



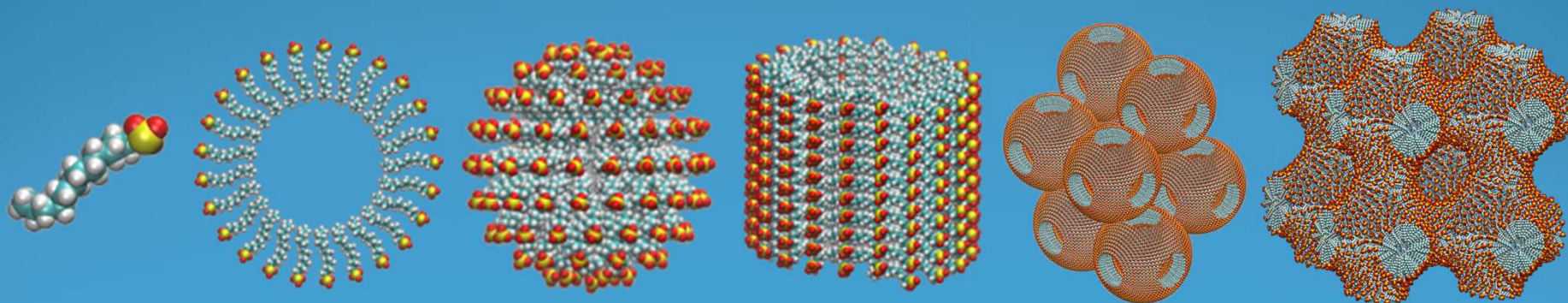
hapespyer: a versatile Python-driven toolchain to model soft matter - ALC Project -

Andrey Brukhno,

Michael Seaton, John Purton, Valeria Losasso

– *Scientific Computing, STFC/UKRI, Daresbury*

Tim Snow – *Diamond*, James Douth – *ISIS, RAL, Harwell*



<https://www.scd.stfc.ac.uk/Pages/Shapespyer.aspx>

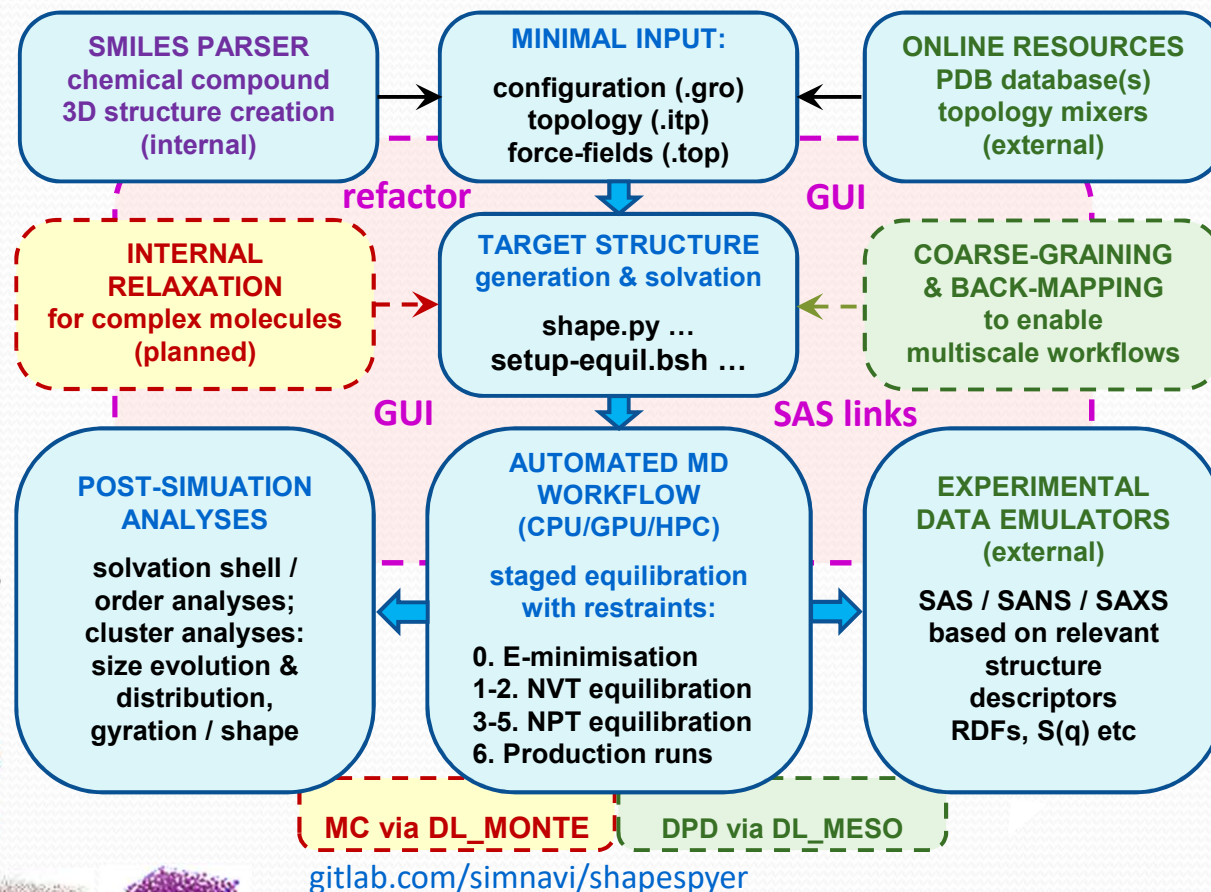
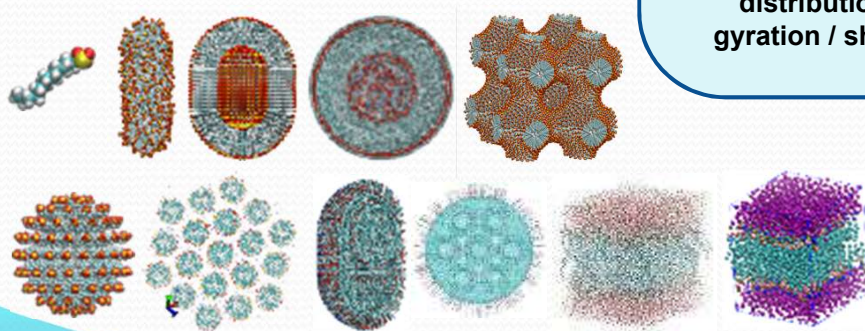
<https://gitlab.com/simnavi/shapespyer>

SHAPESPYER: a Python-driven framework for soft matter simulations

Andrey Brukhno, Michael Seaton, John Purton, Valeria Losasso, *SCD, STFC/UKRI*,
Tim Snow, *Diamond*, and James Douch, *ISIS, STFC/UKRI*

Project overview

- **Generation, simulation & analyses** of pre-equilibrated molecular structures for functional soft matter research
- **Target structures / trajectories** for academic and industrial R&D; Linking with SANS, SAXS experiments
- **Provide automated workflows** Python library, APIs, Bash scripts
- **Partners / collaborators:**
Ales Kutsepau, *ESS, Denmark*
Maggie Holme, *Chalmers, Sweden*
Hanna Barriga, *Karolinska Institutet, Sweden*
Tom Headen, *ISIS, UK – MuSSiC software*
SasView Team, *International*

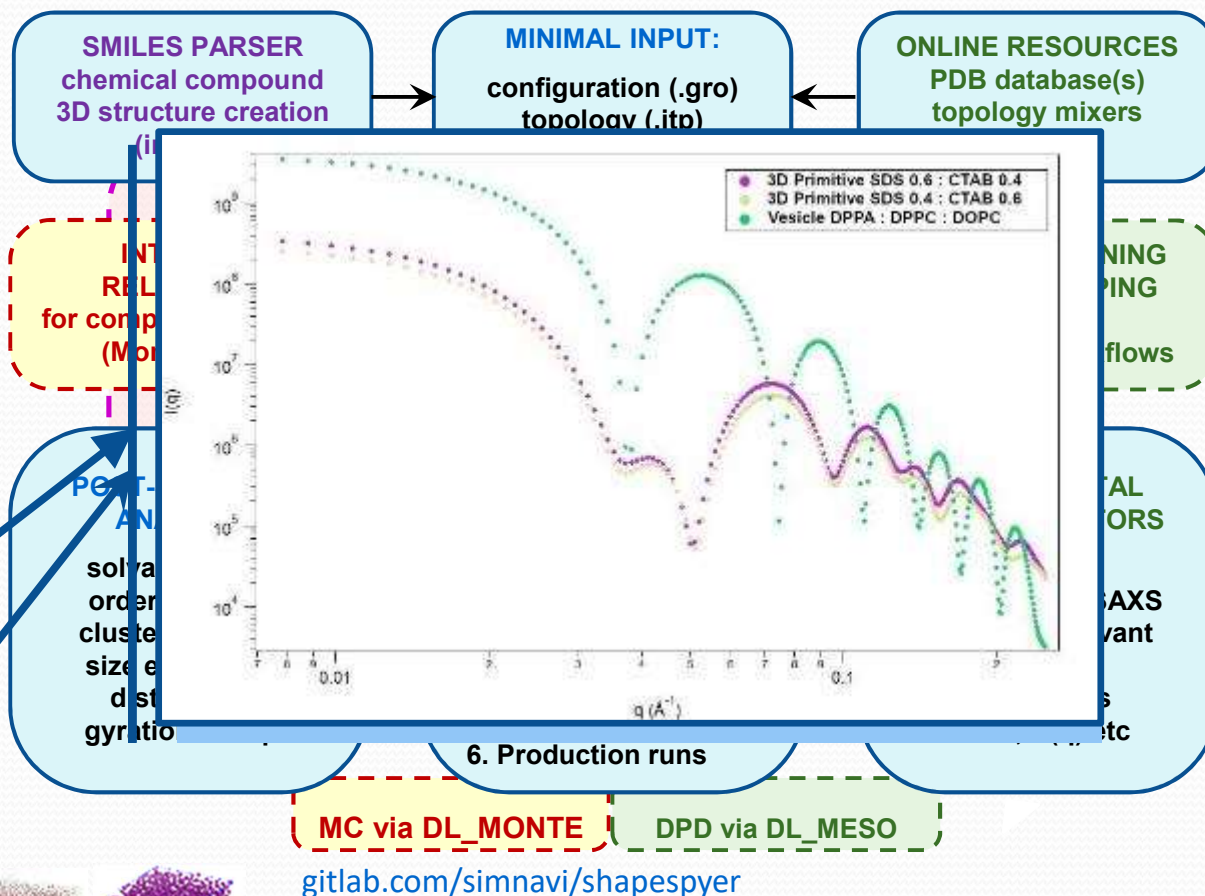
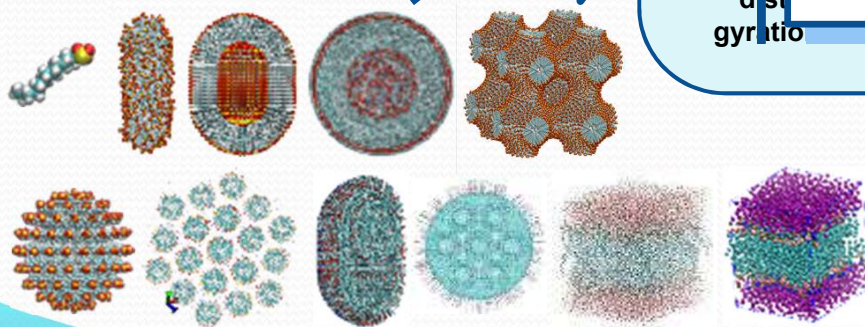


