

Structure setup for TranSIESTA calculations

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Tel Aviv SIESTA/TranSIESTA workshop



10. September 2014



Outline

- 1 General considerations
- 2 Simple example – 1D chain
- 3 The Electrode
 - Self-energies
 - Constructing an electrode
- 4 Building ones first structure
 - Electrode
 - Molecule
 - Intermediate
 - Intermediate electrode layers
 - Finalising simulation
- 5 FDF flags for structural setup
 - Repetition (Bloch's theorem)

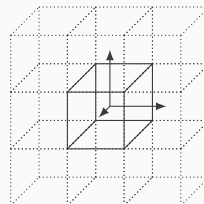


TranSIESTA setup vs. SIESTA setup

Periodicity

SIESTA

- Fully periodic in 3 (all) cell directions
- Periodicity handled by k -points

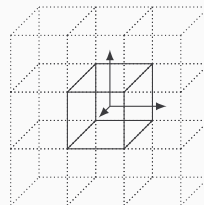


TranSIESTA setup vs. SIESTA setup

Periodicity

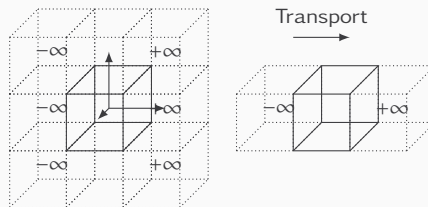
SIESTA

- Fully periodic in 3 (all) cell directions
- Periodicity handled by k -points

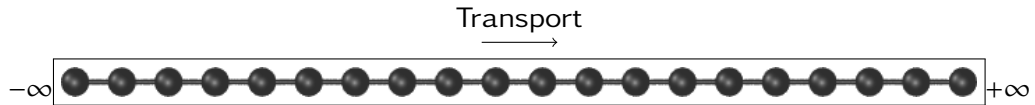


TranSIESTA

- Periodic in 2 cell directions
- Periodicity handled by k -points
- Semi-infinite in 1 cell direction
- Semi-infinite directions handled by self-energies (Σ)

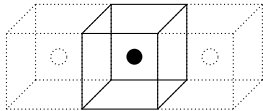


The perfect chain

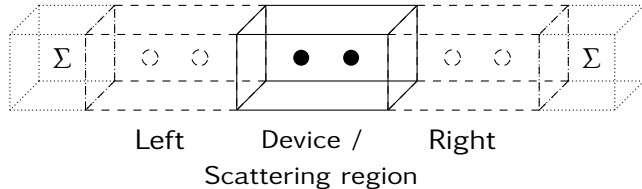


- Perfect systems can be handled equivalently, yet with different methods
- However, SIESTA is the best method for fully periodic systems when *not* applying a bias

SIESTA $k \rightarrow \infty$



TranSIESTA $k = 1$



The electrodes

Semi-infinite — *bulk*

Self-energies Σ , VERY IMPORTANT

We utilise the method by Sancho, Sancho, and Rubio, DOI: 10.1088/0305-4608/15/4/009 which is an iterative scheme for calculating the bulk/surface self energies.

- It requires only principal cell interactions

$$\begin{bmatrix} H_{00} & H_{01} & 0 & \dots & \\ H_{10} & H_{11} & H_{12} & 0 & \dots \\ 0 & H_{21} & H_{22} & H_{23} & \ddots \\ \vdots & 0 & \ddots & \ddots & \ddots \end{bmatrix}$$

- Sets a lower boundary on cell size in transport direction
- No limitation on two other direction cell sizes
- High k -point sampling in transport direction and same k -point sampling in transverse directions



Electrodes

Your first setup

- ❶ An electrode is a *pure* SIESTA calculation with a high number of k -points in the transport direction.
 - Why is that?
- ❷ Solve it with `SolutionMethod` `diagon` using the `transiesta` executable (we only use `transiesta` to get the TSHS-file)
- ❸ Ensure only principal cell interactions! (see *WARNING* in output)
- ❹ Same k -point sampling in the transverse directions *are* required



