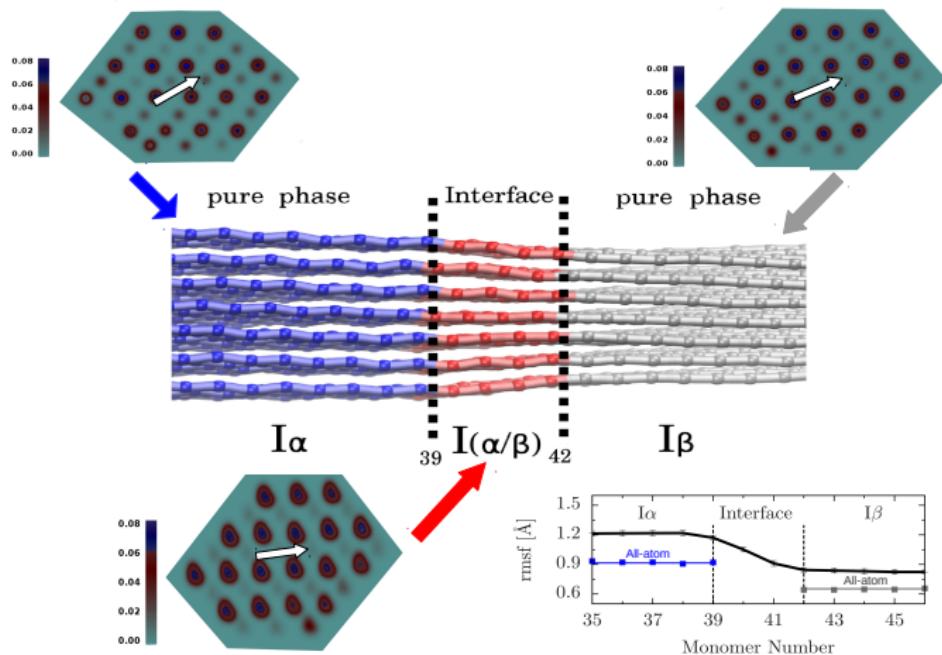
Coexisting $I(\alpha/\beta)$ crystalline phases [A2]



Structural evidence that
 $I\beta$ phase is minima in *free
energy*, can we estimate the
difference in ΔF ?

CG Model of Cellulose

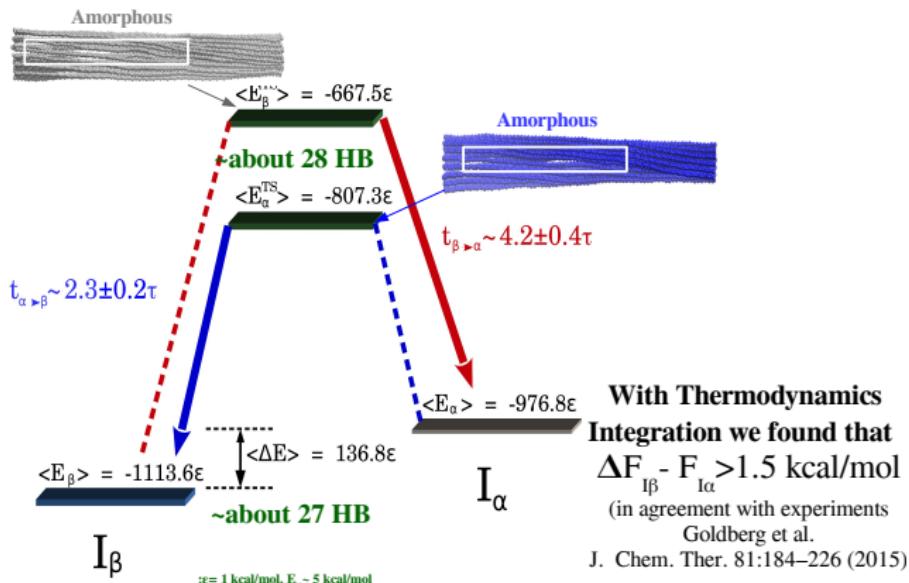
Coexisting $I(\alpha/\beta)$ crystalline phases [A2]



