Practical aspects of software for MD simulations workshop

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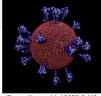
Laboratory for molecular structural dynamics





GORDON BELL PRIZE

- Special prize for HPC Covid-19 research
- NAMD winner in 2020
 - System size 305 million atoms
 - Summit and Frontera supercomputers
- Influenza virus simulations
 - 160 million atoms

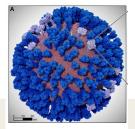


The resulting model of SARS-CoV-2.

Image courtesy of Rommie Amaro and







AŽMAN COMPUTATIONAL CENTRE

- · Located inside the National chemistry institute
- Prof. dr. Andrej Ažman pioneer of computational quantum chemistry in Slovenia (former Yugoslavia)
- > 15 Tflops



- Biosciences
- Material sciences
- Engineering



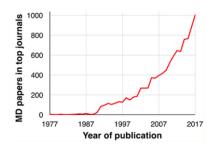




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MD SOFTWARE

- > 50 different software which enable MD simulations
- · Typically free to use for academic users
- The need to efficiently parallelise on HPC infrastructure
- Most popular software packages:
 - CHARMM
 - NAMD
 - GROMACS
 - AMBER
 - LAMMPS





CHARMM IN NAMD

- CHARMM: one of the oldest programs for molecular dynamics of biological systems. Name implies both the software suite and the forcefield
- Easy to use scripting language:
 - A lot of ready made modules for analysis etc.
- Interoperable with NAMD:
 - Scripts for analysis can be reused

```
bomlev -1

! Read topplogy and parameter files
stream toppar.str

open read unit 1 card name step5_assembly.psf
read ppf card unit 1

open read unit 1 card name step6.6_equilibration.cor
read coor card unit 1

open read unit 11 file name recentrd.dcd

trajectory iread 11 nread 1 skip 5000 begin 175000

traj read

open write card unit 10 name frame175k.pdb
write coor pdb unit 10
```







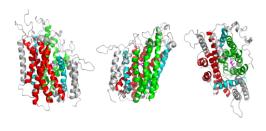
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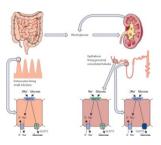
SYSTEM OF INTEREST

- SGLT1 sodium glucose cotransporter 1
- Physiological and pathophysiological importance
 - Oral rehydration therapy
 - Therapeutics for diabetes
 - Other diseases



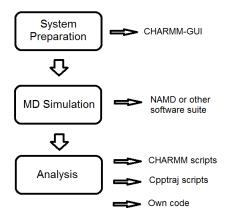








BASIC WORKFLOW





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