

NANOSIM

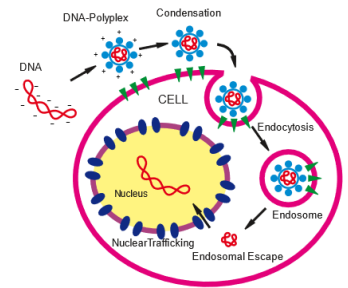
Laboratory for Simulations of Nanostructured Systems

<http://phys.ubbcluj.ro/~tbeu/nanosim.html>

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- **Gene therapy** – remarkable potential to cure genetic or acquired diseases
- **Central mechanism** – DNA condensation into **polyplexes** capable of **transfection**
- **Genetic vectors** (gene carriers):
 - wrap / condensate / protect DNA
 - release DNA inside the cell
- **Polyethylenimine** $[-CH_2-NH-CH_2-]_n$
 - large buffering capacity
 - simple engineering
- **DNA-PEI polyplexes** – ruled by electrostatics:
 - phosphate groups of DNA (-)
 - amino groups of PEI (+)
- **Main aim** – **investigate DNA-PEI condensation** required scale > 2 000 000 atoms



Gene transfer via non-viral vectors.
After Lungwitz et al. Biopharmaceutics 60 (2005) 247.

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Modeling levels of PEI

- **Ab initio**
 - Quantum mechanical (QM) calculations on **PEI models**
 - **~25 Å, ~50 atoms**
- **Atomistic (AA)**
 - **Development of a CHARMM FF for PEI**
 - Reference data: QM calculations
 - MD simulations of solvated PEI chains
 - Validation: experimental data
 - **~100 Å, ~100 000 atoms**
- **Coarse-Grained (CG)**
 - **Development of a MARTINI FF for PEI**
 - Reference: AA simulations
 - MD simulations of solvated PEI chains and DNA-PEI polyplexes
 - Validation: AA and experimental data
 - **~250 Å, ~450 000 beads** (equivalent to ~2 000 000 atoms)

• Gaussian 09

• ffTk 1.1
• NAMD 2.13• Gromacs 2018.1
• NAMD 2.13

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The CHARMM Force Field

- **Atomistic force field** based on **atom** and **residue types**
- **Intramolecular (bonded) terms** – between atom types: **CHARMM parameters to be optimized**

$$U_{\text{bonded}} = \sum_{\text{bonds}} k_b (b - b_0)^2 + \sum_{\text{angles}} k_\theta (\theta - \theta_0)^2 + \sum_{\text{dihedrals}} k_\psi [1 + \cos(n\psi - \delta)]$$

- **Intermolecular (non-bonded) terms:**

$$U_{\text{non-bonded}} = \sum_{\text{atoms } i,j} \left\{ \frac{q_i q_j}{\epsilon_0 r_{ij}} + \epsilon_{ij} \left[\left(\frac{r_{ij}^{\text{min}}}{r_{ij}} \right)^{12} - 2 \left(\frac{r_{ij}^{\text{min}}}{r_{ij}} \right)^6 \right] \right\}$$

$$r_{ij}^{\text{min}} = (r_i^{\text{min}} + r_j^{\text{min}})/2, \quad \epsilon_{ij} = \sqrt{\epsilon_i \epsilon_j}$$

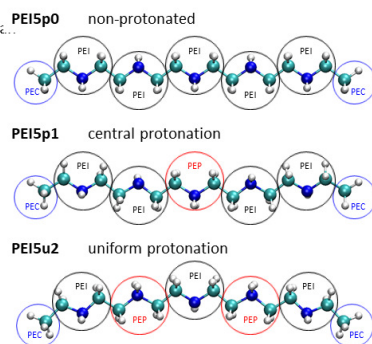
K. Vanommeslaeghe, ... A. D. MacKerell Jr., J. Comput. Chem., 2010, **31**, 671.

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Atomistic CHARMM model for PEI

- **Reference QM properties:**
ab initio calculations on **PEI models** Gauss...
MP2/6-31G(d)
- **Residue types:**
 - **PEI** – generic PEI monomer $[-CH_2-NH-CH_2-]$
 - **PEP** – protonated monomer $[-CH_2-NH_2^+-CH_2-]$
 - **PEC** – terminal CH_3 group
- **Atom types:**
 - NH1, HN1, CH2, HC2 (PEI)
 - NH2P, HN2P, CH2P (PEP)
 - CH3, HC3 (PEC)



Beu, Farcaș, J. Comput. Chem. 38, 2335 (2017).

Beu, Ailenei, Farcaș, J. Comput. Chem. 39, 2564 (2018).