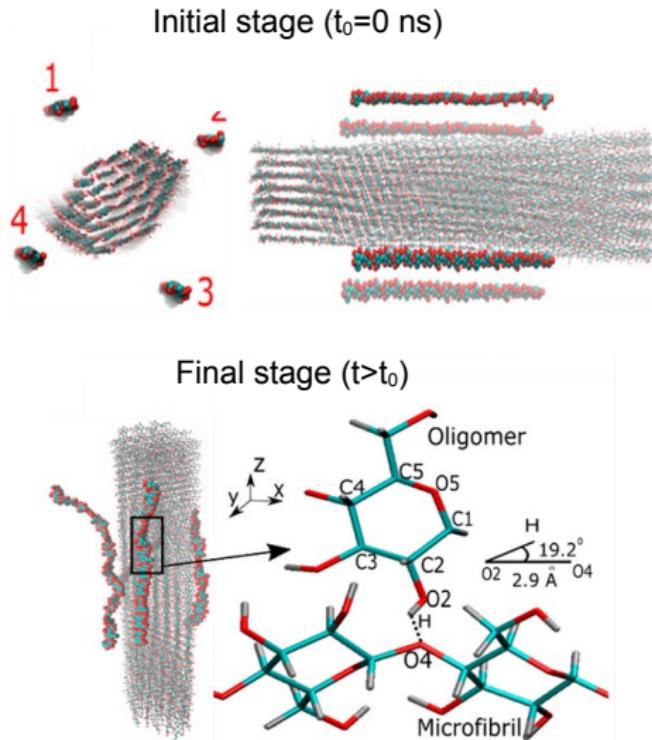
CG Model of Cellulose

Amorphous state during interconversion of I α \rightarrow I β at RT [A2]

Energy difference says that $E_{I\beta} < E_{I\alpha}$

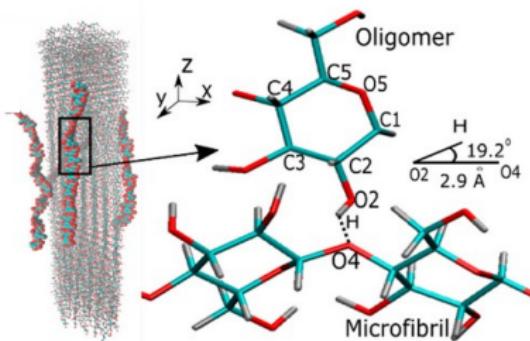


Molecular Insights into Self-assembly Process of Cellulose

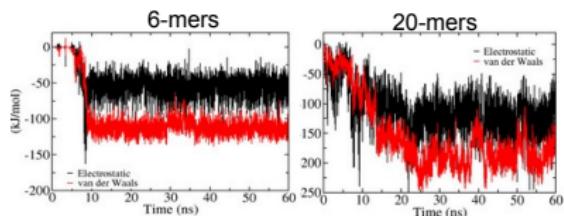


Molecular Insights into Self-assembly Process of Cellulose

Final stage



Energetic Fluctuations



Hydrogen bonds

6-mers

20-mers

$O_nH \cdots O_m$	$C_nH \cdots O_m$	$O_nH \cdots O_m$	$C_nH \cdots O_m$
O3-H...O6		O2H...O3	C2H...O3
O6H...O2		O6H...O2	C1H...O6
O2H...O6		O2H...O6	C5H...O6
O6-H...O3		O4H...O6	C2H...O4
		O3H...O6	C2H...O4
		O2H...O4	
		O6H...O6	

Atomic Fluctuations

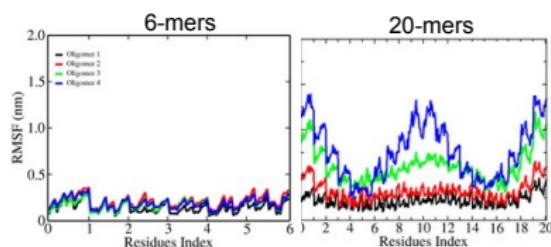


Table of Contents

1 Motivation

- From idea to realisation: The computational microscope
- Method Development
 - Gō-like Approach
 - GōMartini

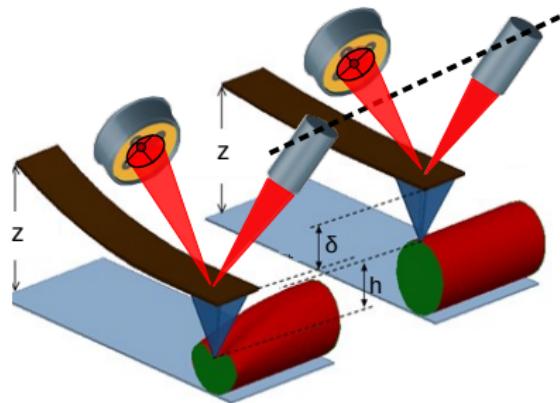
2 Modelling and Simulation of Biomolecular Systems

- Cellulose fibrils: Structure and Dynamics
 - Biotechnological relevance of cellulose
 - Molecular Structure of Cellulose I
 - CG Model of Cellulose
 - Molecular Insights into Self-assembly Process of Cellulose
- Nanomechanics of biological fibrils through simulations
 - Continuum Mechanics at the Nanoscale
 - Nanomechanics of β -Amyloid Fibrils