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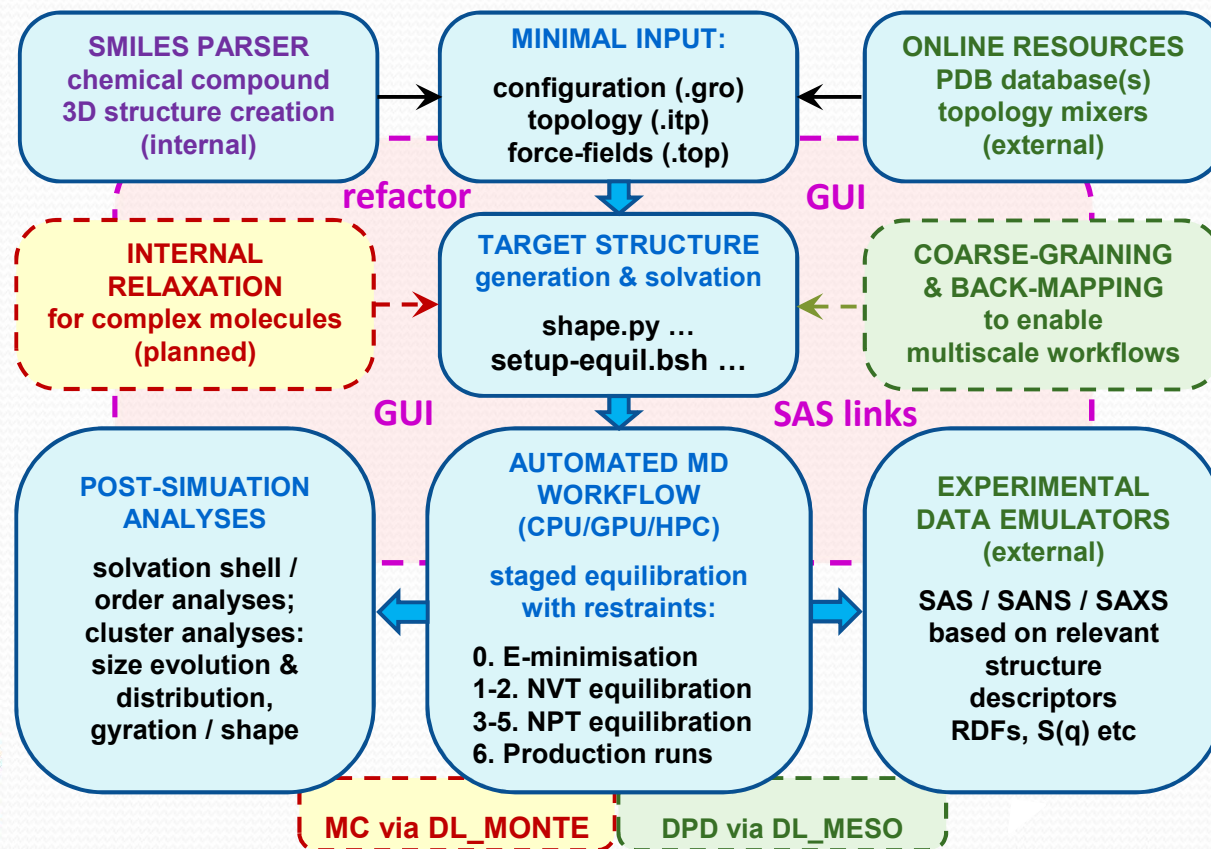
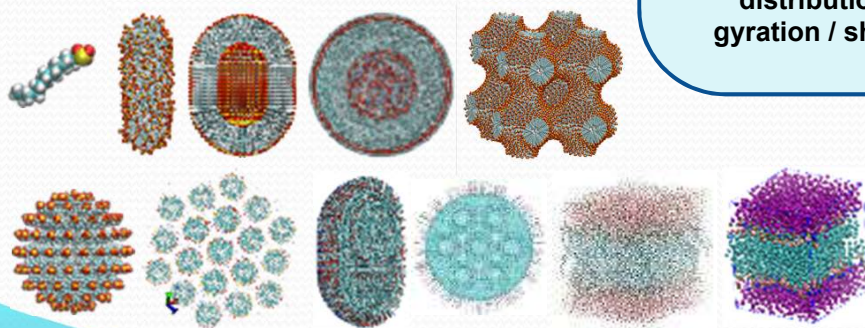


SHAPESPYER: a Python-driven framework for soft matter simulations

Andrey Brukhno, Michael Seaton, John Purton, Valeria Losasso, *SCD, STFC/UKRI*,
Tim Snow, *Diamond*, and James Douth, *ISIS, STFC/UKRI*

Project roadmap (2024-25)

- **Scientific Computing Dept / ISIS (UK)**
MC / DPD workflows - **A Brukhno / M Seaton**
Topol. / FFs – **M Demir / S Beck / C Yong**
Mono- & Bi-layer / NAMD – **V Losasso**
Links to SasView – **A Brukhno / T Snow**
- **Chalmers (Sweden) / ESS (Denmark)**
GUI via easyScience – **A Kutsepau**
SMILES module refactor => sub-package
Links to SANS, SAXS experiments
- **Partners / collaborators:**
Maggie Holme, Chalmers, Sweden
Hanna Barriga, Karolinska Institutet, Sweden
Tom Headen, ISIS, UK – MuSSiC software
SasView Team, International



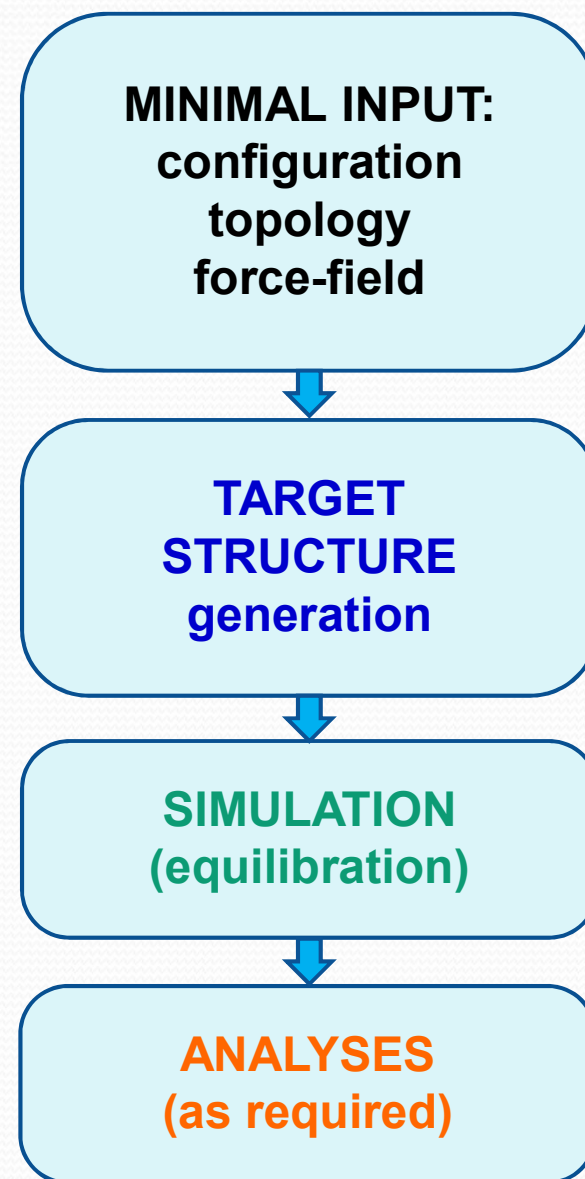
www.scd.stfc.ac.uk/Pages/Shapespyer.aspx
gitlab.com/simnavi/shapespyer



andrey.brukhno@stfc.ac.uk

Project overview

- **What is it about?**
Generation and analyses of pre-equilibrated molecular nano-structures (soft matter systems)
- **Objectives:**
Create and deploy a semi-automated workflow: Python package / APIs & Bash scripts
- **Scope:**
Providing simulation trajectories => reference structures for SAS (SANS, SAXS) & other scattering techniques and associated analyses
- **Partners:**
 - **Hanna Barriga**, *Karolinska Institutet, Sweden*
 - **Margaret Holme**, *Chalmers, Sweden*
 - **Lorna Dugan**, *University of Leeds, UK*
 - **Jian Lu**, *University of Manchester, UK*
 - **Tom Headen, H. Bindu Kolli**,
Disordered Materials, ISIS, UK



Workflow via Python (+lib) & bash scripts

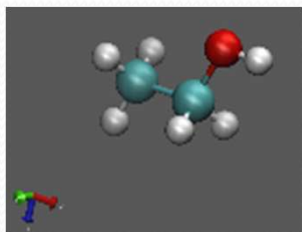
- **Core scripts for semi-automated preparation and running of simulations**
 - **shape.py** – generates a variety of structures, starting with a single molecule input (SMILES, configuration / topology)
 - **gmx-setup-equil.bsh** – adds ionic species, solvates the structure and creates the topology / force-field input for the entire system
 - **gmx-equilibrate.bsh** – runs equilibration in a few stages: energy minimisation (0), NVT (1, 2) / NPT (3 - 5) with *gradually relieved position (shape) restraints*, it also allows to proceed with subsequent production runs
- **Core utilities for automated analysis in parallel workflows via task-farming**
 - **ana-gyration.bsh** – gyration analysis & principal moments of inertia (PCA)
 - **ana-clusters.bsh** – cluster size, number and distribution analysis (a few scripts)
 - **gmx-ana-solvation.py** – solvent, atom groups content in a spherical cavity
 - **shapespyer/scripts/** – Gromacs, NAMD and DL_MESO (DPD) workflows

Molecule chemical structure from SMILES

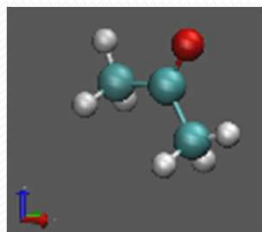
SMILES string parser => no need to search through databases

Shapspyer generates 3D coordinates for relatively simple molecules (rings**)

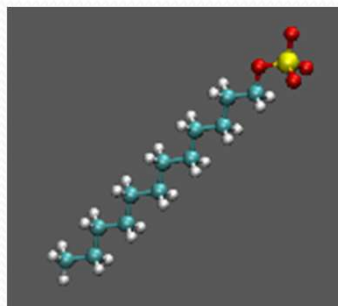
shape.py ... -i 'smiles.sml' --shape='smiles' -r 'ETHANOL'