Electrodes

Your first setup

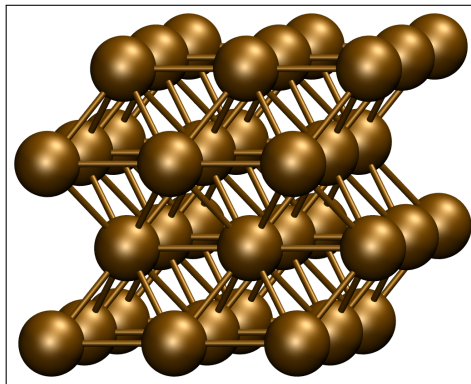
- 1 An electrode is a *pure* SIESTA calculation with a high number of k -points in the transport direction.
- 2 The structure needs to be periodic in the transport direction
- 3 Solve it with `SolutionMethod` `diagon` using the `transiesta` executable (we only use `transiesta` to get the TSHS-file)
- 4 Ensure only principal cell interactions! (see *WARNING* in output)
- 5 Same k -point sampling in the transverse directions *are* required



Benzene dithiol (BDT)

Electrode

- BDT attached to Gold electrodes
- We utilise 100 surface (AB-stacking)
- Decide k -point sampling in transverse direction (converge)



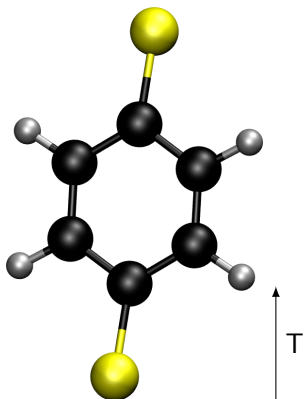
↑
T



Benzene dithiol (BDT)

BDT

Define the molecule



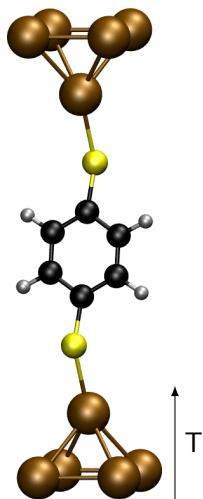
- Relax structure using SIESTA (lecture tomorrow)



Benzene dithiol (BDT)

Intermediate connect

Attach gold connection to the molecule



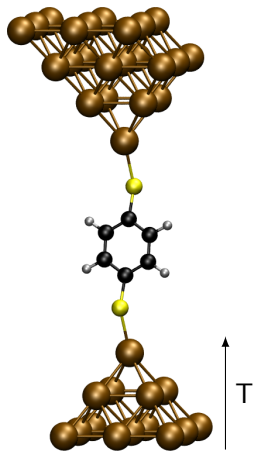
- Consider stacking of *pyramids*
 - A-BDT-A
 - A-BDT-B
 - B-BDT-B
- Relax structure *again*, constrain the *pyramids*



Benzene dithiol (BDT)

Intermediate electrode layers

Attach a couple of electrode layers



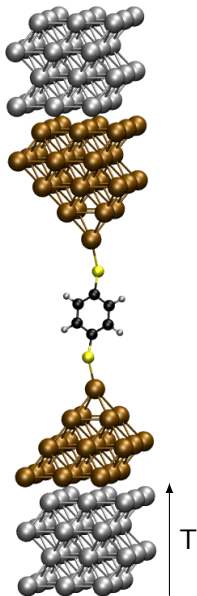
- *Follow the stacking!*
- *Relax structure again, constrain the electrode layers*



Benzene dithiol (BDT)

Attach electrode and more intermediate layers

Attach the electrodes on both sides (converge number of intermediate layers)



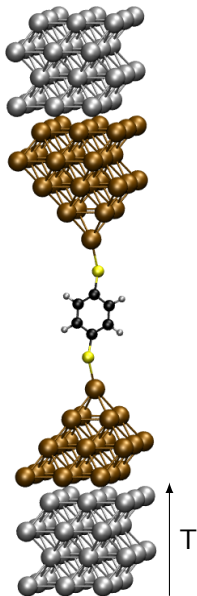
- Follow the stacking!
- Relax structure *again*, constrain the *electrode layers*
- Determining the extra number of layers:
 - Consider the molecule as a “defect”
 - The defect has a screening length in the central region (the extra electrode layers)
 - Ensure that the electrodes “behave as bulk” electrodes (away from defect)



Benzene dithiol (BDT)

Attach electrode and more intermediate layers

Attach the electrodes on both sides (converge number of intermediate layers)



