

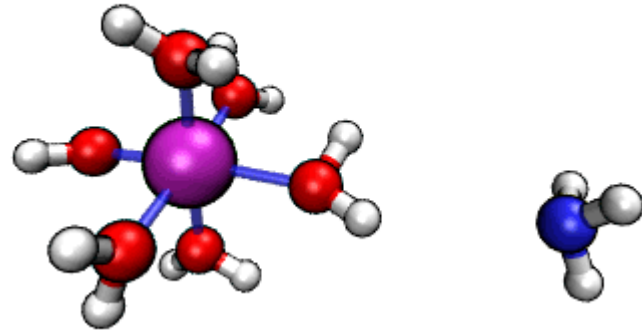
***Ab initio* Molecular Dynamics with ORCA**



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Why another AIMD code?

- There exist several dozen AIMD codes (*CP2k, CPMD, ...*)
- We do not want to get into competition with those.
- **Different focus:**
 - No plane waves, just Gaussian atom centered basis functions
 - No periodic boundary conditions
 - Huge variety of electron structure methods (*HF, DFT, Semiempirics, MP2, CASSCF, DMRG, MRCI, CCSD*)
 - QM/MM directly in ORCA (*no external code/driver*)
 - Semiempirics MD (*xTB or PM3*) is interesting for large systems



The ORCA MD Module

- Standard ORCA input files are **keyword-based** (*not scripts*):

```
! MP2 RHF def2-TZVP TightSCF

%mp2
  MaxCore 100
end

%paras
  rCO = 1.20
  ACOH = 120
  rCH = 1.08
end

* int 0 1
  C 0 0 0 0.00 0.0 0.00
  O 1 0 0 {rCO} 0.0 0.00
  H 1 2 0 {rCH} {ACOH} 0.00
  H 1 2 3 {rCH} {ACOH} 180.00
*
```

The ORCA MD Module

- Standard ORCA input files are **keyword-based** (*not scripts*):
- Specifying „MD“ in the simple input switches on the MD module.
- All input for the MD module is found within „%md . . . end“

```
! MD BLYP D3 def2-SVP
%md
  initvel 300_K
  timestep 0.5_fs
  thermostat berendsen 300_K timecon 10.0_fs
  dump position stride 1 filename "trajectory.xyz"
  run 2000
end
* xyz 0 1
O   -2.03740   -1.21799   -0.08342
H   -1.06493   -1.04408   -0.02285
H   -2.37327   -1.07034    0.83692
O   -1.65042    1.84243    0.07893
H   -0.72656    1.49786   -0.01029
H   -2.07086    1.65422   -0.79801
*
```

The ORCA MD Module

- Standard ORCA input files are **keyword-based** (*not scripts*):
- Specifying „MD“ in the simple input switches on the MD module.
- All input for the MD module is found within „%md ... end“

```
! MD BLYP D3 def2-SVP

%md
  initvel 300_K
  timestep 0.5_fs
  thermostat berendsen 300_K timecon 10.0_fs
  dump position stride 1 filename "trajectory.xyz"
  run 2000
end

* xyz 0 1
  O   -2.03740   -1.21799   -0.08342
  H   -1.06493   -1.04408   -0.02285
  H   -2.37327   -1.07034    0.83692
  O   -1.65042    1.84243    0.07893
  H   -0.72656    1.49786   -0.01029
  H   -2.07086    1.65422   -0.79801
*
```

**This part is a
script –
it runs from top
to bottom!**

The ORCA MD Module

- While the overall ORCA input file is **keyword-based**, the MD input (inside „%md . . . end“) is a **script** which is executed during the ORCA run.
- The language of the MD input is **SANscript** (*which I am currently developing*)

<https://brehm-research.de/sanscript>

The ORCA MD Module

SANscript example program:

```
VAR tape : Character[]
    pos, p : Integer
    a : String

a := "+++++++[->+++++++<]>+.<++++[->++++<]>+++.<+++[->+++<]>+++++.++.----- .+++++
    ++.<+++++[->-----<]>-----.<+++++[->-----<]>-.<+++++[->++++<]>+++ .----- .+++ .+
    ++.---.++++.++++.----- .++++.-.-.++.++++.<+++++[->-----<]>----- .---.<"

pos := 0
p := 0
tape.resize 1

WHILE p < a.length DO
    IF      a[p] = ']' THEN IF tape[pos] <> 0 THEN WHILE a[p] <> '[' DO p-- ENDDO ENDIF
    ELSEIF a[p] = '+' THEN tape[pos]++
    ELSEIF a[p] = '-' THEN tape[pos]--
    ELSEIF a[p] = '.' THEN Print tape[pos]
    ELSEIF a[p] = '<' THEN pos--
    ELSEIF a[p] = '>' THEN pos++ IF pos >= tape.size THEN tape.add 0 ENDIF
ENDIF
    p++
ENDDO
```