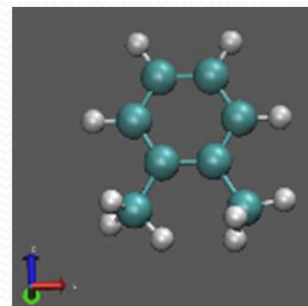
CCO
Ethanol



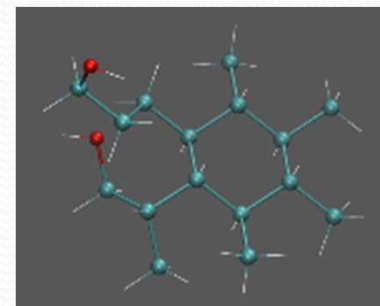
CC(=O)C
Acetone



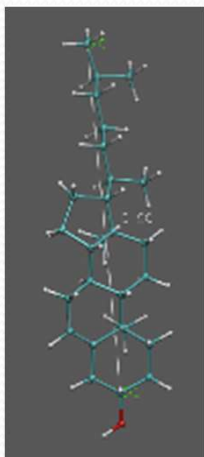
CC{11}OS(=O)(=O)[O-]
SDS



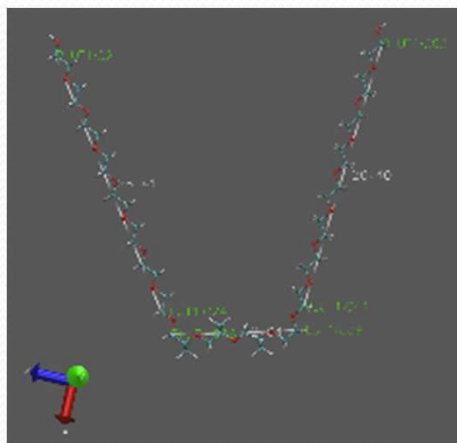
c1(C)c(C)cccc1
Orthoxylene



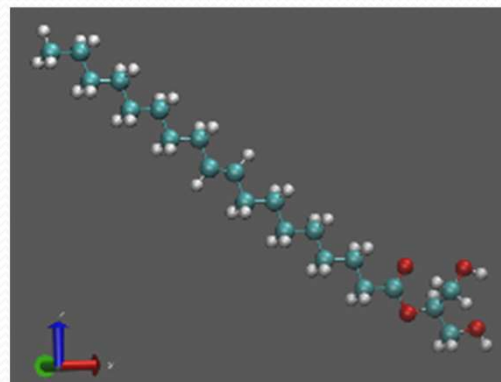
CC1C(R1)C(R2)C(R3)C(R4)C1C
Cyclohexane**



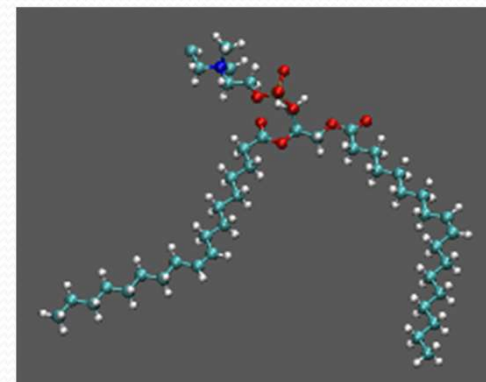
Cholesterol:**
[C27H46O]



Pluronic P123*:
PEO{n}-PPO{m}-PEO{n}



Monoolein:
[C21H40O4]



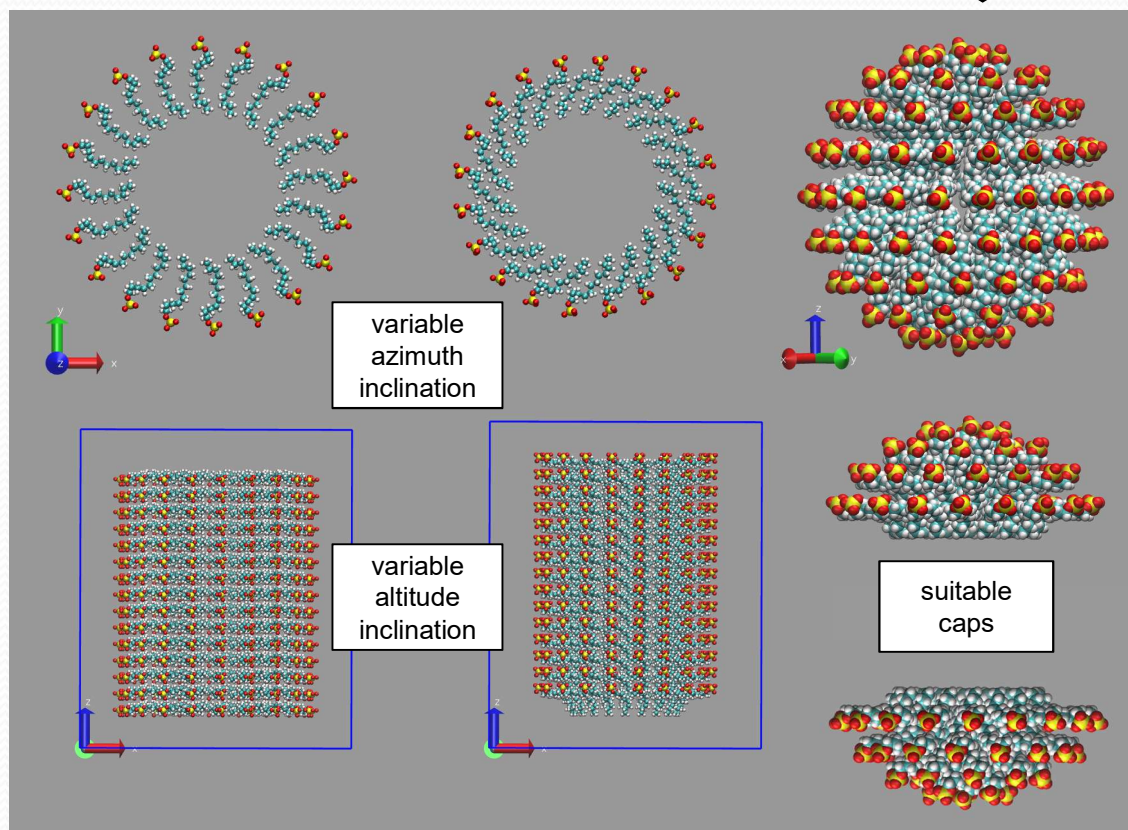
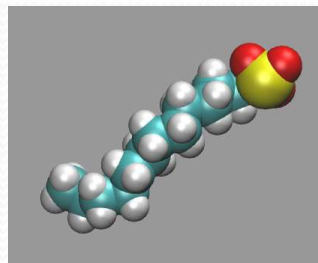
DOPC lipid:
[C44H84NO8P]

Workflow

Example: SDS

sodium-dodecyl-sulphate

- the most ubiquitous surfactant / detergent



INPUTS:

template molecule(s)
config.pdb / .gro / .xyz /
smiles.sml

force-fields

CHARMM / OPLS / Gromos
topology.top, molecule.itp

shape.py

ring (disc)
ball / ves. (sphere / micelle)
rod (cylinder / stack)
lattice (cubic, FCC, hex.)

gmsetup-equil.bsh

add ionic species & water
overall topology for system

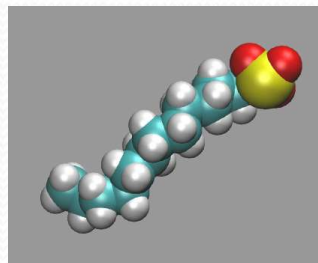
gm-equilibrate.bsh

runs equilibration
5 stages (1ns) → production

Workflow

Example: SDS

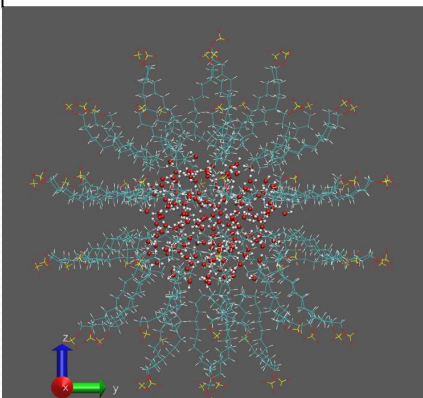
sodium-dodecyl-sulphate



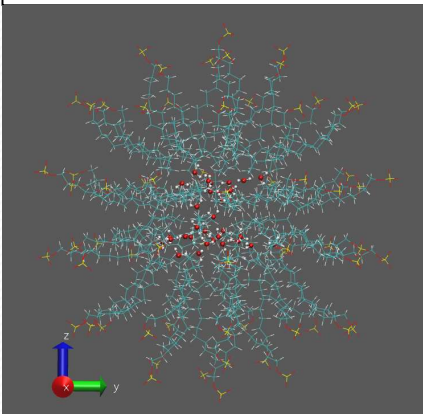
[ana-solvation.py](#)

solvent content analysis
within a given radius or shell

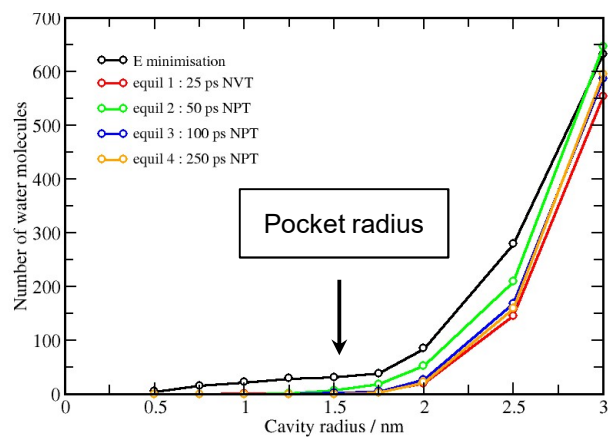
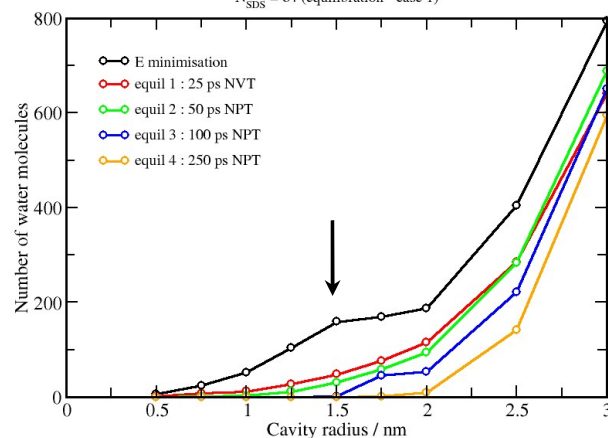
Initial structure 1 (64 mols)
water content