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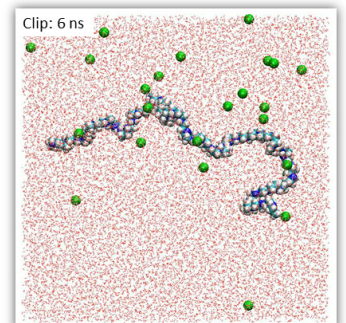
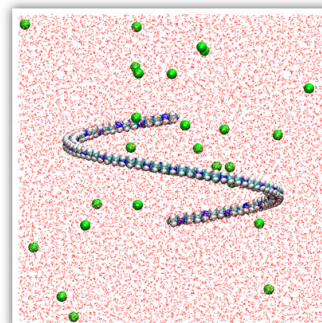
MD simulations of solvated PEI

Reference Simulation Set:

- PEI 27-mer, 39-mer, 51-mer
- Protonation fractions: 0, 1/4, 1/3, 1/2

NPT simulations ~70000 atoms

PME (Particle-Mesh-Ewald) electrostatics
400 ns data collection (time step 2 fs)



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- Coarse-grained force field based on **bead types**

- Intramolecular (bonded) terms – between bead types:

MARTINI parameters to be optimized

$$U_{\text{bonded}} = \frac{1}{2} \sum_{\text{bonds}} K_b (b - b_0)^2 + \frac{1}{2} \sum_{\text{angles}} K_\theta (\theta - \theta_0)^2 + \sum_{\text{dihedrals}} K_\psi [1 + \cos(n\psi - \delta)]$$

- Intermolecular (non-bonded) terms:

$$U_{\text{non-bonded}} = \sum_{\text{beads } i,j} \left\{ \frac{q_i q_j}{\epsilon_0 r_{ij}} + \epsilon_{ij} \left[\left(\frac{r_{ij}^{\text{min}}}{r_{ij}} \right)^{12} - 2 \left(\frac{r_{ij}^{\text{min}}}{r_{ij}} \right)^6 \right] \right\}$$

J. Marrink, H. J. Risselada, ... and A. H. de Vries, J. Phys. Chem. B, **2007**, 111, 7812.

- MARTINI force field:

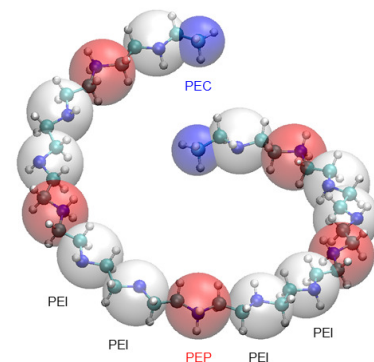
- ~4 heavy atoms → **bead**
- 10-fold reduction of objects
- 10-fold increase of time step

- Standard bead types → vdW interactions: Q-charged, P-polar, N-nonpolar, C-apolar

- Q and N subtypes:** d-donor, a-acceptor, da-both, 0-none
- P and C:** 5 degrees of polarity
- Small "S"** and tiny "T" variants
- Interaction levels (strengths): 10

- Bead types tested for PEI:

- PEI – Nda, Nd, N0, SNda, Snd, SNO
- PEP – Qda, Qd, Q0, SQda, Sqd, SQ0
- PEC – same as PEI



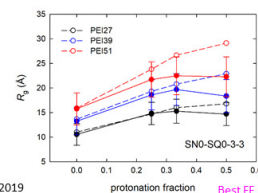
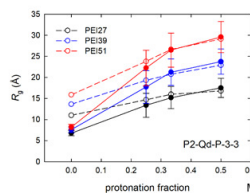
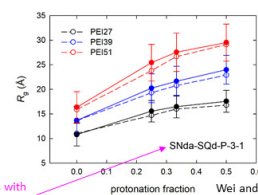
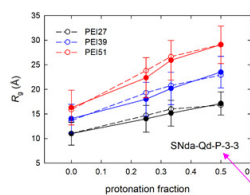
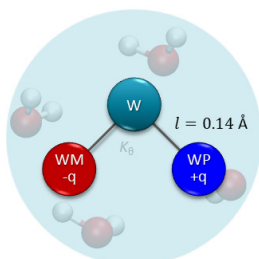
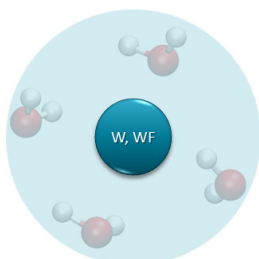
T. A. Beu, A. E. Ailenei, A. Farcaş, Chem. Phys. Lett. 714, 94-98 (2019).

- Standard water:

- W beads** (P4-type) map 4 H₂O mols
- WF beads** (BP4-type "big antifreeze") replace 1 in 10 Ws – to avoid freezing at to high temperatures

- Polarizable water:

- (W, WM, WP) beads** map 4 H₂O mols
- W-WM and W-WP distances constrained
- W – only Lennard-Jones interactions
- WM and WP – only Coulomb interactions



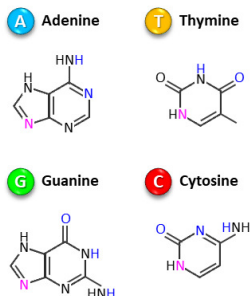
Best FF models with polarizable water

Wei and Luijten 2015 proposed Snda-SQd

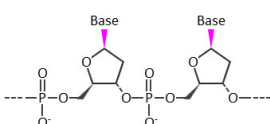
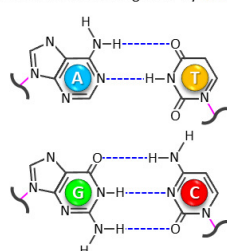
Best FF model with standard water