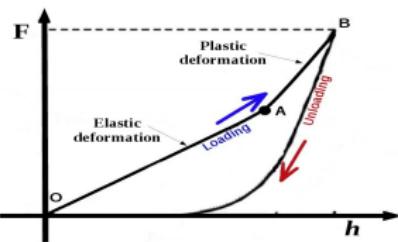
3 Summary

Continuum Mechanics at the Nanoscale

AFM-indentation

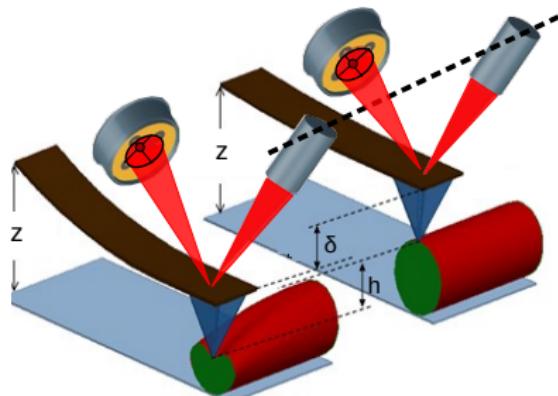


Compliance curve

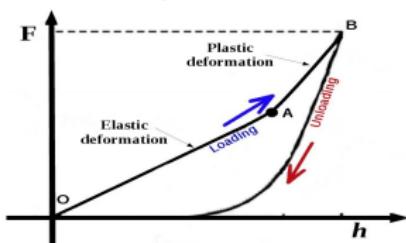


Continuum Mechanics at the Nanoscale

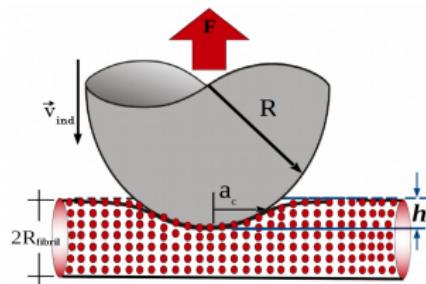
AFM-indentation



Compliance curve



Elastic Theory (Hertz 1882)



Applied for an **elastic half-space, homogeneous and frictionless** material.

The theory predicts:

$$F = \frac{4Y^* R^{1/2} h^{3/2}}{3}$$

With Y as the elastic modulus

Continuum Mechanics at the Nanoscale



Letter | Published: 18 June 2005

The breakdown of continuum models for mechanical contacts

Binquan Luan & Mark O. Robbins

Nature 435, 929–932 (16 June 2005) | Download Citation

Abstract

Forces acting within the area of atomic contact between surfaces play a central role in friction and adhesion. Such forces are traditionally calculated using continuum contact mechanics¹, which is known to break down as the contact radius approaches atomic dimensions. Yet contact mechanics is being applied at ever smaller lengths, driven by



Letter | Published: 26 February 2009

Friction laws at the nanoscale

Yifei Mo, Kevin T. Turner & Izabela Stilufarska

Nature 457, 1116–1119 (26 February 2009) | Download Citation

Abstract

Macroscopic laws of friction do not generally apply to nanoscale nanoscale friction experiments^{4,5,6,7}. We demonstrate that the breakdown of continuum mechanics can be understood as a result of the rough (multi-asperity) nature of the contact, and show that roughness theories^{8,9,10} of friction can be applied at the nanoscale.

Continuum Mechanics at the Nanoscale

nature

Letter | Published: 16 June 2005

The breakdown of continuum models for mechanical contacts

Binquan Luan & Mark D. Robbins

Nature 435, 929–932 (16 June 2005) | Download Citation ↗

Abstract

Forces acting within the area of atomic contact between surfaces play a central role in friction and adhesion. Such forces are traditionally calculated using continuum contact mechanics¹, which is known to break down as the contact radius approaches atomic dimensions. Yet contact mechanics is being applied at ever smaller lengths, driven by

nature

Letter | Published: 26 February 2009

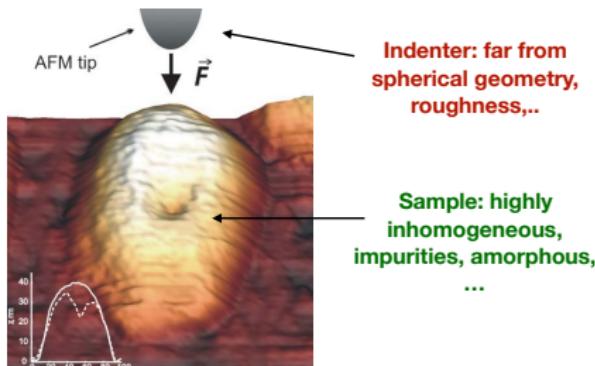
Friction laws at the nanoscale

Yifei Mo, Kevin T. Turner & Izabela Szlufarska

Nature 437, 1116–1119 (26 February 2009) | Download Citation ↗

Abstract

Macroscopic laws of friction do not generally apply to nanoscale nanoscale friction experiments^{4,5,6,7}. We demonstrate that the breakdown of continuum mechanics can be understood as a result of the rough (multi-asperity) nature of the contact, and show that roughness theories^{8,9,10} of friction can be applied at the nanoscale.



Nanoindentation of bacteriophage capsid. Taken from W.H. Roos et al.: Cell Mol. Life Sci. 64, 1484. 2007.