Initial structure 2 (64 mols)
water content



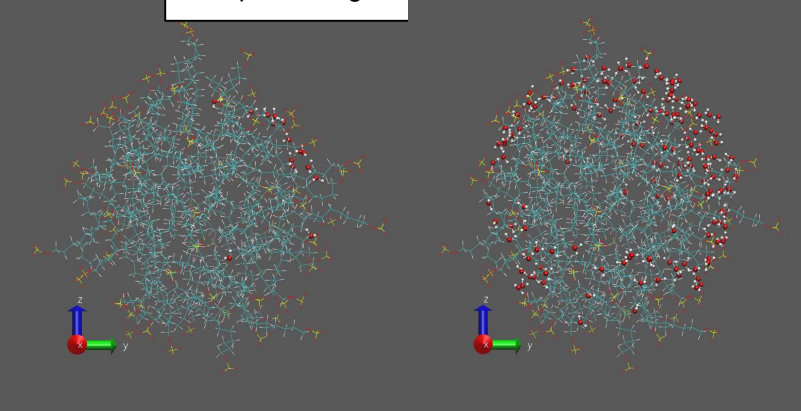
Spherical cavity occupancy inside / around a micelle
 $N_{\text{SDS}} = 64$ (equilibration - case 1)



R = 2 nm

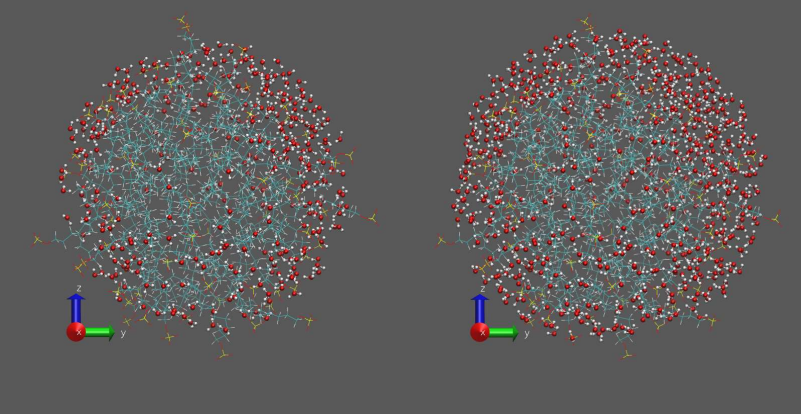
Eq: 5-th stage

R = 2.6 nm



R = 2.8 nm

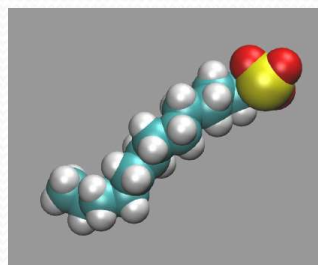
R = 3.0 nm



Workflow

Example: SDS

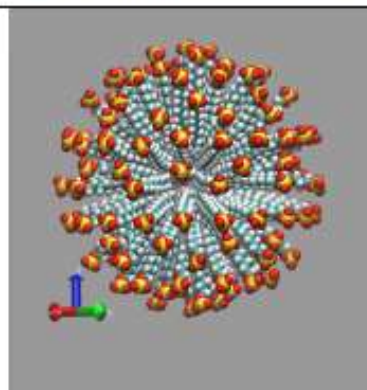
sodium-dodecyl-sulphate



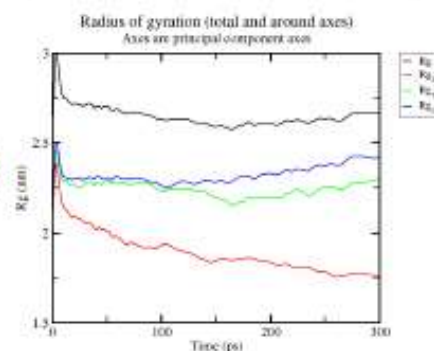
ana-gyration.bsh

radius of gyration analysis
around the 3 principal axes

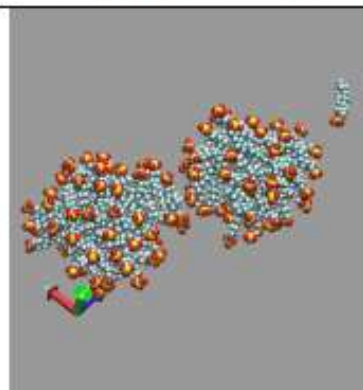
Initial structure with 126 mols



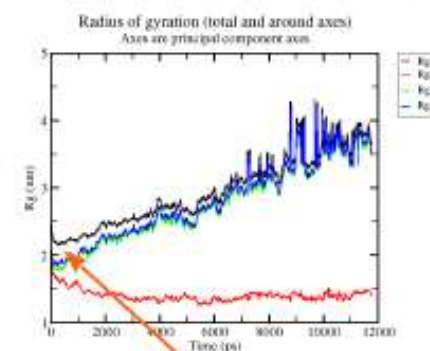
Equilibration: 300 ps



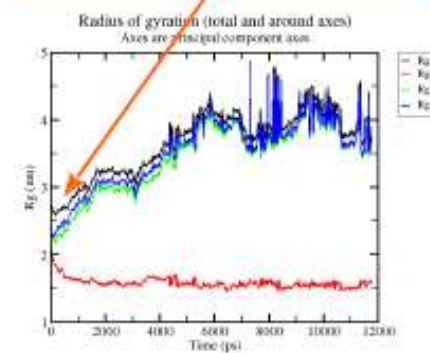
Equilibration: 735 ps



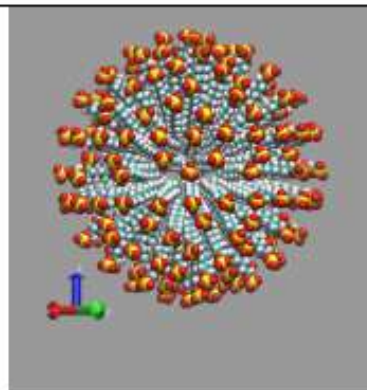
Production: 1 ns (2)



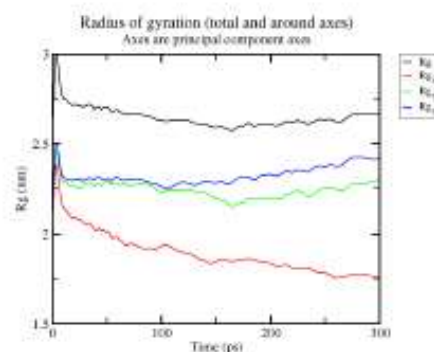
The SDS micelle splits!



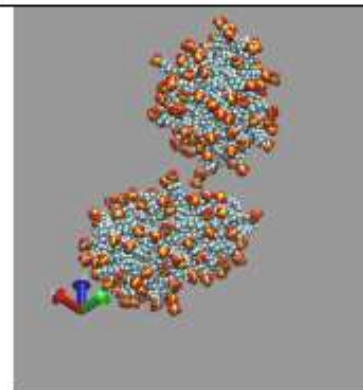
Initial structure with 180 mols



Equilibration: 300 ps



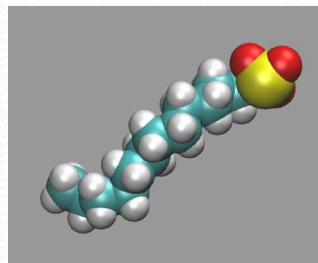
Equilibration: 435 ps



Workflow

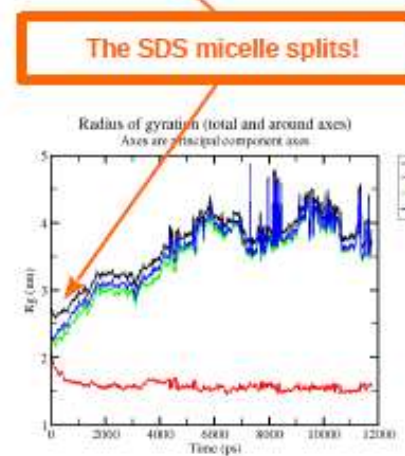
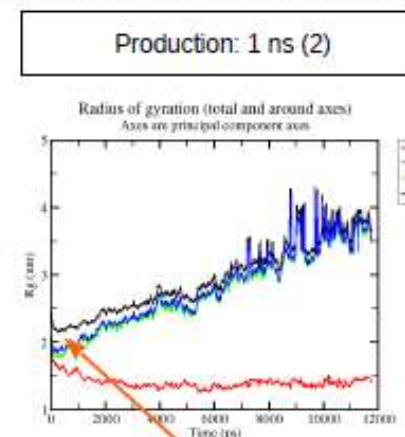
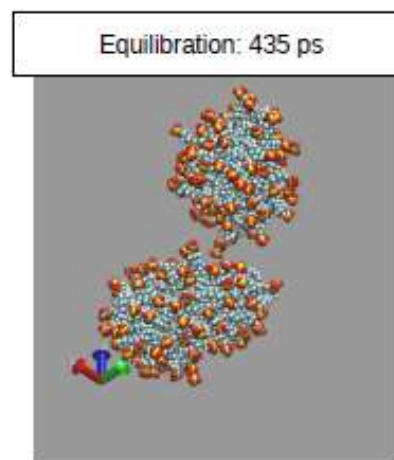
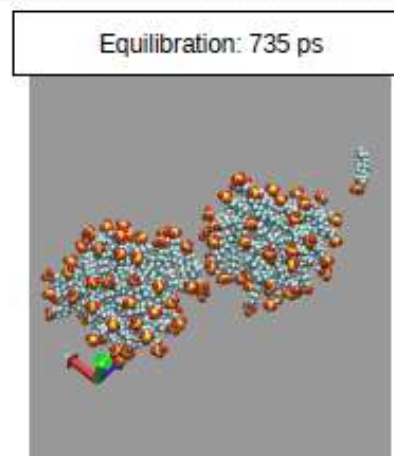
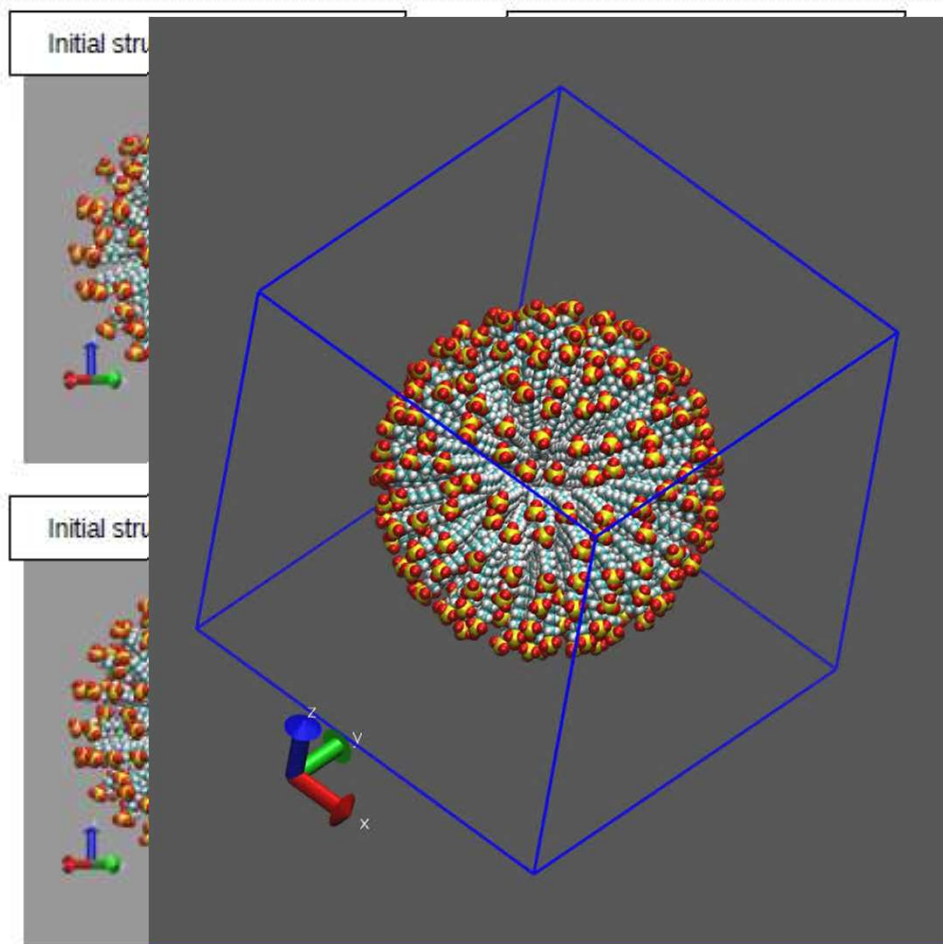
Example: SDS