Mahajan and Tang 2019 proposed P2-Qd

DNA – polymer composed of nucleotides

Nucleotides: nucleobase
sugar (deoxyribose)
phosphate group

Sugar phosphate backbone

DNA strands held together by **H-bonds**

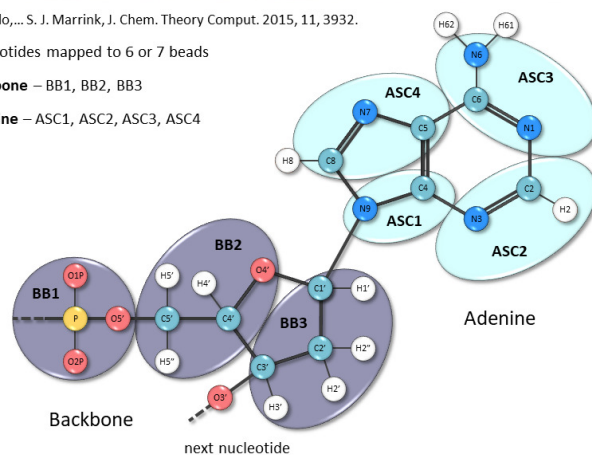
After Andy Brunning – www.compoundchem.co.uk

J. J. Uusitalo, ... S. J. Marrink, J. Chem. Theory Comput. 2015, 11, 3932.

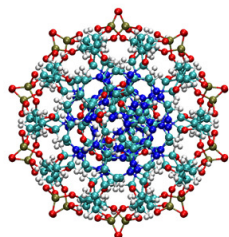
- Nucleotides mapped to 6 or 7 beads

- Backbone – BB1, BB2, BB3

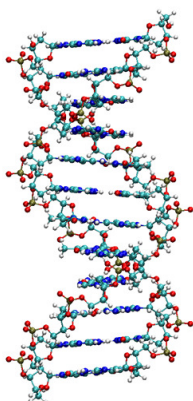
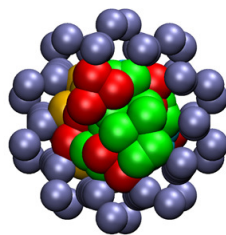
- Adenine – ASC1, ASC2, ASC3, ASC4



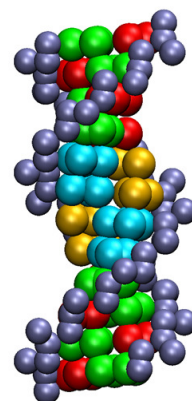
AA CHARMM model



CGCGAATTCGCG
GCGCTTAAGCGC

CG MARTINI model
Home-made "martinization" code

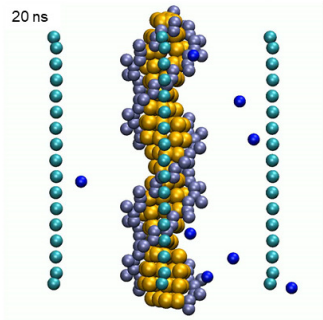
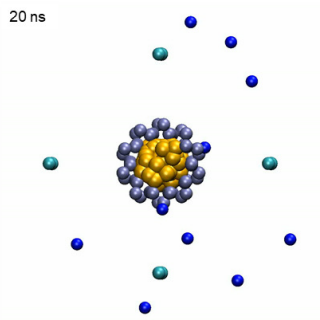
A Adenine T Thymine
G Guanine C Cytosine



Formation of DNA-PEI complexes

2 Drew-Dickerson dodecamers + 4 PEI15 protonated 1/2
8100 beads (~32000 atoms) – 96% polarized water
Simulation box: 68 x 68 x 68 Å (PBC), time step 10 fs

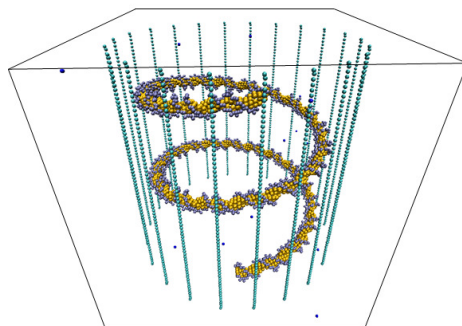
Nucleobase
Backbone
PEI
Na



Condensation of DNA-PEI polyplexes

30 Drew-Dickerson dodecamers + 22 PEI 65-mers protonated 1/2
440 000 beads (~1 800 000 atoms) – 98% polarizable water
Simulation box (PBC): 260 x 260 x 260 Å, time step 10 fs

