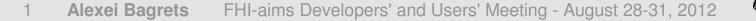


Hands-on session: brief introduction into AITRANSS

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What is AITRANSS ?



• AITRANSS (*ab initio* transport simulations) : project under continuous development at Inst. of Nanotechnology (INT) of the Karlsruhe Inst. of Technology (KIT) since 2002

 when combined with FHI-aims, is a postprocessor module: enables calculation of electron transmission across molecular junctions based on a Landauer formalism

• advanced options to appear in future releases (spin-polarized transport, out-of-equilibrium response, etc.)

• when using AITRANSS, please cite the reference:

Andreas Arnold, Florian Weigend, and Ferdinand Evers, "Quantum chemistry calculations for molecules coupled to reservoirs: Formalism, implementation, and application to benzenedithiol." J. Chem. Phys. **126**, 174101 (2007).



Source of code & supporting materials



- Code is placed at the subdirectory **aitranss**/ of the FHI-aims release
- aitranss/ contains
 source/: with Fortran90 code & Makefile
 tcontrol.script/: contains a script to create a mandatory input
 file tcontrol
 electrodes.library/: library of fcc Au clusters modeling electrodes
 archetypical examples (benzene-dithiol, alkyl
 wire) with input & (partially) output files
- Documentation: look at README file and Chapter 5 of FHI-aims manual



Compiling the AITRANSS module



- Prerequisite: Fortran90/95 compiler, compiled LAPACK & BLAS libraries (e.g. Intel's MKL)
- Use an example Makefile found at /source, and adjust it accordingly
- Encouraged is to use compiler options aka "-openmp" to build a multithreaded code based on OpenMP directives
- For now (hands-on session) use precompiled binary file(s) and scripts: see next page for details



Links to binary files, scripts, visualization tool



- To be able to execute precomplied binary files of FHI-aims and aitranss, and related scripts, please, create symbolic links (or, alternatively, copy files) mkdir bin ; cd bin
 - ln -s /home/bude/k0019299/bin/aims.scalapack.mpi.x .
 - ln -s /home/bude/k0019299/bin/aitranss.x .
 - ln -s /home/bude/k0019299/bin/tcontrol.aims.x .
 - ln -s /home/bude/k0019299/bin/aims2pdb .
- Edit your .bashrc file, add a line: export PATH=~/bin:\$PATH
- To be able to use a simple structure visualization tool Rasmol (supporting a PDB format), create a symbolic link (or copy the binary file)
 cd bin
 - ln -s /home/bude/k0019299/bin/rasmol .



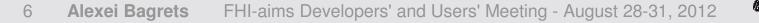
Hands-on session: collection of examples



- Please, create a working directory and copy a collection of examples, e.g.
 mkdir aitranss.tutorial
 - cd aitranss.tutorial
 - cp -r /home/bude/k0019299/aitranss.tutorial/examples .

Collection contains three directories:

- Simplest example, benzene-dithiol (au-c6h6-au): takes ~ 25 min. wall time
- Further example, alkyl wire (au-alkyl_chain-au): takes ~ 50 min. wall time
- Exercises (exercise.alkyl.wires): 7 different molecular structures, to be tested during free time