sodium-dodecyl-sulphate



ana-gyration.bsh

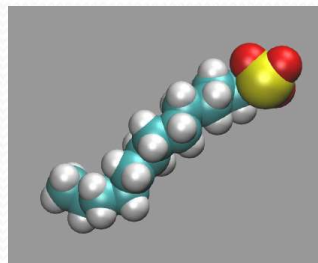
radius of gyration analysis
around the 3 principal axes



Workflow

Example: SDS

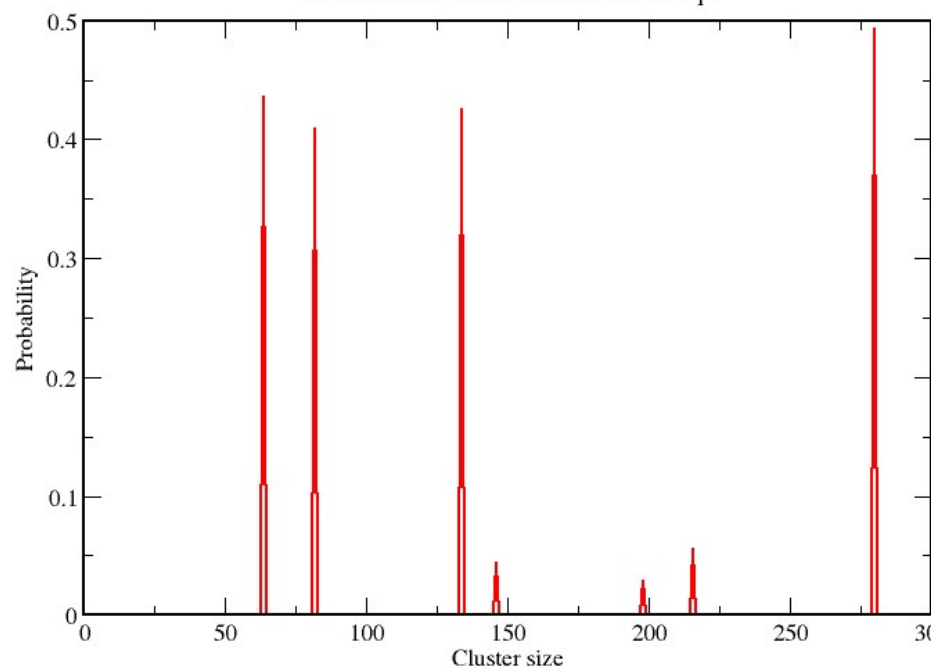
sodium-dodecyl-sulphate



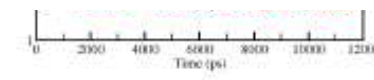
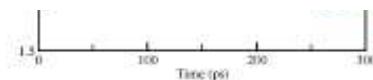
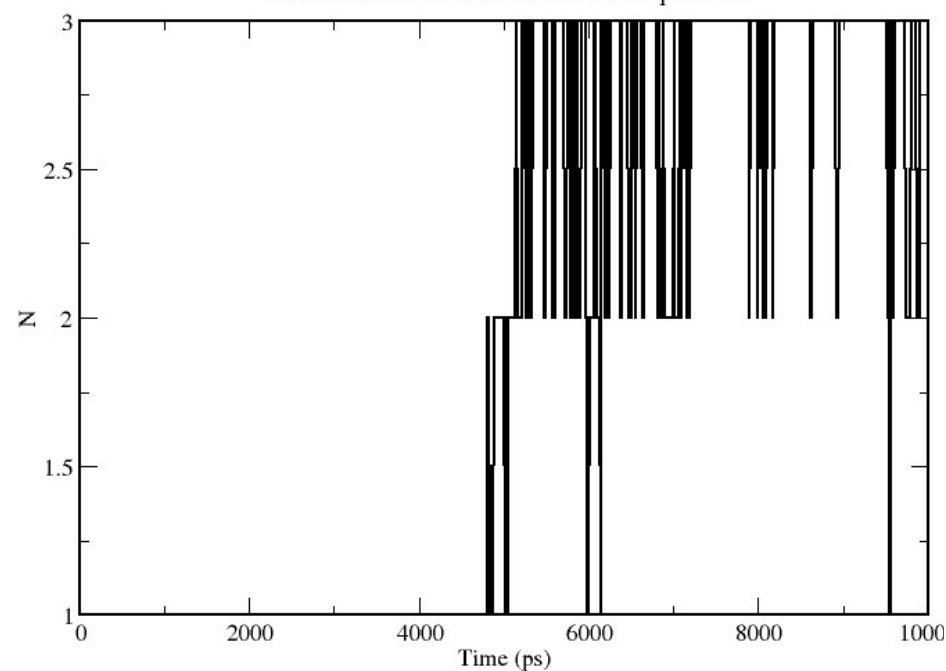
ana-clusters.bsh

cluster size and distribution
analysis along a trajectory

Cluster size distribution
SDSmic280-NAT440-CLA160-wTIP3-eq6

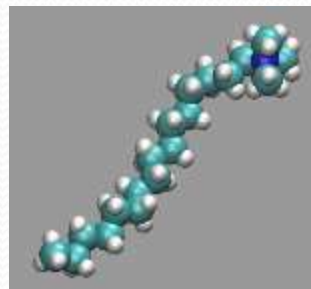


Number of clusters
SDSmic280-NAT440-CLA160-wTIP3-eq6 Nclust

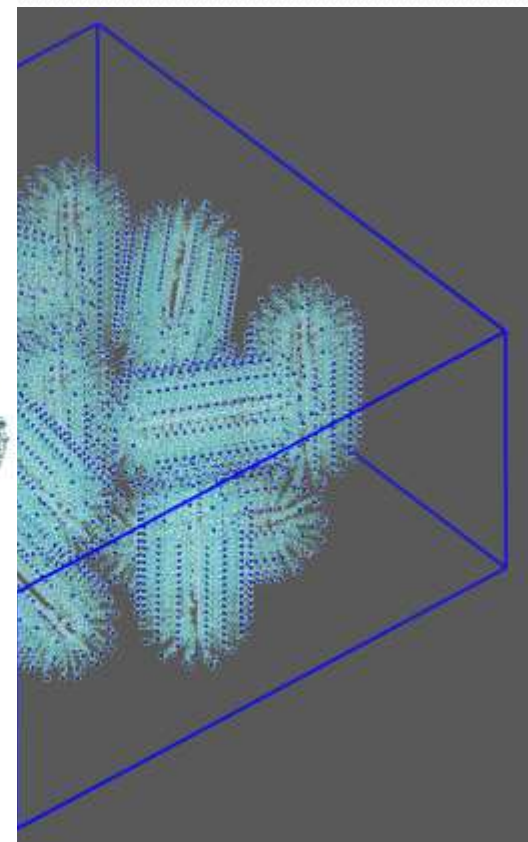
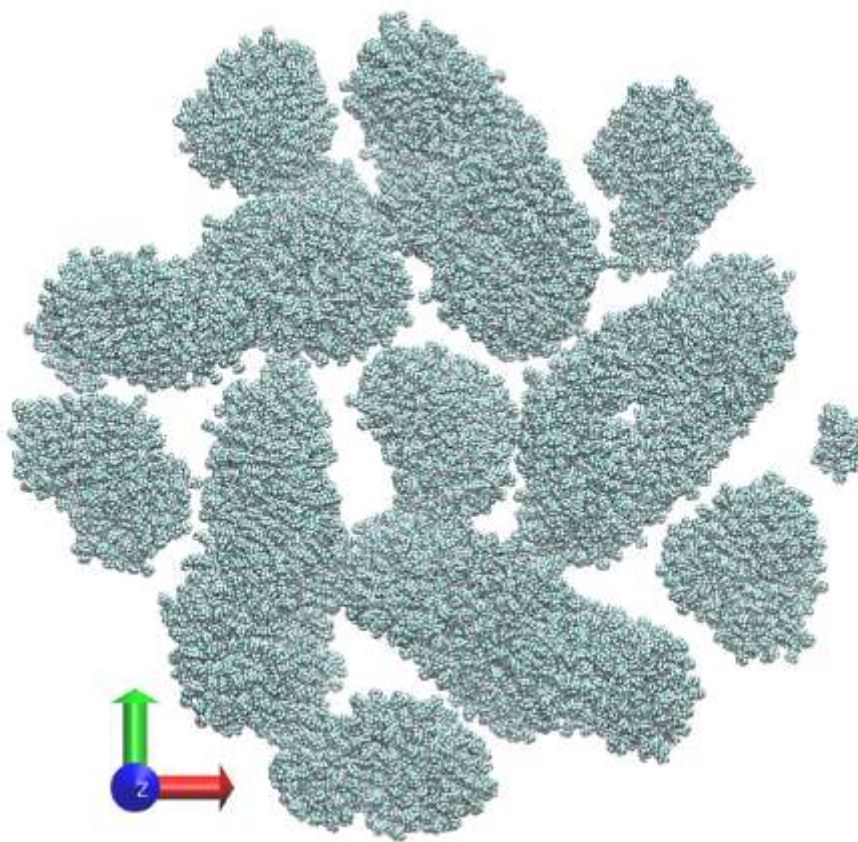
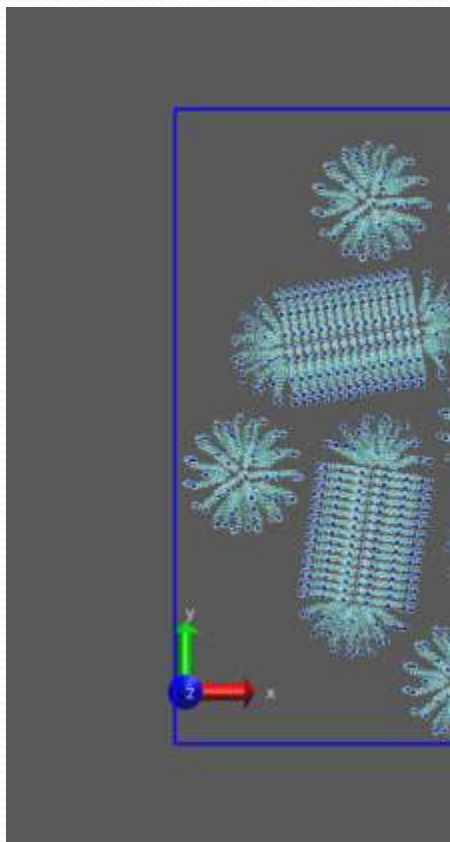