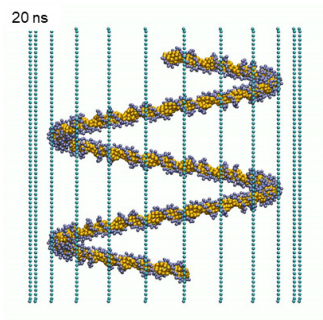
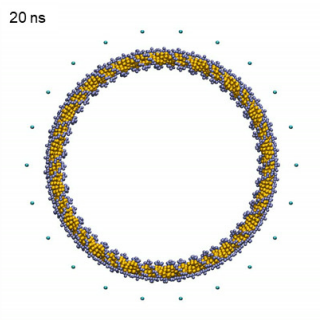
Nucleobase
Backbone
PEI
Na



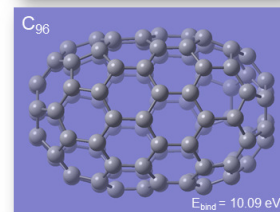
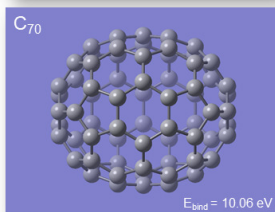
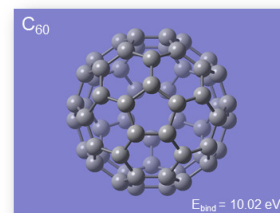
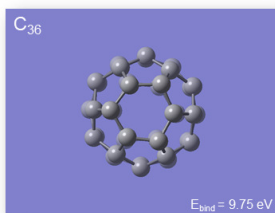
Condensation of DNA-PEI polyplexes

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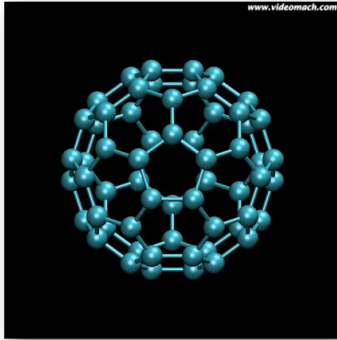
Nucleobase
Backbone
PEI



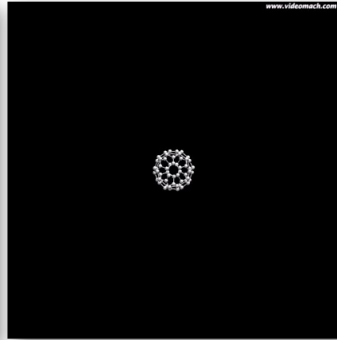
Radiation-induced fragmentation of fullerenes



C60
qtot = +10e, Eexc = 50 eV

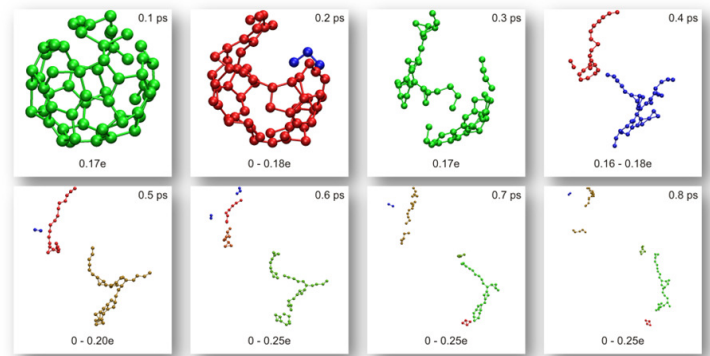


C60
qtot = +10e, Eexc = 100 eV



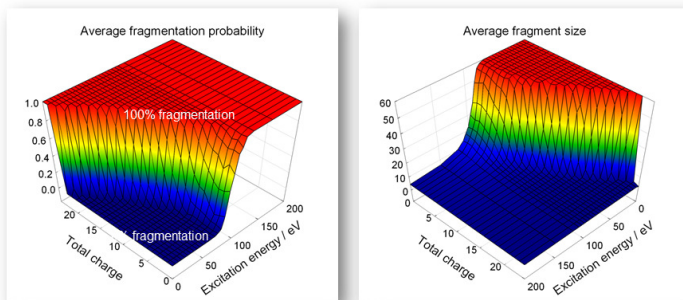
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Fragmentation probability (for each parameter combination) – ratio of dissociative trajectories to total number of trajectories

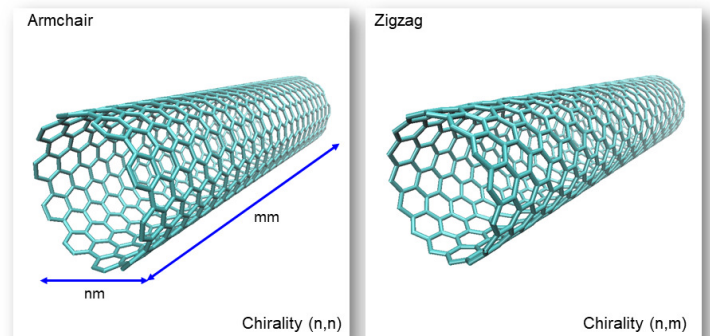
Phase transition: fragmentation-less regime ($p = 0$) → saturation regime ($p = 1$)

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1991 – **Discovery of multi-wall CNTs** – S. Iijima, Nature **354**, 56 (1991).