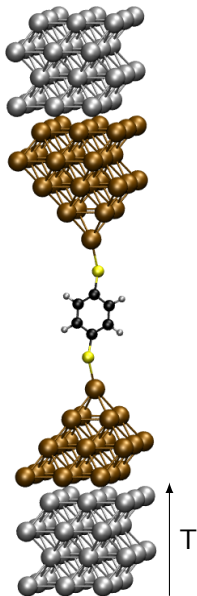
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 - Consider the molecule as a “defect”
 - The defect has a screening length in the central region (the extra electrode layers)
 - Ensure that the electrodes “behave as bulk” electrodes (away from defect)
- What does a metallic electrode require:
 - ① Bad screening → many electrode layers
 - ② Good screening → few electrode layers
- What does a semi-conducting electrode require:
 - ① Bad screening → many electrode layers
 - ② Good screening → few electrode layers



Benzene dithiol (BDT)

Attach electrode and more intermediate layers

Attach the electrodes on both sides (converge number of intermediate layers)



- Follow the stacking!
- Relax structure *again*, constrain the *electrode layers*
- Determining the extra number of layers:
 - Consider the molecule as a “defect”
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 - Ensure that the electrodes “behave as bulk” electrodes (away from defect)
- What does a metallic electrode require:
 - 1 Bad screening → many electrode layers
 - 2 Good screening → few electrode layers
- What does a semi-conducting electrode require:
 - 1 Bad screening → many electrode layers
 - 2 Good screening → few electrode layers



Structure setup

Electrodes (yes you can use the same electrodes on *both* sides)

```
%block AtomicCoordinatesAndAtomicSpecies
  0. 0. 0.00  1 # 1
  0. 0. 1.42  1 # 2
  0. 0. 2.84  1 # 3
  0. 0. 4.26  1 # 4
%endblock AtomicCoordinatesAndAtomicSpecies
```

System, *always* consecutive

```
%block AtomicCoordinatesAndAtomicSpecies
  0. 0. 0.00  1 # 1
  0. 0. 1.42  1 # 2
  0. 0. 2.84  1 # 3
  0. 0. 4.26  1 # 4
  0. 0. 5.68  1 # 5
  0. 0. 7.10  1 # 6
  0. 0. 8.52  1 # 7
  0. 0. 9.94  1 # 8
  0. 0. 11.36 1 # 9
  0. 0. 12.78 1 # 10
  0. 0. 14.20 1 # 11
  0. 0. 15.62 1 # 12
  0. 0. 17.04 1 # 13
  0. 0. 18.46 1 # 14
  0. 0. 19.88 1 # 15
  0. 0. 21.30 1 # 16
%endblock AtomicCoordinatesAndAtomicSpecies
```

Left electrode

Device

Right electrode

```
# Define the left electrode
TS.HSFileLeft elec/siesta.TSHS
# Define the right electrode
TS.HSFileRight elec/siesta.TSHS
# any relative paths are usable
```



Structure setup

Electrodes (yes you can use the same electrodes on *both* sides)

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Left electrode

Device

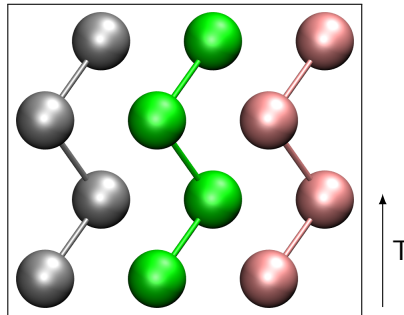
Right electrode

```
# Define the left electrode
TS.HSFileLeft elec/siesta.TSHS
# Define the right electrode
TS.HSFileRight elec/siesta.TSHS
# any relative paths are usable
```



Electrodes using Bloch's theorem

- In case the electrode has simple periodicity in the transverse direction it is encouraged to utilise Bloch's theorem to reduce electrode size



- Requires number of repeated times larger Monkhorst-Pack grid in each direction
- Faster calculation time of electrodes
- Heavily reduces computation time of self-energies

```
# first unit-cell vector  
TS.ReplicateLeftA1 3  
# second unit-cell vector  
TS.ReplicateLeftA2 3
```



Reducing self-energy region

For short orbital range, and atomic plane stacking creates long electrode we can reduce self-energy region (a stacking of ABAB with short orbital cutoff is a good candidate!)