Workflow

Example: CTAB 4528 mols
Cetyl-trimethyl-ammonium-bromide

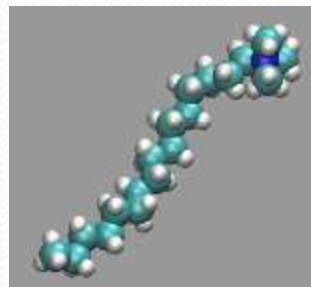


ana-clusters.bsh
ana-gyration.bsh

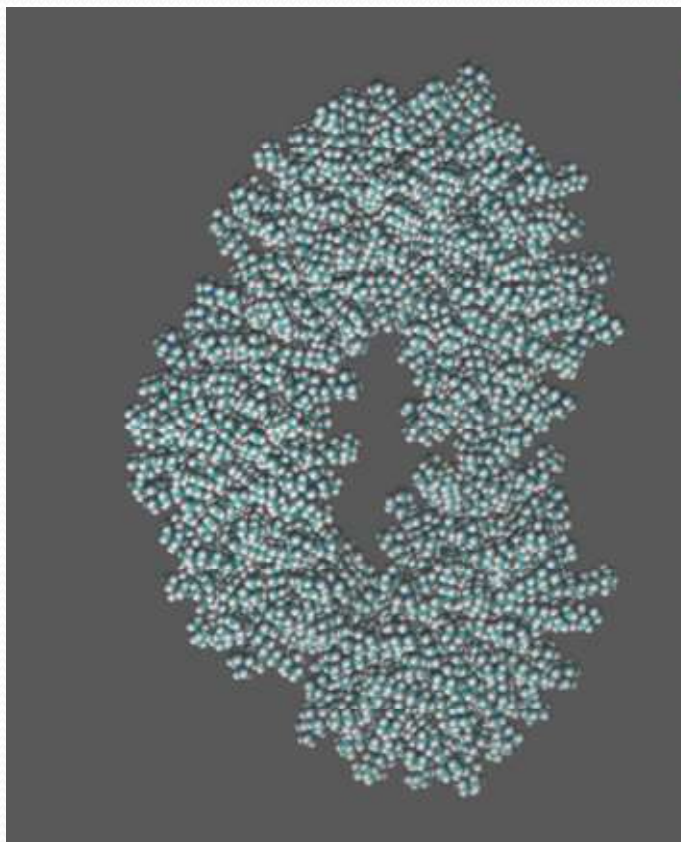


Workflow

Example: CTAB 4528 mols
Cetyl-trimethyl-ammonium-bromide

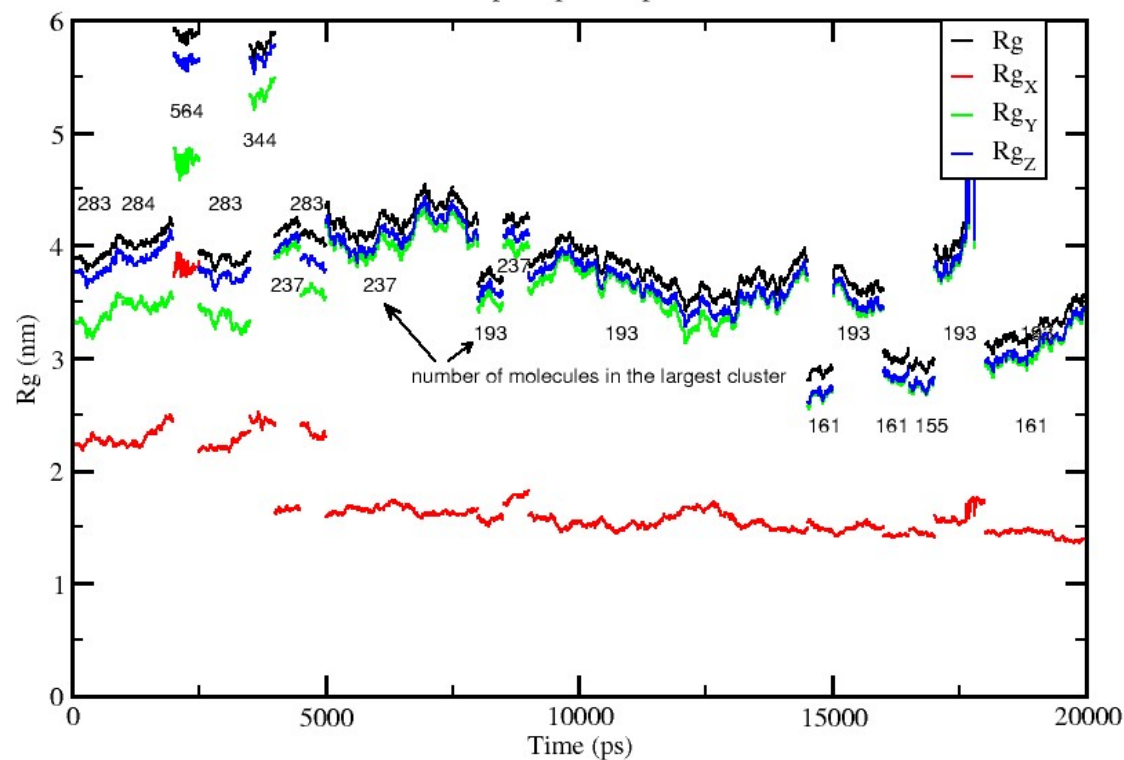


↓
ana-clusters.bsh
&
ana-gyration.bsh



Radius of gyration for the largest cluster

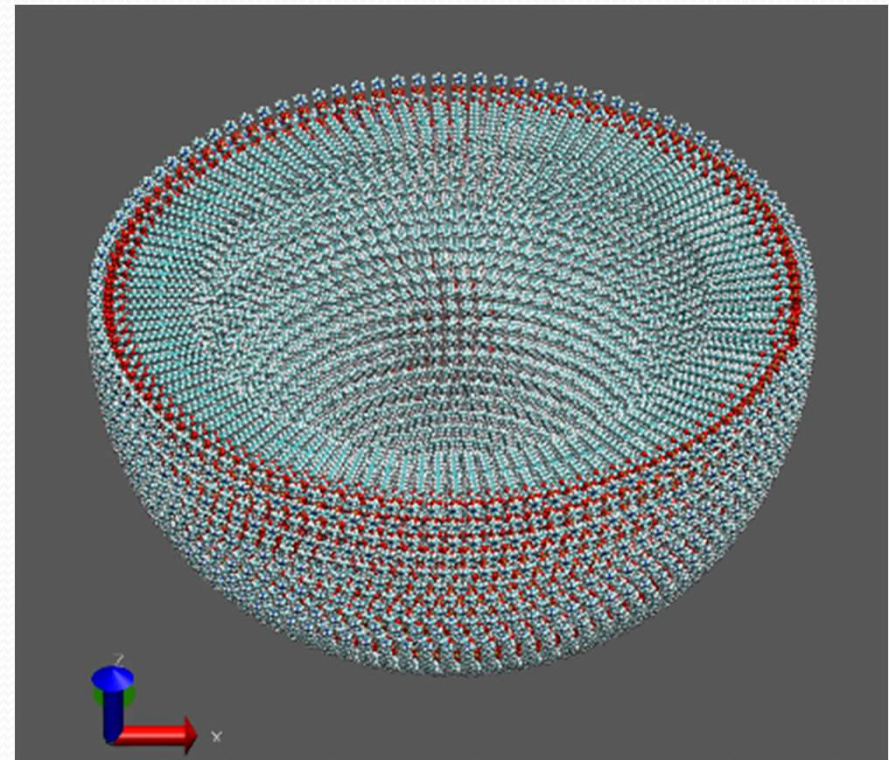
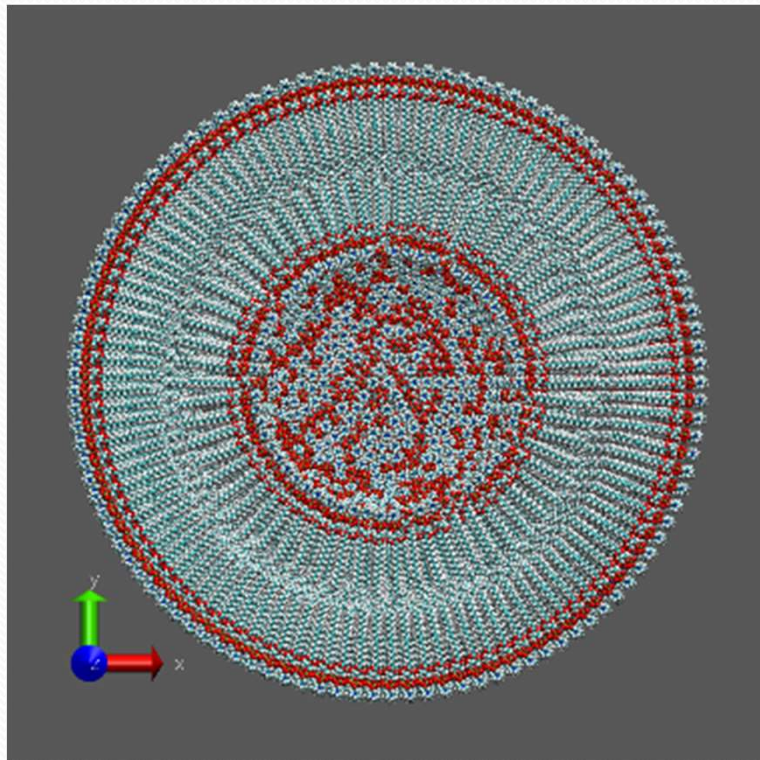
Axes are principal component axes