1993 – **Synthesis of single-wall CNTs** – S. Iijima & T. Ichihashi, Nature, **363**, 603 (1993).



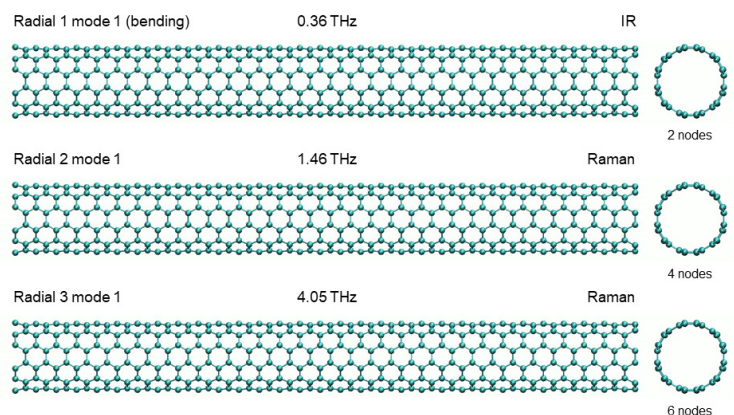
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- **Extreme length-to-diameter ratio** up to 132,000,000:1
a few nm in diameter, up to a mm long.
- **Exceptional material properties** – strength, stiffness, toughness, electrical and thermal conductivity etc.
- **Stiffness** (Young's modulus) up to 1000 GPa – **5x stiffer than steel**.
- **Metallic or semiconducting character** depending on the CNT structure.
- **Gas flow** exceeds predictions of the Knudsen diffusion model by **> 1 order**.
- **Water flow** exceeds values from continuum hydrodynamics by **> 3 orders**.
- **Huge flow rates** of solvents ~ **independent of pore length**.
- **Quasi-frictionless transport**.
- **Wide variety of applications:** filtration, electronics, catalysis, molecular sensing etc.

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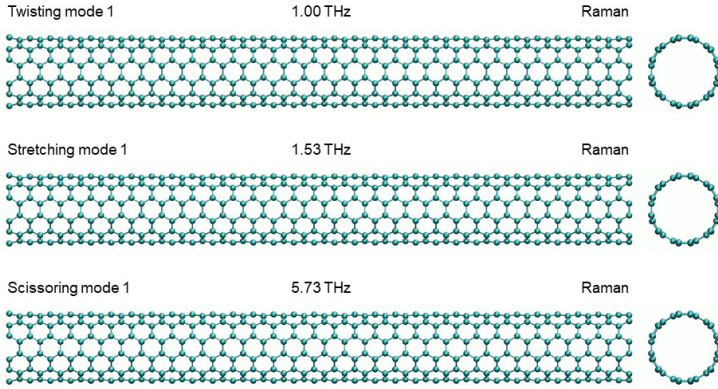
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Carbon nanotubes as mass resonators

CNT (6,6) 30 – twisting, stretching, and scissoring

Introduction to MD simulations



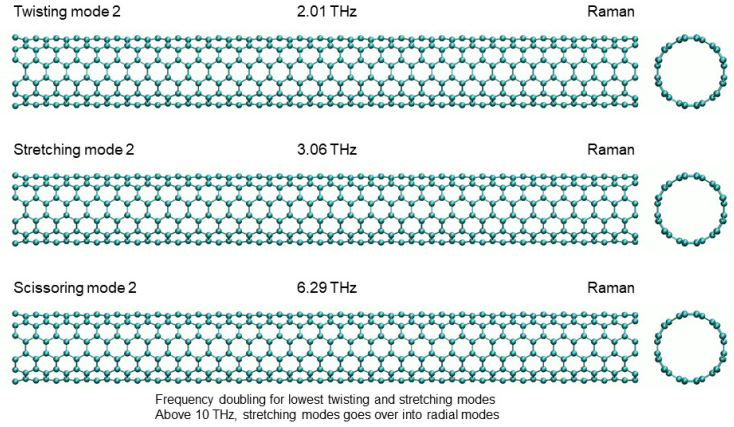
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Carbon nanotubes as mass resonators

CNT (6,6) 30 – twisting, stretching, and scissoring

Introduction to MD simulations



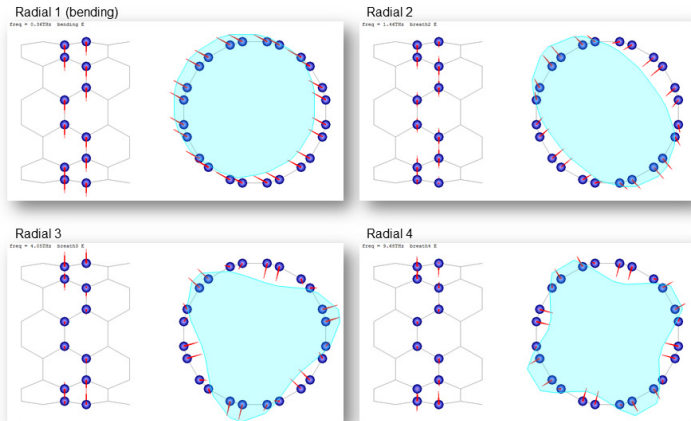
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Carbon nanotubes as mass resonators