Continuum Mechanics at the Nanoscale

nature

Letter | Published: 16 June 2005

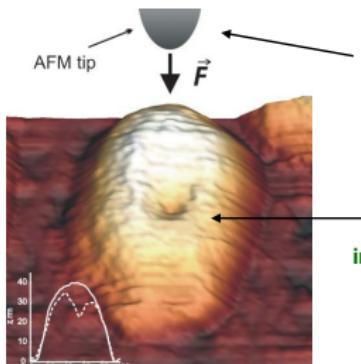
The breakdown of continuum models for mechanical contacts

Binquan Luan & Mark D. Robbins

Nature 435, 929–931 (16 June 2005) | Download Citation ↗

Abstract

Forces acting within the area of atomic contact between surfaces play a central role in friction and adhesion. Such forces are traditionally calculated using continuum contact mechanics¹, which is known to break down as the contact radius approaches atomic dimensions. Yet contact mechanics is being applied at ever smaller lengths, driven by



Nanoindentation of bacteriophage capsid. Taken from W.H. Roos et al.: Cell Mol. Life Sci. 64, 1484. 2007.

nature

Letter | Published: 26 February 2009

Friction laws at the nanoscale

Yifei Mo, Kevin T. Turner & Izabela Szlufarska

Nature 457, 1116–1119 (26 February 2009) | Download Citation ↗

Abstract

Macroscopic laws of friction do not generally apply to nanoscale nanoscale friction experiments^{4,5,6,7}. We demonstrate that the breakdown of continuum mechanics can be understood as a result of the rough (multi-asperity) nature of the contact, and show that roughness theories^{8,9,10} of friction can be applied at the nanoscale.

What if?



Design computer simulation

Aims

Validate the continuum model

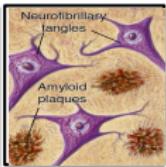
Ideal Experimental conditions

...

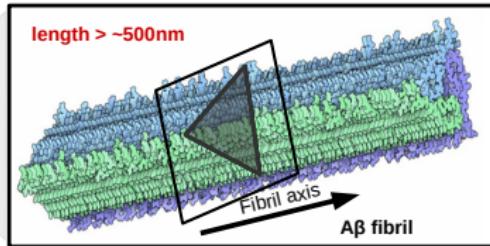
Sample: highly inhomogeneous, impurities, amorphous,

...

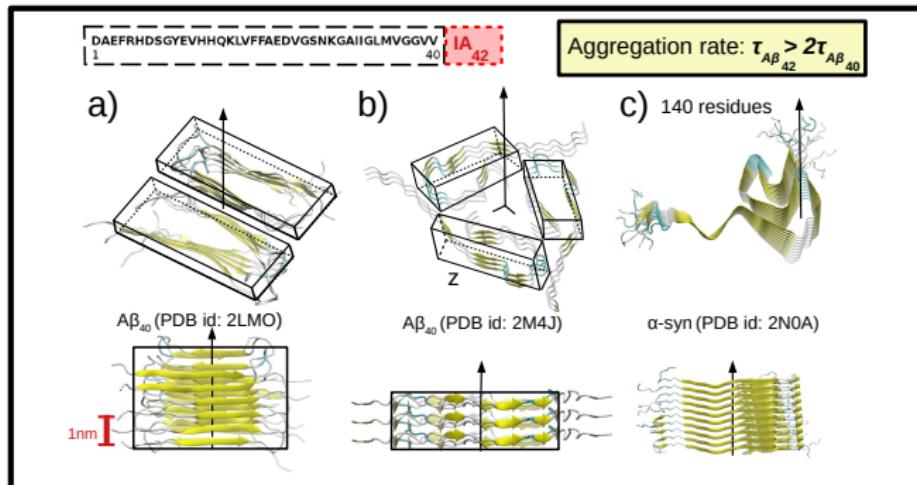
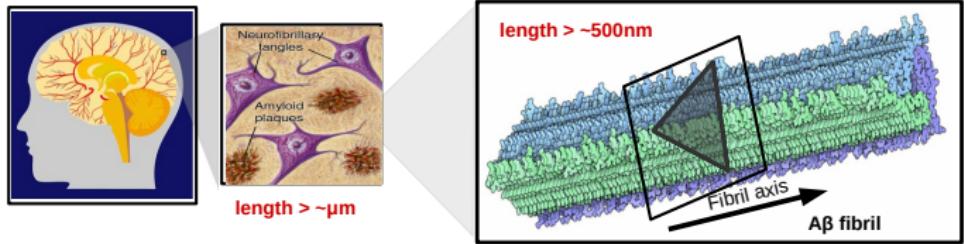
Nanomechanics of Amyloid Fibrils



length > $\sim \mu\text{m}$



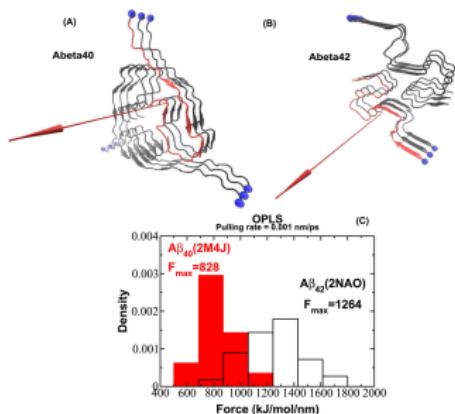
Nanomechanics of Amyloid Fibrils



Nanomechanics of β -Amyloid Fibrils

Kouza M. et al. (J. Chem. Phys. 148, 215106 (2018)) proposed that in $A\beta$:

"The higher the mechanical stability the faster the fibril formation takes places".

