Preparing an MD simulation

the procedures – briefly

Marcus Elstner and Tomáš Kubař

2017, June 2

Work plan

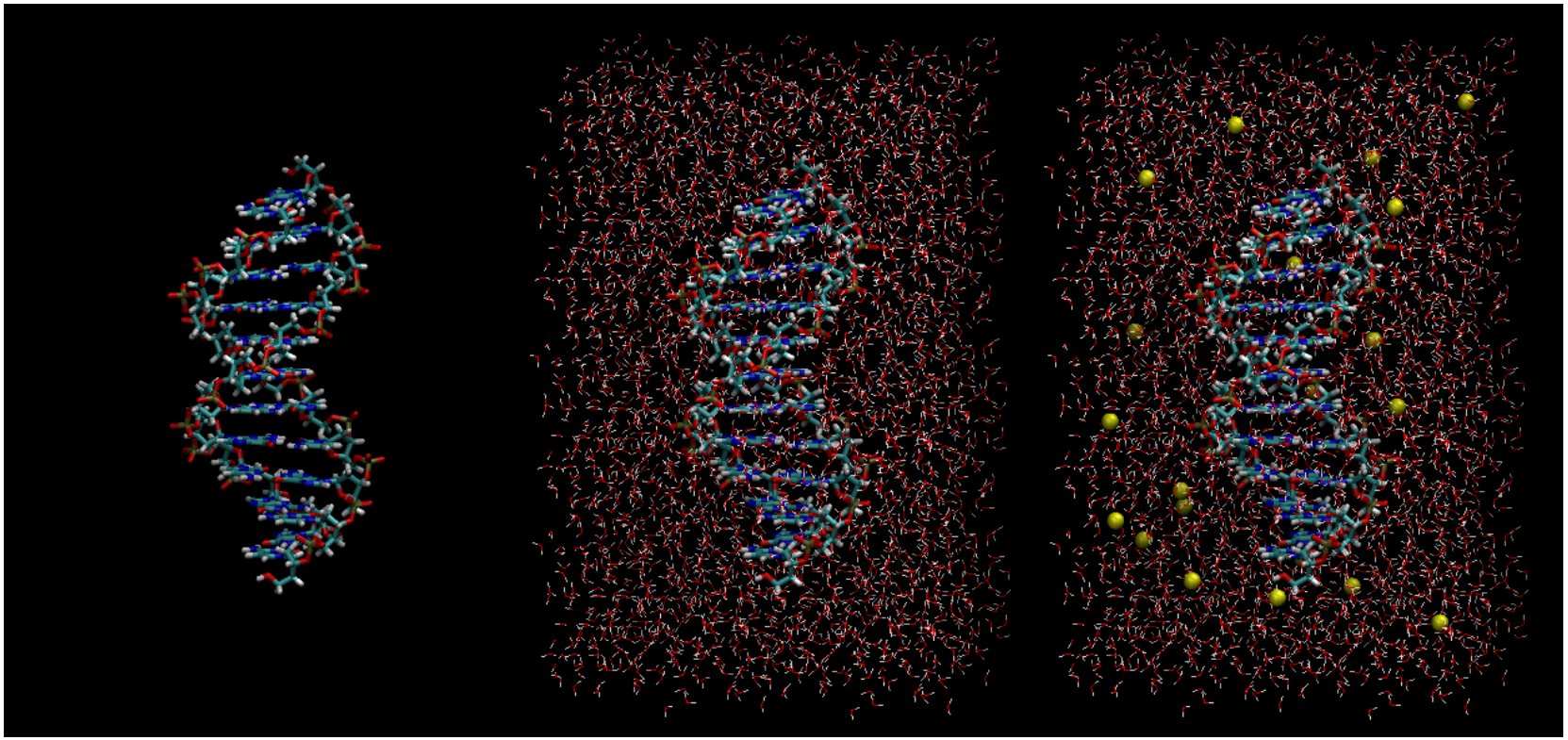
1. build the initial structure
2. bring the system into thermodynamic equilibrium
3. perform the productive simulation
4. analyze the trajectory

Tools to build the structure

- do it yourself
- specific programs within simulation packages
- 'universal' visualization programs – VMD, Molden, Pymol
- databases of biomolecular systems – PDB, NDB
- specialized web services – Make-NA
- tools to create periodic box and hydrate system

Tools to build the structure

build the solute, solvate it and add counterions



Why equilibrate?