Fundamental modes

Introduction to MD simulations



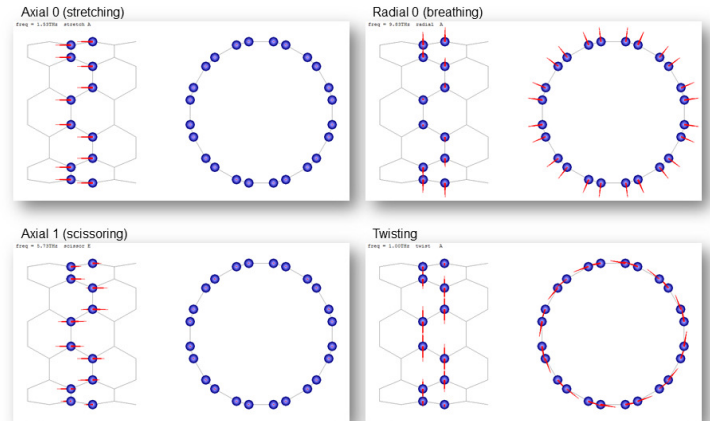
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Carbon nanotubes as mass resonators

Fundamental modes

Introduction to MD simulations



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Carbon nanotubes as mass resonators

Merit functions

Introduction to MD simulations

- **Twisting** – cumulated (axial) vector products of transversal displacements

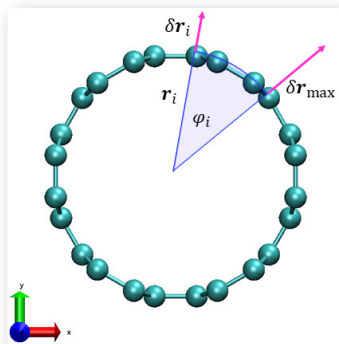
$$F_t = \sum_{\Delta_z} \left| \sum_{i \in \Delta_z} (x_i \cdot \delta x_i - y_i \cdot \delta y_i) \right|$$

- **Radial Fourier analysis**

$$F_r^n = 1 - \sum_{\Delta_z} \sum_{i \in \Delta_z} \left| \cos n\varphi_i - \frac{\delta r_i}{\delta r_{\max}} \right|$$

- **Axial Fourier analysis**

$$F_z^n = 1 - \sum_{\Delta_z} \sum_{i \in \Delta_z} \left| \cos n\varphi_i - \frac{\delta z_i}{\delta z_{\max}} \right|$$



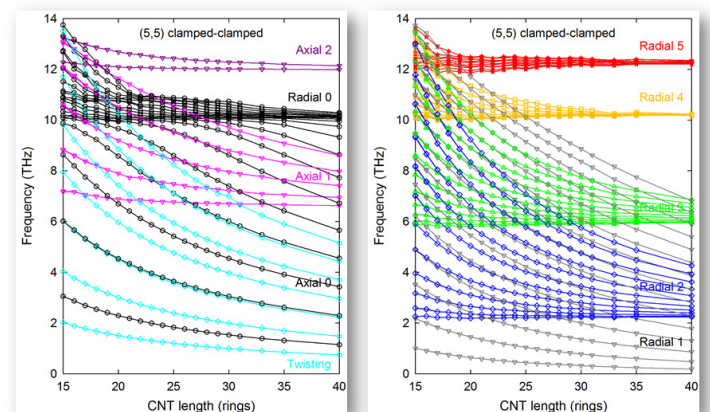
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Carbon nanotubes as mass resonators

Length-dependence of normal frequencies for damped-damped CNTs

Introduction to MD simulations



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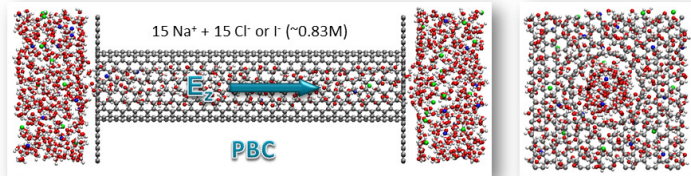
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Carbon nanotubes for filtration/separation applications

CNT model

Introduction to MD simulations

Chirality	r_{pore}	$r_{\text{pore}}^{\text{eff}}$	z_{pore}	$z_{\text{pore}}^{\text{eff}}$	x_{cell}	y_{cell}	z_{cell}	$V_{\text{pore}}^{\text{eff}} / V_{\text{fill}}^{\text{eff}}$	No. of C atoms
(8,8)	5.42	3.74	30.09	31.76	14.89	14.74	47.21	0.09	1368
(9,9)	6.09	4.42	30.09	31.76	14.89	14.74	46.58	0.13	1436
(10,10)	6.77	5.10	30.09	31.76	14.89	14.74	45.85	0.17	1522
(11,11)	7.45	5.77	30.09	31.76	14.89	14.74	45.01	0.22	1606
(12,12)	8.12	7.45	30.09	31.76	14.89	13.51	45.19	0.28	1630