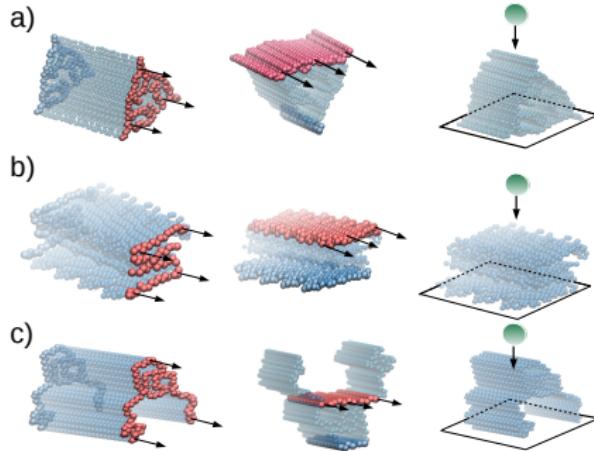


- ① Can we capture energetic difference between $A\beta_{40}$ and $A\beta_{42}$ within the **CG model**?
- ② Can we validate the mechanical stability and fibrils formation correlation within the **CG model**?

All-atom simulation of unbinding forces. Histograms clearly show that the force peak moves toward higher values for $A\beta_{42}$ compared with $A\beta_{40}$ (Taken from Kouza et al.)

Nanomechanics of β -Amyloid Fibrils

We have explored five $A\beta$ and one α -syn fibrils in the CG model [A3]



Left side shows tensile, middle panel shearing, and right panel indentation processes.

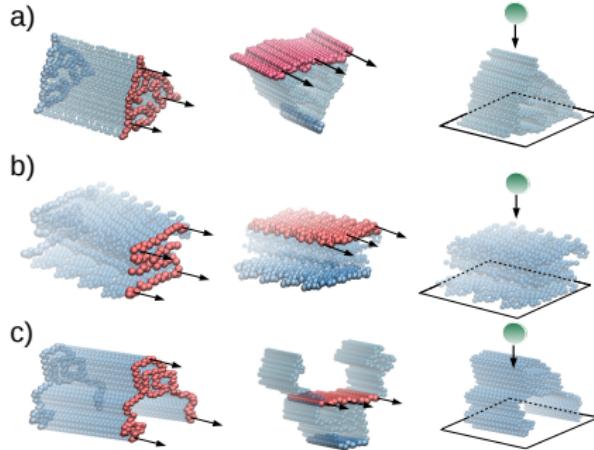
We found by simulations that $A\beta_{42}$ is mechanically more stable than $A\beta_{40}$ and β A fibrils present a mechanical anisotropy.

Elastic moduli

Tensile (Y_L)/PDB id	Symmetry	$A\beta_{40}$	$A\beta_{42}$	α -syn
2LMO	2-fold	1.6 ± 0.1		
2MJ4	3-fold	3.1 ± 0.1		
2MVX	2-fold	1.5 ± 0.1		
5OQV	2-fold		2.0 ± 0.2	
2NAO	2-fold		2.7 ± 0.2	
2NOA	—			2.3 ± 0.2
Avg (GPa)		—	2.0	2.4
Exp		—	—	—
Shear (S)/PDB id				
2LMO	2-fold	0.6 ± 0.3		
2MJ4	3-fold	1.2 ± 0.2		
2MVX	2-fold	0.4 ± 0.1		
5OQV	2-fold		1.3 ± 0.2	
2NAO	2-fold		1.8 ± 0.1	
2NOA	—			0.7 ± 0.2
Avg (GPa)		—	0.7	2.2
Exp		—	0.1 ± 0.02	—
Indentation (Y_I)/PDB id				
2LMO	2-fold	3.0 ± 0.1		
2MJ4	3-fold	6.0 ± 0.2		
2MVX	2-fold	5.0 ± 0.1		
5OQV	2-fold		7.0 ± 0.3	
2NAO	2-fold		16.0 ± 0.4	
2NOA	—			13.0 ± 0.1
Avg (GPa)		—	5.0	11.0
Exp		—	—	3.2 ± 0.8
				2.2 ± 0.6

Nanomechanics of β -Amyloid Fibrils

We have explored five $A\beta$ and one α -syn fibrils in the CG model [A3]



Left side shows tensile, middle panel shearing, and right panel indentation processes.