Spherical vesicles

[DPPA 0.4 / DPPC 0.6]_{int} : [DPPC 0.3 / DOPC 0.7]_{ext}

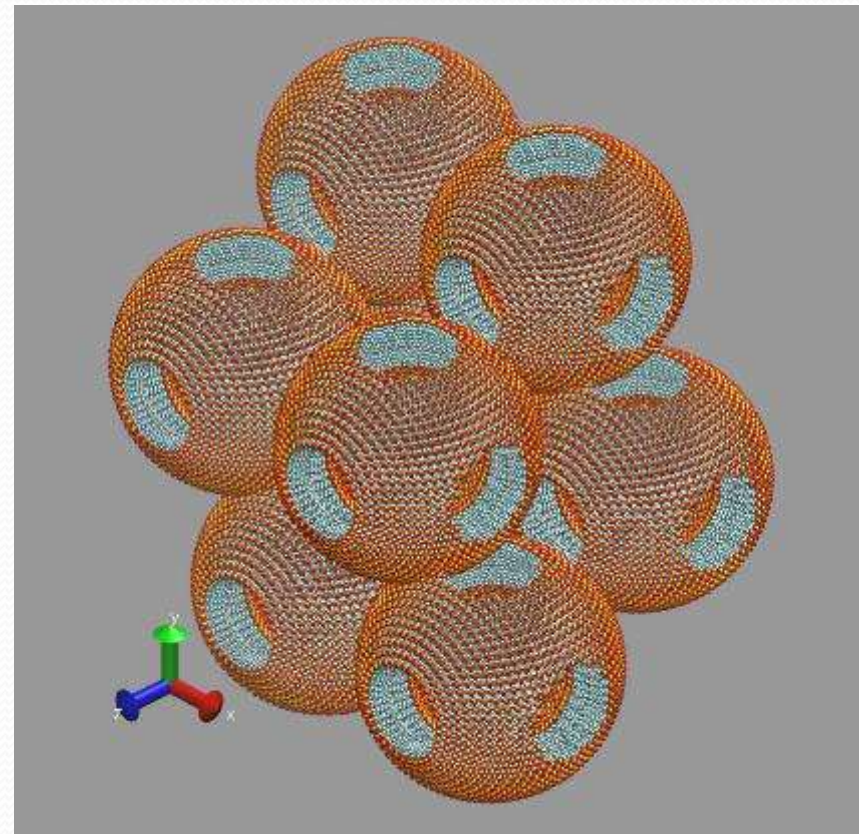
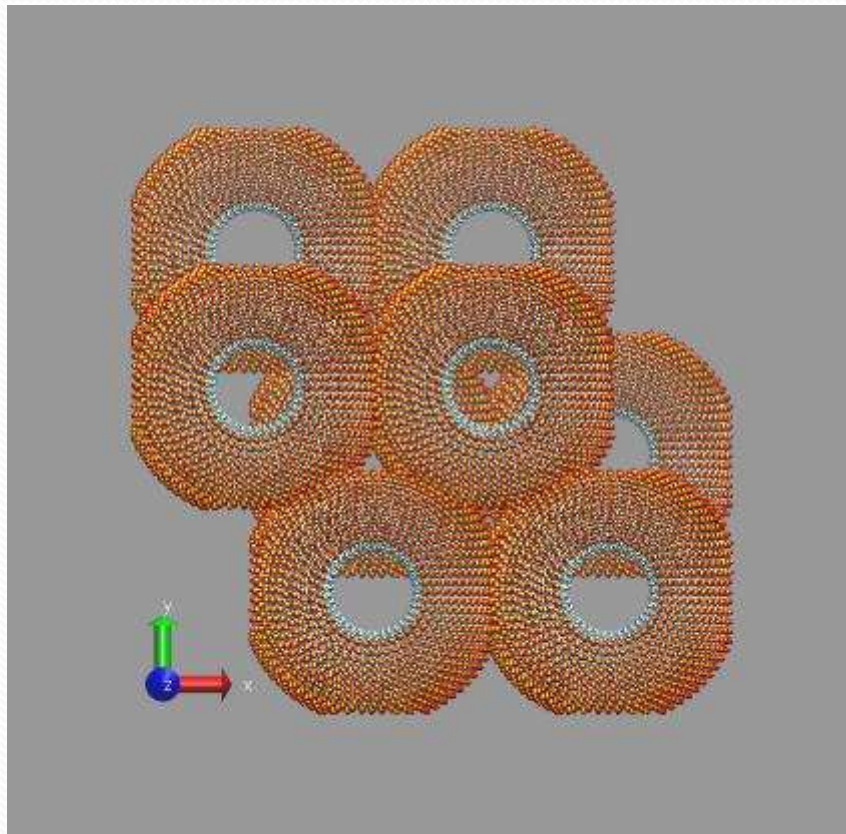
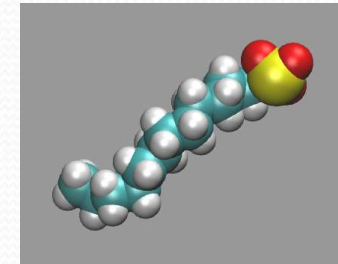
shape.py ... --shape='ves' --frc='40,60,0:0,30,70'



Nano-aggregates on a lattice

Simple Cubic, FCC, Hexagonal

shape.py ... --nx # --ny # --nz #

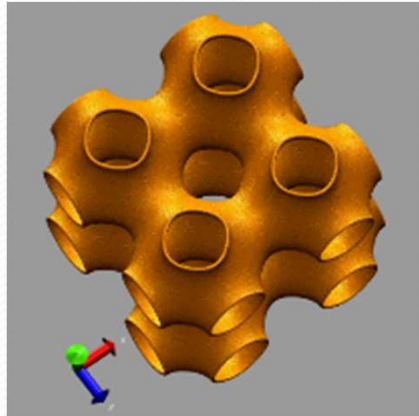


Nanostructures on Schwarz minimal surfaces

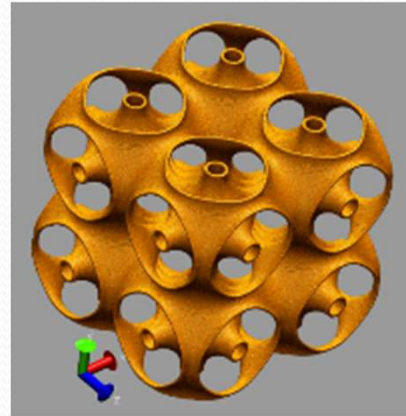
3D surfaces with zero average curvature => minimum surface tension

Shapeways can generate any analytically defined surface: $F(x,y,z) = \text{const}$

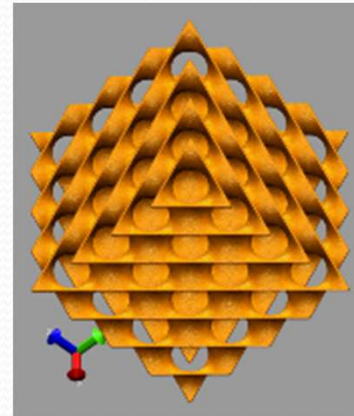
[surface3d.py](#) ...