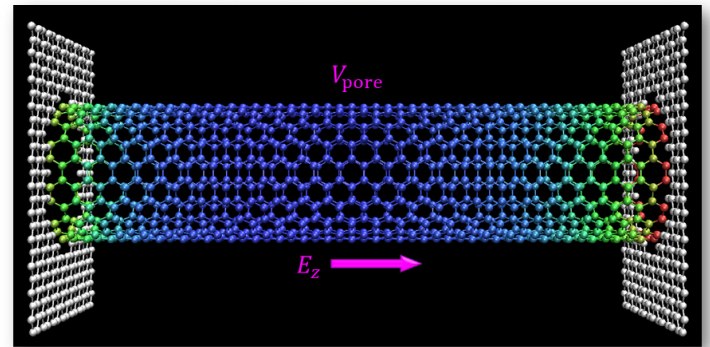
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Carbon nanotubes for filtration/separation applications

Polarized pore charge distributions – “Charge-hopping” Monte Carlo method

Introduction to MD simulations



- Constrained minimum for the total Coulomb energy with fixed total charge / voltage
- Interactions: (1) between charges and electric fields, (2) between charges, (3) self-energies.
- Multiple Monte Carlo threads, averaged at the end.

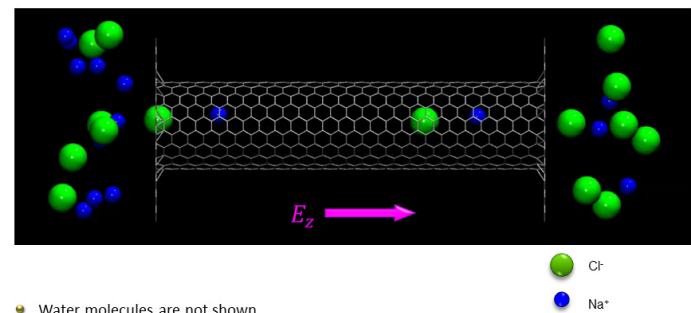
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Carbon nanotubes for filtration/separation applications

Typical run

Introduction to MD simulations



- Water molecules are not shown
- 6 ns of a trajectory are presented

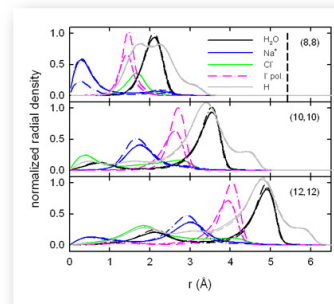
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Carbon nanotubes for filtration/separation applications

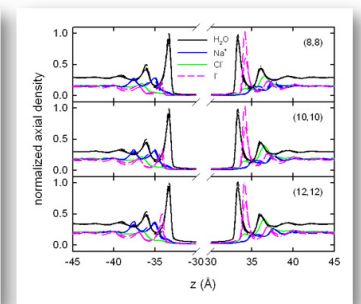
Solution structuring

Introduction to MD simulations

Radial density profiles



Axial density profiles



Similar radial / axial structuring of the solution.

I⁻ is optimally hydrated by the water boundary layer; polarizability enhances maxima.

Cl⁻ resides preferentially on the interior side of the Na⁺ layer.

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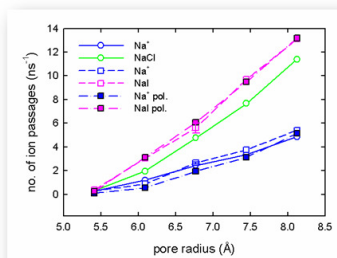
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Carbon nanotubes for filtration/separation applications

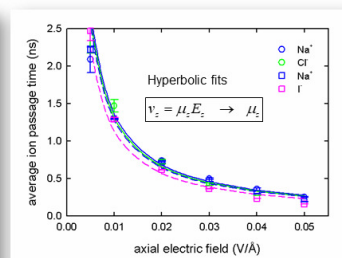
Transport properties

Introduction to MD simulations

Average number of ion passages as a function of the pore radius



Average ion passage time as function of the axial electric field



Net currents for NaI exceed those for NaCl by up to 30% – anion selectivity.

The I⁻ ions travel preferentially along cylindrical layers of larger radius than the Cl⁻ ions.

Partial Na⁺ currents are solute independent.