We found by simulations that $A\beta_{42}$ is mechanically more stable than $A\beta_{40}$ and β A fibrils present a mechanical anisotropy.

Elastic moduli

Tensile (Y_L)/PDB id	Symmetry	$A\beta_{40}$	$A\beta_{42}$	α -syn
2LMO	2-fold	1.6 ± 0.1		
2MJ4	3-fold	3.1 ± 0.1		
2MVX	2-fold	1.5 ± 0.1		
5OQV	2-fold		2.0 ± 0.2	
2NAO	2-fold		2.7 ± 0.2	
2NOA	—			2.3 ± 0.2
Avg (GPa)		—	2.0	2.4
Exp		—	—	—
Shear (S)/PDB id				
2LMO	2-fold	0.6 ± 0.3		
2MJ4	3-fold	1.2 ± 0.2		
2MVX	2-fold	0.4 ± 0.1		
5OQV	2-fold		1.3 ± 0.2	
2NAO	2-fold		1.8 ± 0.1	
2NOA	—			0.7 ± 0.2
Avg (GPa)		—	0.7	2.2
Exp		—	0.1 ± 0.02	—
Indentation (Y_I)/PDB id				
2LMO	2-fold	3.0 ± 0.1		
2MJ4	3-fold	6.0 ± 0.2		
2MVX	2-fold	5.0 ± 0.1		
5OQV	2-fold		7.0 ± 0.3	
2NAO	2-fold		16.0 ± 0.4	
2NOA	—			13.0 ± 0.1
Avg (GPa)		—	5.0	11.0
Exp		—	—	3.2 ± 0.8
				2.2 ± 0.6

Summary

- ① Biomolecular simulation is now feasible at large length and time scales quite close to *in vitro* cell experiments. Certainly it will serve as the computational microscope to observe biophysical responses in complex systems under non-equilibrium conditions (e.g. mechanical or thermal induced processes).
- ② The GōMartini approach is a very powerful tool for the simulation of large conformational changes in biomolecular complexes.
- ③ Biomechanics of biological fibrils at the nanoscale can be studied by the coarse-grained MD simulations.
- ④ We showed that in fibrils composed by β A exists a high degree of anisotropy in terms of the elastic moduli (i.e. Tensile vs indentational) and it depends on the direction of deformation.

Acknowledgments

Collaborators

Coarse-grained development for Biomolecules

- Prof. S.-J. Marrink (Groningen, Netherland)
- Dr. Paulo Telles de Souza (CRNS, France)
- Dr. Sebastian Thallmair (FIAS, Germany)
- Dr. Mateusz Chwastyk (IFPAN, Poland)

Bioengineering and probing cells by SMFS

- Prof. Michale E. Nash (ETH Zurich, Switzerland)
- Prof. David Alsteen (The Université Catholique de Louvain, Belgium)
- Prof. Marta Bally (Umeå University, Sweden)

Former Team Members



Dr. Rodrigo Moreira
(BCAM, Spain)



Dr. Thu Tran
(Ho Chi Minh University, Vietnam)



Dr. Krishnan Sangasmewaram
(Lodz University of Technology, Poland)

Funding and Computational Resources

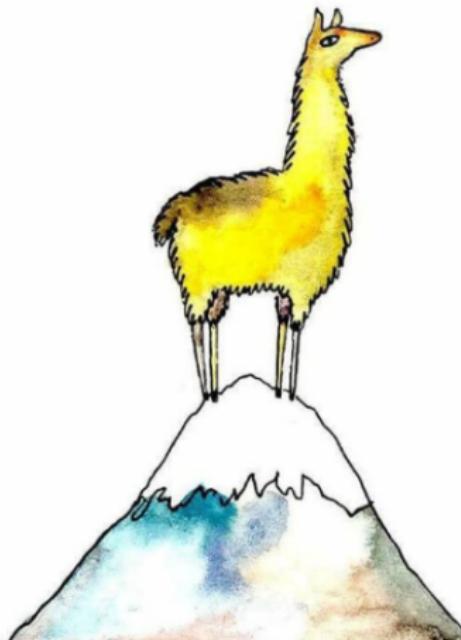


Rzeczypospolita
Polska



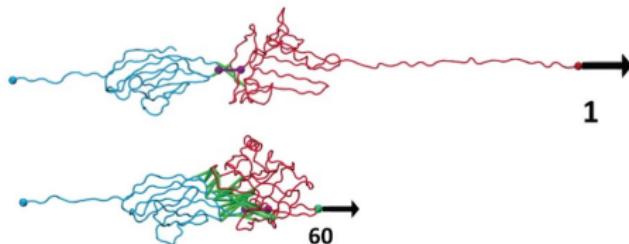
Thanks for your attention:

THE DAY WILL COME,
THE UNIVERSE WILL **GRANT YOU**
WITH A LLAMA

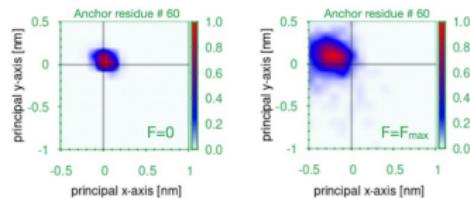
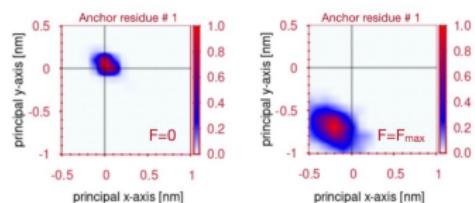


GōMARTINI applications for biomolecular complex

GōMartini pathways



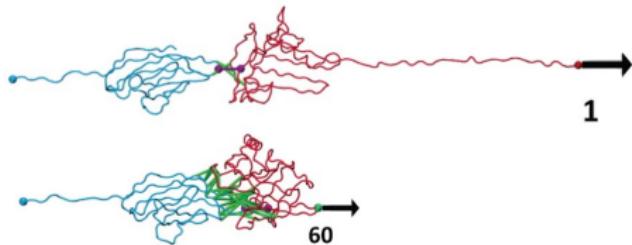
Anticalin center-of-mass



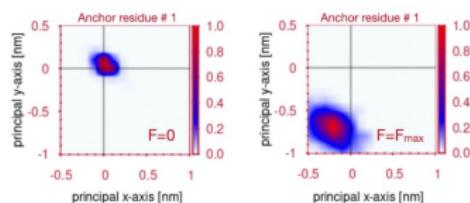
[11] Z. Liu, R. Moreira, A. Dujmović, H. Liu, B. Yang, A. B. Poma, and M. A. Nash, Nano Letters 22(1), 179 (2021).

GōMARTINI applications for biomolecular complex

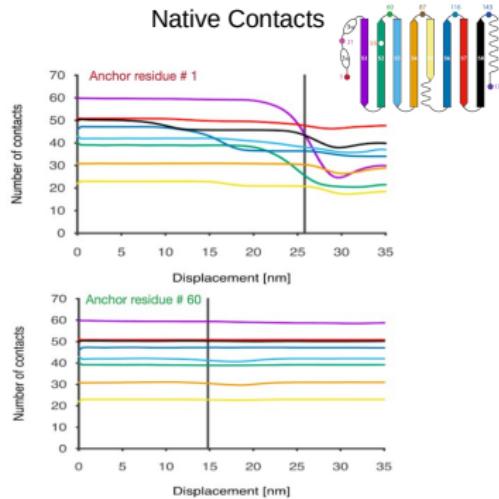
GōMartini pathways



Anticalin center-of-mass



Native Contacts



[11] Z. Liu, R. Moreira, A. Dujmović, H. Liu, B. Yang, A. B. Poma, and M. A. Nash, Nano Letters 22(1), 179 (2021).

ADOLFO POMA BERNOLA

(1) Instytut Podstawowych Problemów Techniki Polskiej Akademii Nauk

Procedure for the conferment of the post-doctoral degree of doctor habilitated in the field of **Bioengineering**

Scientific achievement entitled:

Computational Modelling and Simulations of Biomolecular Systems

SUMMARY OF PROFESSIONAL ACCOMPLISHMENTS

• EDUCATION

- 2011 Ph.D. in **Physics**, – *multiscale simulations*
Johannes Gutenberg University, Mainz, Germany 
Supervisor: Prof. Dr. Kurt Kremer and *co-supervisor:* Prof. Dr. Luigi Delle Site
- 2007 M.Sc. in **Physics**, *molecular simulations*
State University of Campinas, São Paulo, Brazil 
Supervisor: Prof. Dr. Maurice de Koning

• CURRENT POSITIONS



since 2018, Assistant Professor
Institute of Fundamental Technological Research (IPPT-PAN), Polish Academy of Sciences

• PREVIOUS POSITIONS

- 2021 – 2022 Group leader
Supported by FNP & MAB-PLUS (*ICRI-bioM*) hosted at the Faculty of Biotechnology and Food Sciences at Lodz University of Technology, Poland
- 2013 – 2018 Assistant Professor
Institute of Physics, Polish Academy of Sciences, Poland
- 2011 – 2013 Postdoctoral Fellow
Department of Physics, University of Rome “La Sapienza”, Italy 

SUMMARY OF PROFESSIONAL ACCOMPLISHMENTS

• AWARDS

- 2022 Lodz University of Technology, Outstanding research I and IV semester, Lodz, Poland
2020 1st Degree Award for Team Achievements (IPPT-PAN)
2019 2nd Degree Award for Scientific achievements (IPPT-PAN)
2017 First Prize, Outstanding Young Research Talk, Cincinnati, USA.