- the initial structure may have high potential energy – dangerous – remove 'close contacts'
- often, static structure available – velocities missing
- often, structure resolved at different conditions (xtal)
- structure of solvent artificially regular – entropy wrong

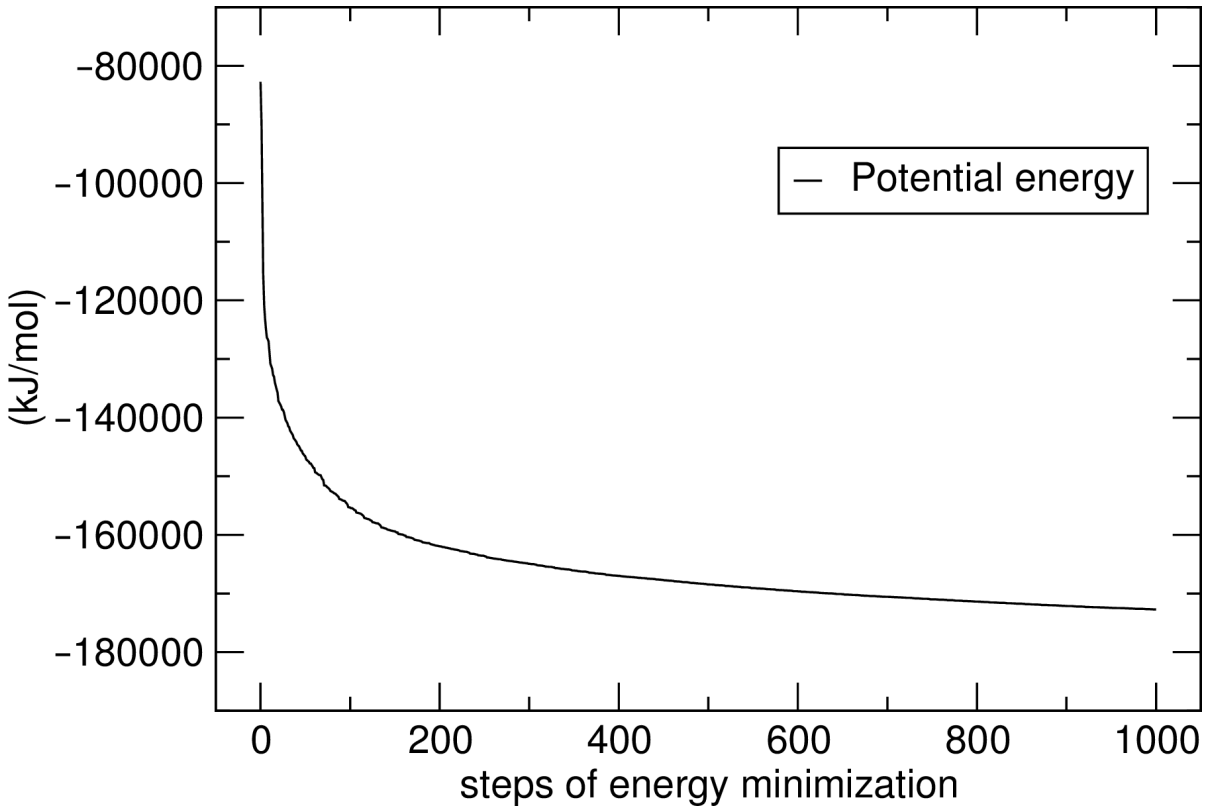
How to equilibrate

1. short energy minimization – remove ‘bad contacts’

Short energy minimization

```
integrator              =  steep
nsteps                  =  1000
pbc                     =  xyz
nstlist                 =  10       ; update pairlist
;
coulombtype             =  PME
vdwtype                 =  Cut-off
rlist                   =  1.0      ; nm
rvdw                    =  1.0      ; nm: cut-off for vdw
rcoulomb                =  1.0      ; nm
;
constraints             =  hbonds
```