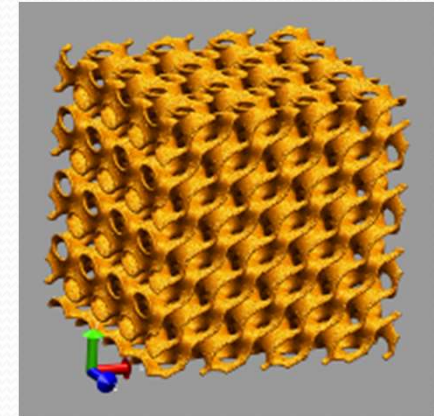
Primitive



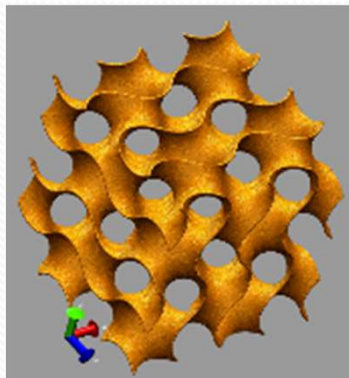
Double Primitive



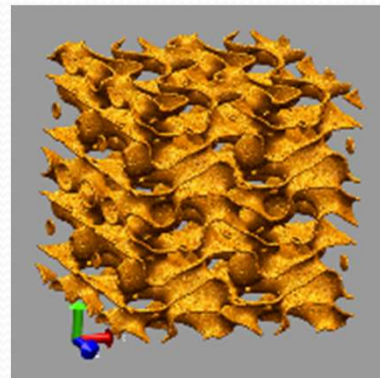
Diamond



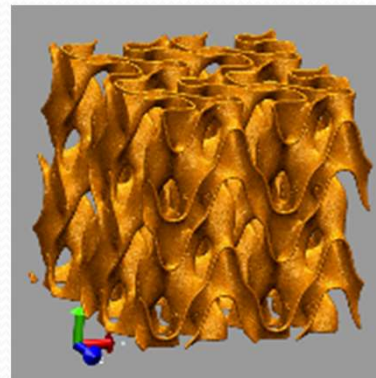
Double Diamond



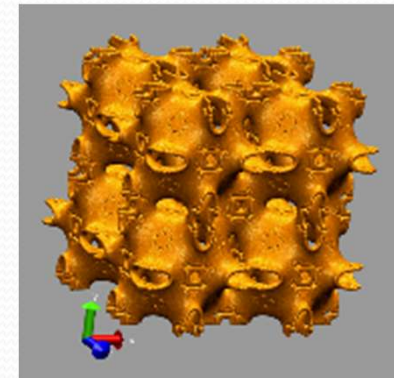
Gyroid



Double Gyroid

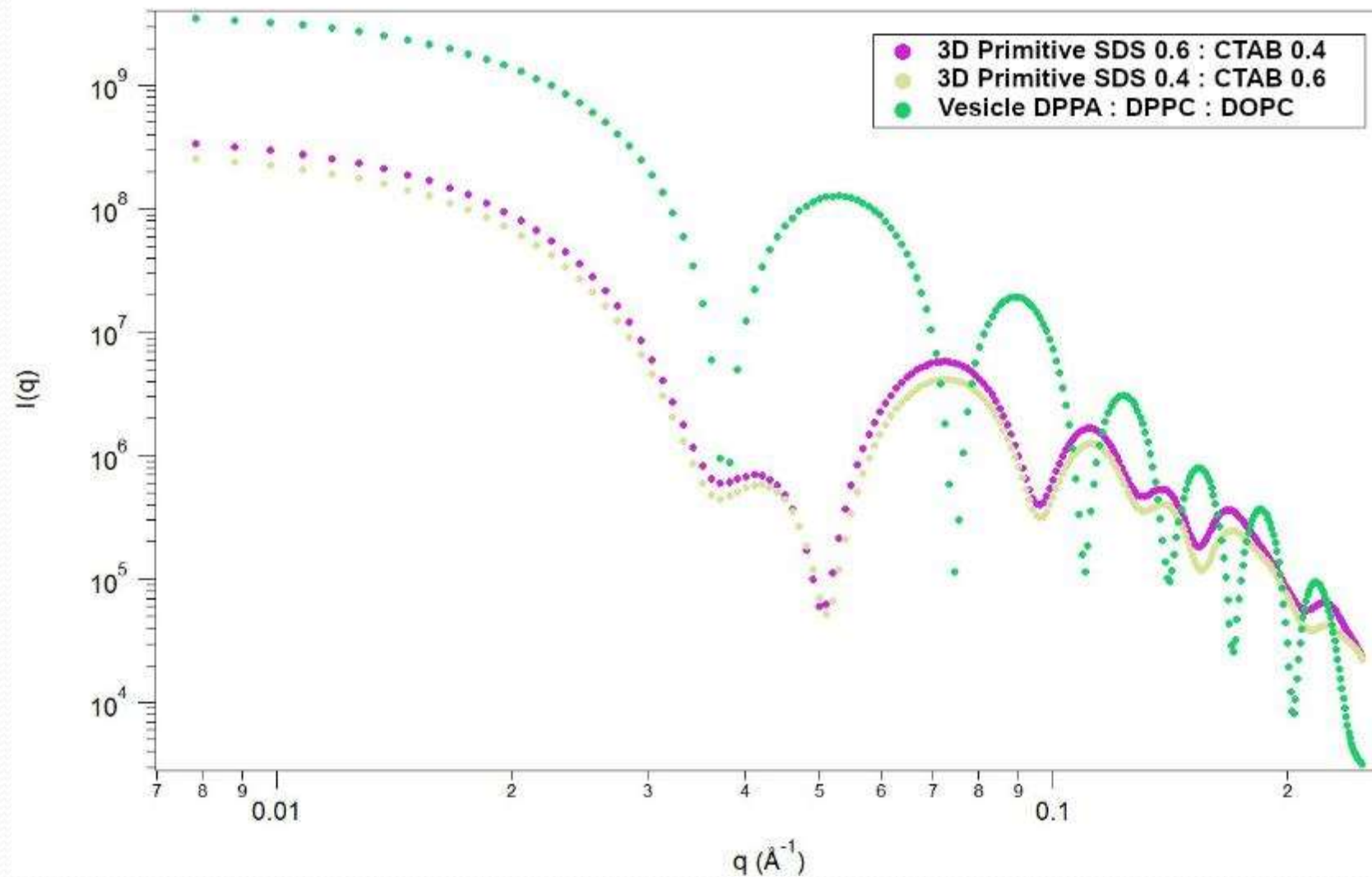


Fischer-Koch



Neovius

Nanostructures on Schwarz minimal surfaces

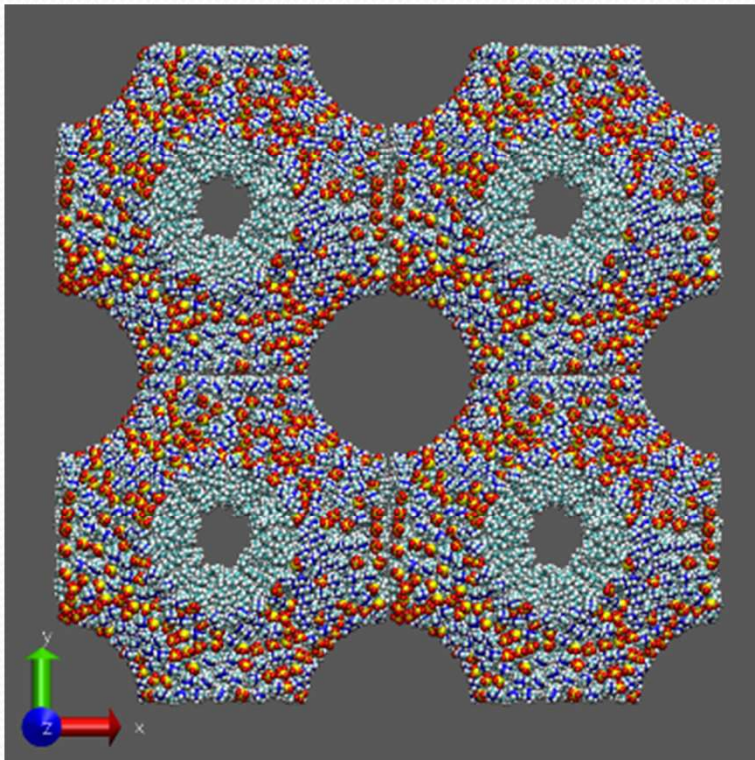


Nanostructures on Schwarz minimal surfaces

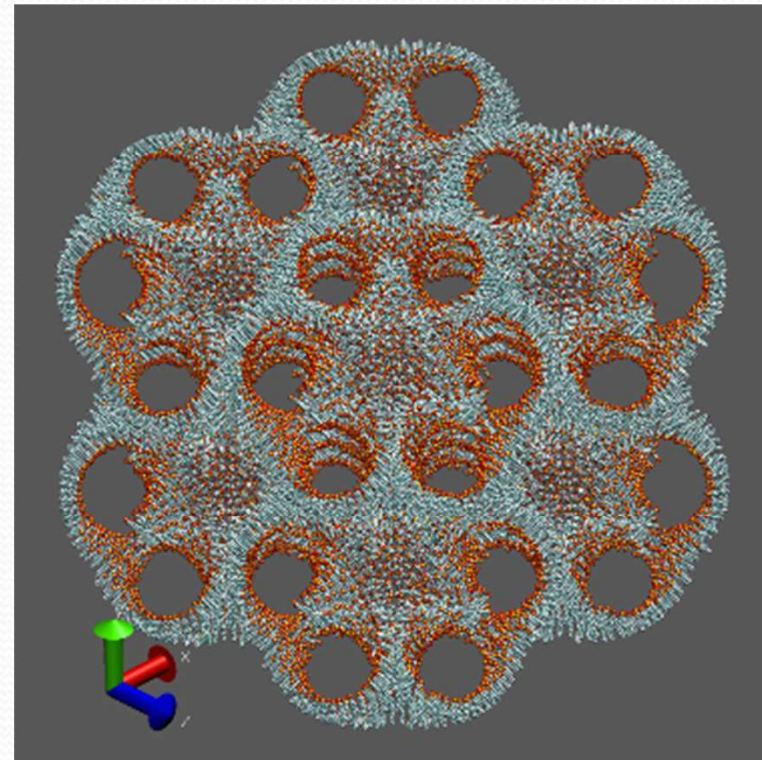
3D surfaces with zero average curvature => minimum surface tension

Shapspyer can generate any analytically defined surfaces: $F(x,y,z) = \text{const}$

[surface3d.py](#) ...



Primitive: unit cell 10 nm



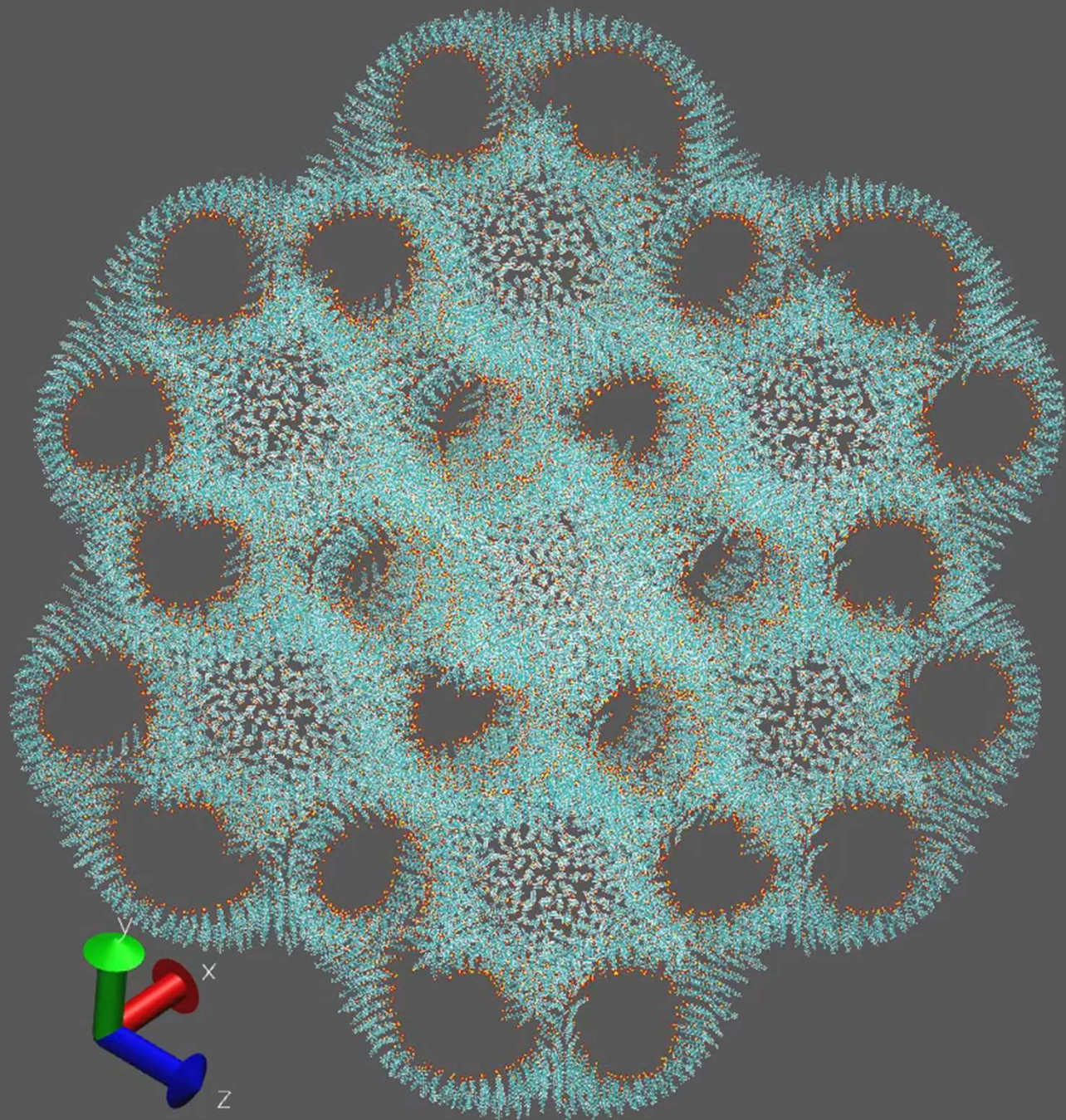
Double Primitive: unit cell 20 nm

Nanostr

3D surfaces w

Shapspyer ca

[surface3d.py](#)



Progress as of May 2025

- Generation and simulation of multicomponent nanostructures ✓
- Parsing SMILES strings for branched molecules ✓
- Assemblies on 3D lattices and minimal surfaces ✓
- Overarching Python framework: library of objects with APIs ✓
- Inputs as dictionaries via popular file format (Yaml, Json) ✓
- Jupyter notebooks with interactive visualization (NGL Viewer) for tutorials ✓ ...
- Coarse-graining functionality: Martini and DPD force-fields ✓ ...
- Molecule topology (bonds/angles) recognition ✓ / *conversion* via *DL_FIELD* ...
- *DL_MESO (DPD) / DL_POLY (MD) & NAMD workflows have been added* ✓ ...
- *Bespoke structures & simulations in response to users' requests* ...
- *Relaxation engine for atomic groups & GUI being developed* ...