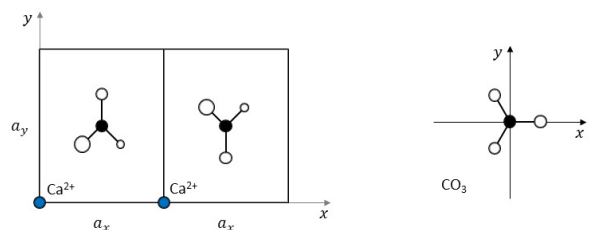
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Solution dynamics of calcite

CaCO₃ unit cell – 1014 plane

Introduction to MD simulations



In-plane unit cell size
 $a_x = 4.0485$, $a_y = 4.991$

Inter-plane distance
 $a_z = 3.036$

Inter-plane shift
 $h_x = -0.76a_x$, $h_y = -\frac{a_y}{2}$

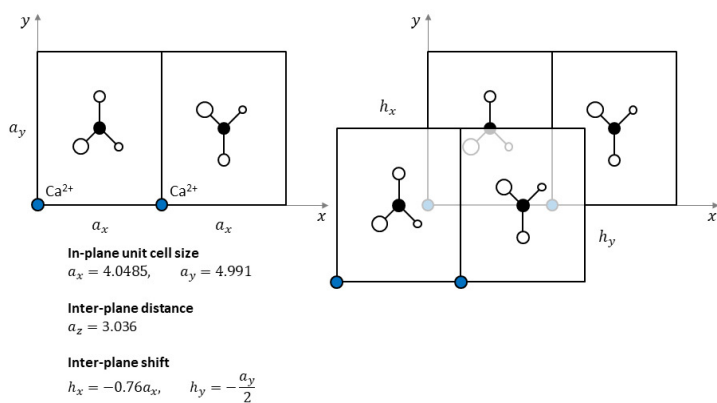
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Solvation dynamics of calcite

CaCO₃ unit cell – 1014 plane

Introduction to MD simulations

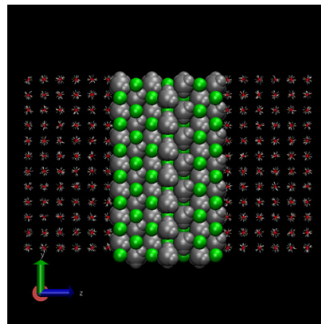


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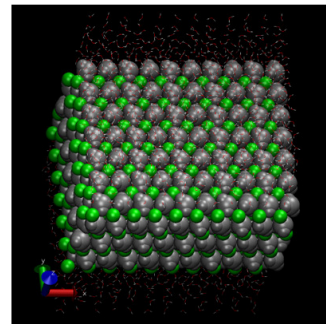
Solvation dynamics of calcite

Introduction to MD simulations

Slab model formed of 7 calcite (CaCO₃) layers and 2 water reservoirs (side view)



Slab model formed of 7 calcite (CaCO₃) layers and 2 water reservoirs (top view)



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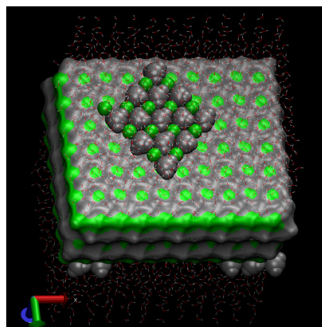
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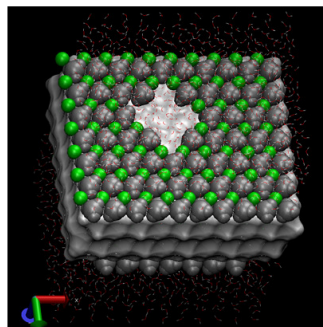
Solvation dynamics of calcite

Introduction to MD simulations

Slab model formed of 7 calcite (CaCO₃) layers with etch island



Slab model formed of 7 calcite (CaCO₃) layers with etch pit

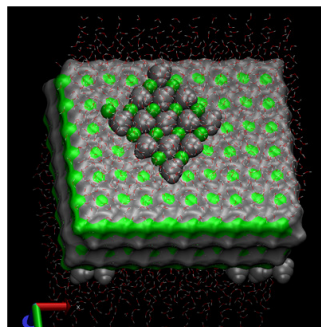


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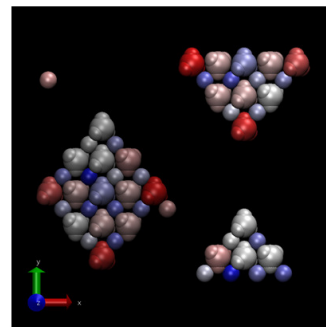
Solvation dynamics of calcite

Introduction to MD simulations

Slab model formed of 7 calcite (CaCO₃) layers with etch island



Solvation rates (blue – low, red – high)



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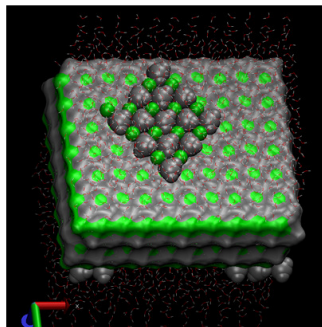
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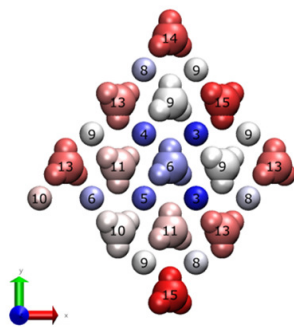
Solvation dynamics of calcite

Introduction to MD simulations

Slab model formed of 7 calcite (CaCO₃) layers with etch island



Solvation rates (blue – low, red – high)



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