Short energy minimization



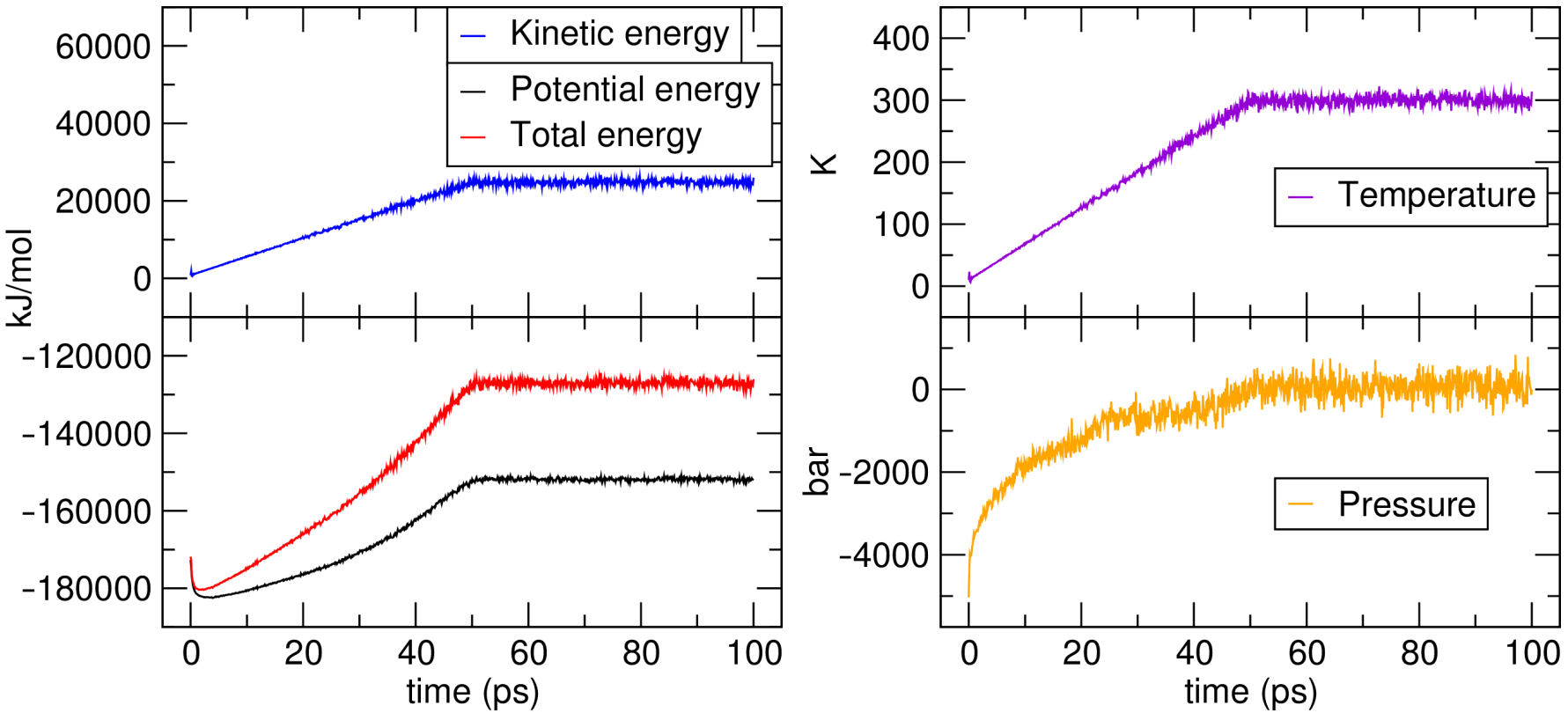
How to equilibrate

1. short energy minimization – remove 'bad contacts'
2. assignment of velocities – randomly, at some (low) T
3. thermalization – heating the system up to the desired T, possibly gradually, with a thermostat – NVT simulation

Thermalization

```
integrator        =  md
pbc               =  xyz
dt                =  0.002    ; ps
nsteps            =  50000
nstlist           =  10       ; update pairlist
coulombtype       =  PME
vdwtype           =  Cut-off
rlist             =  1.0      ; nm
rvdw              =  1.0      ; nm
rcoulomb          =  1.0      ; nm
;
gen_vel           =  yes
gen_temp          =  10.      ; K
constraints       =  hbonds
;
tcoupl            =  nose-hoover
tc_grps           =  System
tau_t             =  0.5      ; ps
ref_t             =  300.     ; K
;
annealing         =  single
annealing_npoints =  3
annealing_time    =   0.   50. 100. ; ps
annealing_temp    =  10. 300. 300. ; K
```