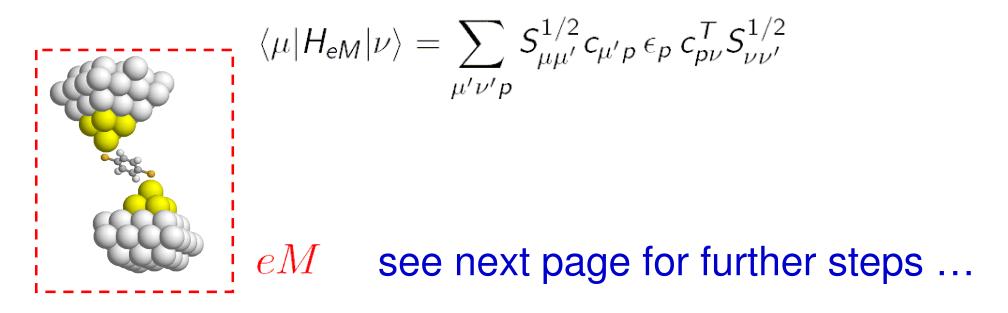




Algorithm behind AITRANSS



- ▶ Do DFT for eM with a quantum chemistry package (here FHI-aims) using local basis set $|\tilde{\mu}\rangle = |\mathbf{x}_n, I\rangle$
- Ask the package to provide the overlap matrix $S_{\mu\nu} = \langle \tilde{\mu} | \tilde{\nu} \rangle$
- Orthogonalize the basis set, $|\mu
 angle=\sum_{
 u}| ilde{
 u}
 angle S_{
 u\mu}^{-1/2}$
- Use KS states $|p
 angle=\sum_{\mu}| ilde{\mu}
 angle c_{\mu p}$ and energies ϵ_{p} to construct





Algorithm behind AITRANSS (continue)

Make the choice for the left/right local leakage function iη(x_n) (look for remarks in the library files and use default set of parameters!), construct

$$\langle \mu | \Sigma_{L/R} | \nu \rangle = -i\eta(\mathbf{x}_n) \delta_{\mu\nu}$$

Calculate transmission as

$$T(E) = \operatorname{Tr}\left[\Gamma_L G(E) \Gamma_R G^{\dagger}(E)\right]$$

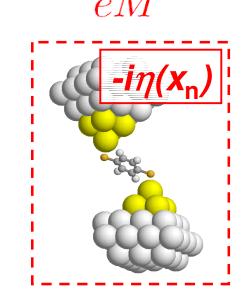
where

$$\langle \mu | G(E) | \nu \rangle = \langle \mu | [E - H_{eM} - \Sigma_L - \Sigma_R]^{-1} | \nu \rangle$$

$$\Gamma_{L/R} = \frac{1}{2i} (\Sigma_{L/R}^{\dagger} - \Sigma_{L/R})$$

For that task, eigenstate representation of the complex-valued operator $(H_{eM} + \Sigma_L + \Sigma_R)$ is used.

Forschungszentrum Karlsruhe in der Helmholtz-Gemeinschaft



HELMHOLTZ

GEMBINSCHAFT

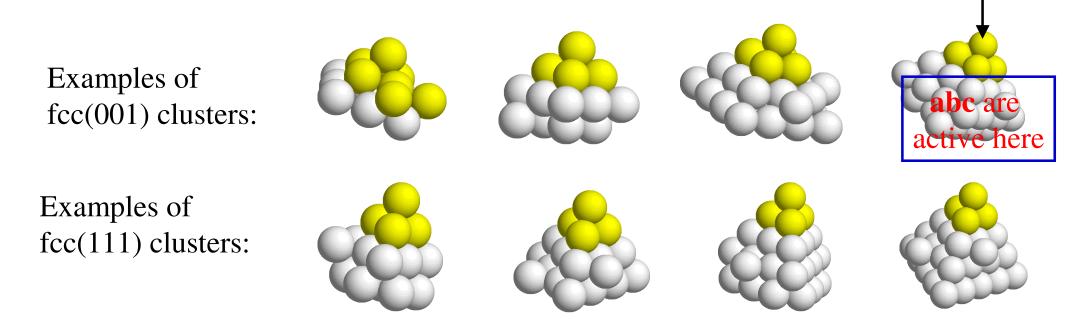


First step: prepare your molecular structure



 use your favorite visualization and modeling tool and build up an "extended molecule" by linking your molecule via anchoring groups to the apex atoms of Au clusters

• "chaotic" clusters are to be found in the aitranss library directory apex atom



• For your convenience, all examples considered in this tutorial already contain extended structures (not isolated molecules)