The ORCA MD Module

SANscript example program:

```
VAR tape : Character[]
    pos, p : Integer
    a : String

a := "+++++++[->+++++++<]>+.<++++[->++++<]>+++.<+++[->+++<]>+++++.++.----- .+++++
    ++.<+++++[->-----<]>----- .<+++++[->-----<]>>-.<+++++[->++++<]>+++ .----- .+++ .+
    ++.--- .++++.++++.----- .++++.-.-.++.++++.<+++++[->-----<]>----- .---.<"

pos := 0
p := 0
tape.resize 1

WHILE p < a.length DO
    IF      a[p] = ']' THEN IF tape[pos] <> 0 THEN WHILE a[p] <> '[' DO p-- ENDDO ENDIF
    ELSEIF a[p] = '+' THEN tape[pos]++
    ELSEIF a[p] = '-' THEN tape[pos]--
    ELSEIF a[p] = '.' THEN Print tape[pos]
    ELSEIF a[p] = '<' THEN pos--
    ELSEIF a[p] = '>' THEN pos++ IF pos >= tape.size THEN tape.add 0 ENDIF
ENDIF
p++
ENDDO
```

It emulates a Turing machine!

→ Proof that SANscript is a Turing-complete language! 😊

The ORCA MD Module

How to run the example? SANSscript interpreter is not yet available...

The ORCA MD Module

How to run the example? SANSscript interpreter is not yet available...

```
! MD
%md
$verbose execute 1$ # reduce printlevel
VAR tape : Character[]
    pos, p : Integer
    a : String

a := "+++++++[->+++++++<]>+.<++++[->++++<]>+++.<+++[->++++<]>+++++.++.-----+.+++++
++.<+++++++[->-----<]>-----.<+++++[->-----<]>-.<+++++[->++++<]>++++.-----+.+++.+
+.++++.++++.-----+.++++.-.-.++.++++.<+++++[->-----<]>-----.-.-.<"

pos := 0
p := 0
tape.resize 1

WHILE p < a.length DO
    IF      a[p] = ']' THEN IF tape[pos] <> 0 THEN WHILE a[p] <> '[' DO p-- ENDDO ENDIF
    ELSEIF a[p] = '+' THEN tape[pos]++
    ELSEIF a[p] = '-' THEN tape[pos]--
    ELSEIF a[p] = '.' THEN Print tape[pos]
    ELSEIF a[p] = '<' THEN pos--
    ELSEIF a[p] = '>' THEN pos++ IF pos >= tape.size THEN tape.add 0 ENDIF
    ENDIF
    p++
ENDDO
end

* xyz 0 1
  Ar 0.0 0.0 0.0
*
```

Just run it in ORCA 😊

The ORCA MD Module

There is now a Turing-complete scripting language inside ORCA

→ In theory, you can solve **any** computational problem with ORCA 😊

The SANscript language is still in development, but standard MD runs already work reliably.

Later, you will be able to have loops / branches / etc. in your MD input, allowing for complicated protocols.

```
! MD BLYP D3 def2-SVP

%md
  initvel 300_K
  timestep 0.5_fs
  thermostat berendsen 300_K timecon 10.0_fs
  dump position stride 1 filename "trajectory.xyz"
  run 2000
end

* xyz 0 1
  ...
*
```

Implemented Features (*ORCA 4.2.1*)

- AIMD with many different electron structure methods (*HF, DFT, MP2, Semiempirics, xTB, CASSCF, ...*)
- Trajectory output in **XYZ, PDB, DCD format**
- **Restart ability** to continue MD runs
- Simple **thermostats** (*Berendsen*)
- Keeping track of **energy drift** / conserved quantity
- Optional **repulsive walls** (*rectangular, elliptical, etc.*)
- **Constraints** (*distances / angles / dihedrals / centers of mass*)
- ORCA-internal **QM/MM** simulations
- **Region features** (*different thermostats for different parts of the system, etc.*)
- Cartesian **L-BFGS optimizer** for very large systems (*10000s of atoms*)

Planned Features

- **More sophisticated thermostats**
(Nose-Hoover-Chains? CSVN?)
- **Restraints** *(currently only constraints implemented)*
- **Metadynamics** *(free energy sampling)*
→ e.g. accurate prediction of pK_A values
- **Calculation of properties** along trajectories
- **Vibrational spectra from AIMD** (IR, Raman, VCD, ROA)
→ many anharmonicities and full solvent influence!

Manual

There is a chapter on the MD module in the ORCA manual (sec. 9.34, „*Detailed Input* → Ab initio Molecular Dynamics Simulations“).

There, you find a list of commands with description of all the options.

The manual of the MD module can also be found on my homepage:

<https://brehm-research.de/orcamd>

A library of input examples will be created in the future.

If you have questions, write a post in the **ORCA forum!**
(*others might have same question; will be interested in answer*)