Thermalization



last 40 ps: $T = 300 \pm 7$ K, $p = 64 \pm 266$ bar

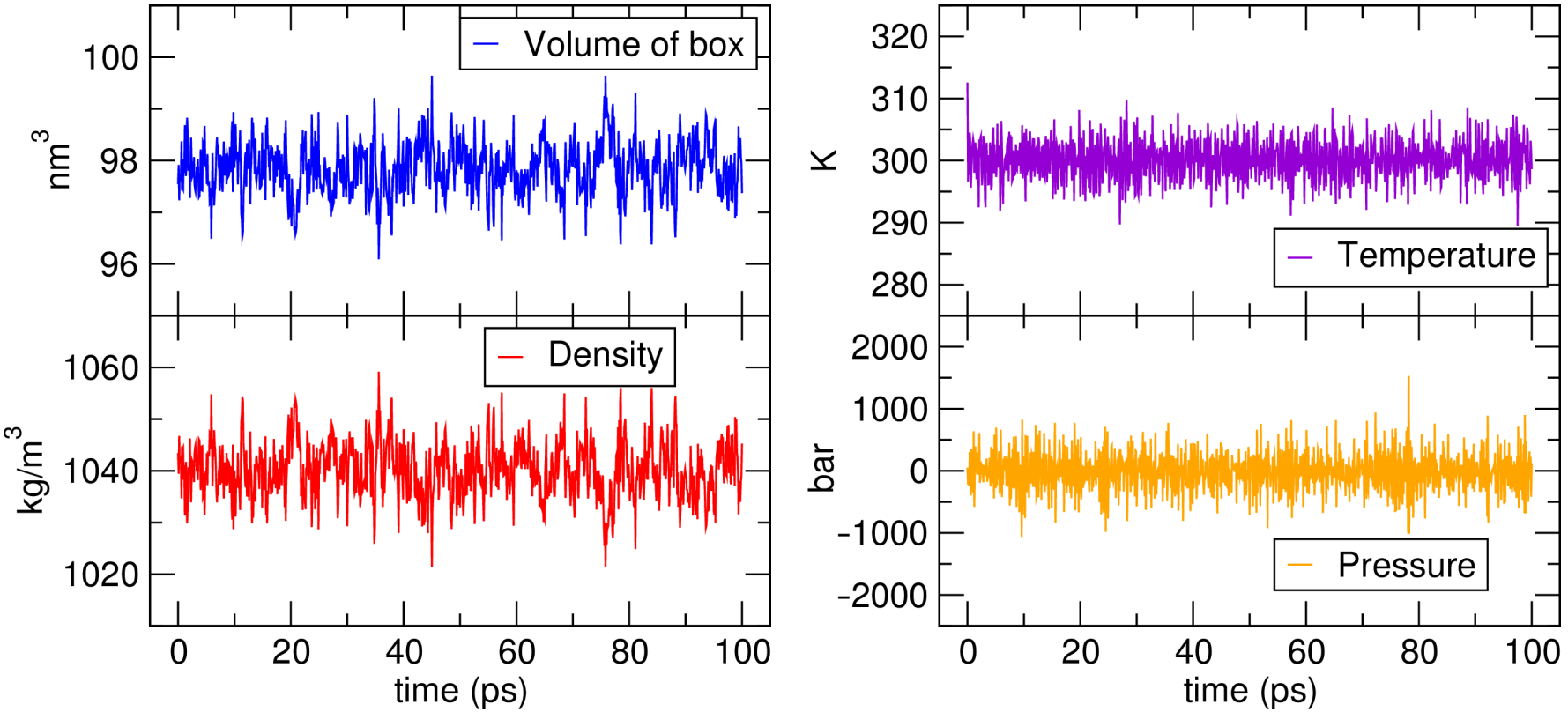
How to equilibrate

1. short energy minimization – remove 'bad contacts'
2. assignment of velocities – randomly, at some (low) T
3. thermalization – heating the system up to the desired T, possibly gradually, with a thermostat – NVT simulation
4. simulation with the same setup as the production – probably NPT, with appropriate thermostat and barostat

Equilibration

```
integrator          =  md
pbc                 =  xyz
dt                  =  0.002
nsteps              =  50000
nstlist             =  10        ; update pairlist
coulombtype         =  PME
vdwtype             =  Cut-off
rlist               =  1.0       ; nm
rvdw                =  1.0       ; nm
rcoulomb            =  1.0       ; nm
;
gen_vel             =  no
constraints         =  hbonds
;
tcoupl              =  nose-hoover
tc_grps             =  System
tau_t               =  0.5       ; ps
ref_t               =  300.      ; K
;
pcoupl              =  parrinello-rahman
tau_p               =  0.5       ; ps
ref_p               =  1.0       ; bar
compressibility     =  4.5e-5    ; 1/bar
```

Equilibration



last 40 ps: $T = 300 \pm 3$ K, $p = -11 \pm 331$ bar

What comes then?

Productive simulation

– easy ☺

Analysis of the trajectory

– let us see...