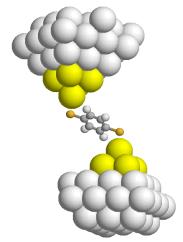


Simple visualization tool: Rasmol



- To visualize your structure, you may use an old-fasion but simple tool called Rasmol (http://www.rasmol.org/software/RasMol_2.7.5/)
- To convert aims-coordinate file to the PDB format, type
 aims2pdb geometry.in (you'll get file called coord.pdb)
- To obtain a picture shown below, (i) type
 rasmol coord.pdb (two windows will pop up);
 - (ii) Choose in the graphical window Display | Ball & Stick ;
 - (iii) Switch to the control window and type in the command line:

```
background white
select 1, 2
spacefill 380
select 1
color yellow
select 2
color white
```



Hint: by clicking on atom, you find its index (look at the control window)



Second step: FHI-aims run (input)



- FHI-aims should be invoked with a cluster type (non-periodic) settings
- Include a line output aitranss into control.in file
- Following parameters are recommended

occupation_type	gaussian	0.01
mixer	pulay	
n_max_pulay	10	
charge_mix_param	0.2	
sc_accuracy_rho	1E-4	

- sc_accuracy_eev 1E-2
- sc_accuracy_etot 1E-6

relativistic zora scalar 1.0e-10





Second step: FHI-aims run (output)



- Invoke FHI-aims, e.g.: nohup mpirun -np 4 aims.scalapack.mpi.x > aims.dft.out&
- After FHI-aims completed its job, following ASCII files will be generated:
 basis-indices.out : indexing of basis functions
 omat.aims :
 contains overlap integrals
 contains Kohn-Sham molecular orbitals &
 energies of the "extended molecule"
- AITRANSS needs also a mandatory file tcontrol, which has to be created with help of a script tcontrol.aims.x



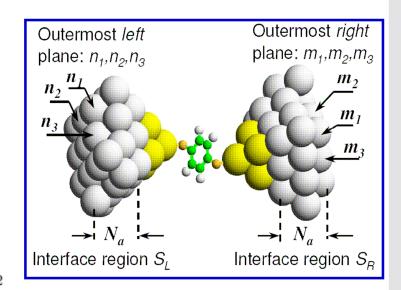


What is needed to run AITRANSS job?



- Files geometry.in, basis-indices.out, omat.aims, mos.aims
- Create a file tcontrol, launch a script tcontrol.aims.x with arguments (consult also README file for parameters):

tcontrol.aims.x -lsurc n_1 -lsurx n_2 -lsury n_3 -rsurc m_1 -rsurx m_2 -rsury m_3 -nlayers N_a -ener E_1 -estep dE -eend E_2



here n_1 , n_2 , n_3 are indices of atoms defining the left outermost atomic plane;

 m_1, m_2, m_3 are indices of atoms defining the right outermost plane ; N_a is number of atomic layers where absorbing boundary conditions are active (value of N_a is to be taken from the header of aitranss library files comprising structures of fcc Au clusters!) ;

 E_1 , E_2 & dE define a window $[E_1, E_2]$ and energy step (in Ha units!) required to output the transmission function T(E)



Final step: AITRANSS calculation and output



- Invoke AITRANSS (without MPI!) :
 nohup aitranss.x > aitranss.out &
- On output, you get two ASCII files

self.energy.in : contains information on the *model self-energy*; data are arranged in 7 columns: atom index, xyz-coordinates (\mathbf{x}_n) , atom symbol, atom target (left/right/empty) and the local leakage rate $\eta(\mathbf{x}_n)$ [in Ha units]

TE.dat : contains ballistic transmission function T(E); data are arranged in 3 columns: *E* in Ha units, $E - E_F$ in eV units, and T(E)results may be visualized with gnuplot, e.g. plot `TE.dat' u 2:3 w 1



Advanced exercise



• Look into directory .../exercise.alkyl.wires: it contains 7 molecular structures: organic molecular wires (alkyl chains) of different length linked to Au electrodes

• Exercise: compute tunneling conductance *G* through all molecules; estimate a decay exponent of *G* as function of CH2 units in the wire; compare your results with those published by C. Li *et al.*, J. Am. Chem. Soc. **130**, 318 (2008)