• ACQUIRED FUNDING AS PI

- 2023 – 2027 NCN OPUS-23, Molecular biomechanics of the SARS-CoV-2 variants: The virus-host cell attachment and immune evasion
2018 – 2022 NCN SONATA-11, Self-assembly and nanomechanical characterization of cellulose microfibril

- Winner of an NCN OPUS-22 and involved as a researcher in 2 international research projects under Horizon 2020

• INVITED CONFERENCES / PRESENTATIONS OVER PAST 5 YEARS (AS SPEAKER)

- 2023 Kick-off meeting of the MimmicLS project by Roza Sweda , Wroclaw, Poland.
2022 BIT-20->22, Torun, Poland
2021 Bionanomechanics Conference 2020 (On-line), Spain
2020 The 5th Workshop of Vietnamese Students in Poland (On-line), COVID-19 session, Warsaw, Poland
2019 European Summit of Industrial Biotechnology (ESIB2019), Flash talk, Graz, Austria
 APS march meeting, Boston, USA.
 Soft Matter and Statistical Physics Seminar–University of Warsaw, Poland.
 Seminarium z fizyki biologicznej i Bioinformatyki, Warsaw, Poland
2018 CECAM/CSM/IRTG School 2018: Machine Learning in Scientific Computing, Nierstein, Germany

Total conferences / presentations (as speaker): >20 (After Ph.D studies)

SUMMARY OF PROFESSIONAL ACCOMPLISHMENTS

• ORGANIZATION OF SCIENTIFIC MEETING

Since 2021 Organization of a bi-weekly PomaLab (On-line) seminar on the *Simulation and Modelling of Biomolecular Systems*, IPPT
(>60 individual participants; 20-40 registrations every seminar)
2021 Bi-weekly ICRI-BioM Seminars at Lodz University of Technology, Poland

• EXPERT AS EVALUATOR

2022 – 2025 NCN and FNP, Poland
Since 2022 COST-Actions, EU
Since 2017 National University of San Marcos (UNMSM), Peru

• EDITORIAL WORK

Editorial Board of the Journal of Structural Biology (JSB/JSBX)

AS EDITOR: Poblete S., Pantano S., Okazaki K.-i., Liang Z., Kremer K. and **Poma A.B.** (2023), Editorial: Recent advances in computational modelling of biomolecular complexes. *Front. Chem.* 11:1200409

• REVIEWING ACTIVITIES

- Chemical Sciences (IF=9.969) • Virus (5.818) • International Journal of Molecular Sciences (6.208) • Cells (7.666) • Biology (5.168)
- Biomolecules (6.064) • Microorganism (4.926) • Pathogens (4.531) • Molecules (4.927) • RSC Advances (4.036) • Vaccines (4.961)
- Physical Chemistry Chemical Physics (3.945) • Future Virology (3.015) • Genes (4.141) • Journal of Physical Chemistry (4.177)
- Journal of Chemical Information and Modeling (6.162) • Journal of Chemical Theory and Computation (6.578) Diagnostics (3.992)
- Applied Science (2.838) • Journal of Molecular Modeling (2.172)

• SUPERVISION

2019 – 2022 As a PI, supervision of 1 Postdoc, at IPPT PAN, Poland
2021 – 2022 As a PI, supervision of 2 Postdocs, at ICRI-BioM Lodz University of Technology

SUMMARY OF PROFESSIONAL ACCOMPLISHMENTS

• BIBLIOMETRIC INFORMATION (2023.05.25)

	Scopus	Web of Science™
Number of citations	831*	791
Number of citations (excl. self-citations)	---	701
H-index	16	15

• MAIN ACHIEVEMENTS FOR HABILITATION

- Poma, A. B.† , Chwastyk, M., Cieplak, M. (2015). Polysaccharide–protein complexes in a coarse-grained model. *J. Phys. Chem. B*, 119(36), 12028–12041.
- Poma, A. B.† , Chwastyk, M., Cieplak, M. (2016). Coarse-grained model of the native cellulose I and the transformation pathways to the I allomorph. *Cellulose*, 23(3), 1573–159.
- Poma, A. B.† , Chwastyk, M., Cieplak, M. (2017). Elastic moduli of biological fibers in a coarse-grained model: Crystalline cellulose and -amyloids. *Phys. Chem. Chem. Phys.*, 19(41), 28195–28206.
- Thu, T. T. M.† , Moreira, R. A., Weber, S. A., Poma, A. B.† (2022). Molecular Insight into the Self-Assembly Process of Cellulose I Microfibril. *Int. J. Mol. Sci.*, 23(15), 8505
- Moreira, R. A.† , Weber, S. A., Poma, A. B.† (2022). Martini 3 Model of cellulose microfibrils: on the route to capture large conformational changes of polysaccharides. *Molecules*, 27(3), 9

Total number according to Czasopisma z listy MEiN (2021-12-30):

The cycle of 5 publications	620
The remaining 21 publications	2630
Total	3250

* Removing one publication *Nat. Commun.* because of the wrong counting. Actual number on 26.05.2023 is 35 citation and not 665 as in Scopus