TS.NumUsedAtomsLeft 3

TS.NumUsedAtomsRight 3

Electrodes (yes you can use the same electrode on *both* sides)

```
%block AtomicCoordinatesAndAtomicSpecies
```

```
0. 0. 0.00 1 # 1
```

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0. 0. 1.42 1 # 2
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Left electrode

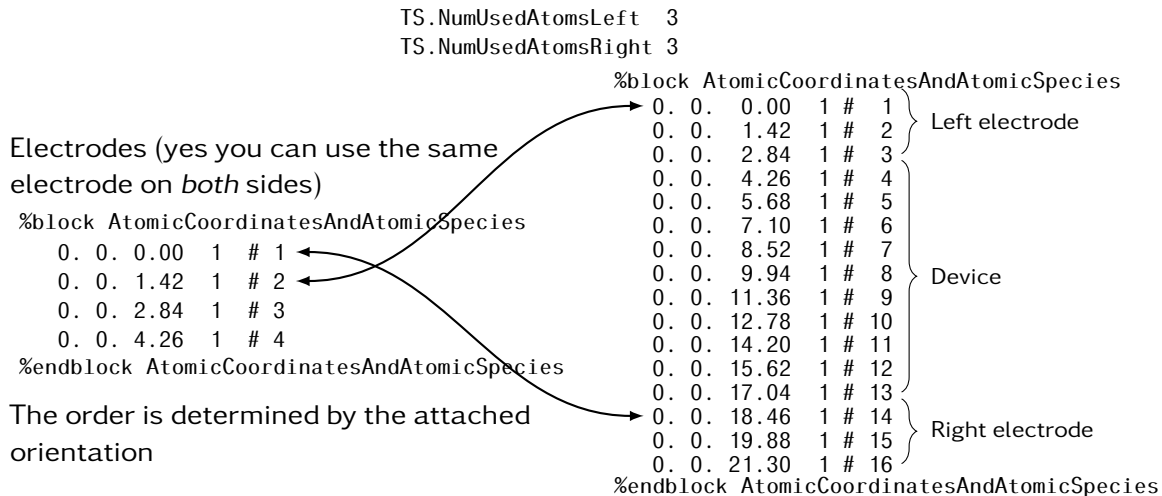
Device

Right electrode



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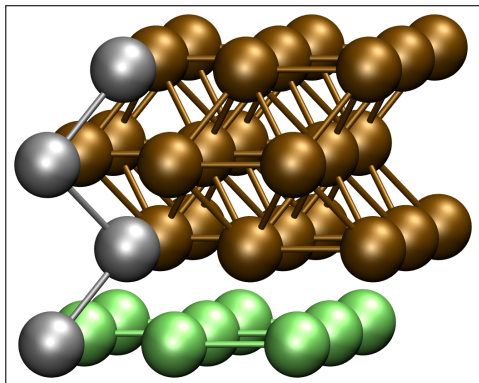


Electrode – All together

A short orbital cutoff, long stacking order, Bloch's theorem applicable

```
# Contains the silver atoms:  
TS.HSFileLeft ../ELEC/siesta.TSHS  
TS.ReplicateLeftA1 3  
TS.ReplicateLeftA2 3  
# Do not use the green atoms:  
TS.NumUsedAtomsLeft 3
```

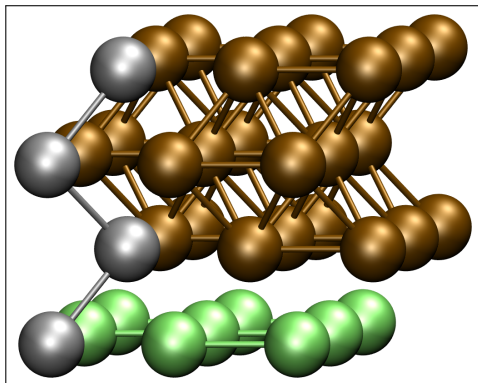
```
# Contains the silver atoms:  
TS.HSFileRight ../ELEC/siesta.TSHS  
TS.ReplicateRightA1 3  
TS.ReplicateRightA2 3  
# Do not use the green atoms:  
TS.NumUsedAtomsRight 3
```



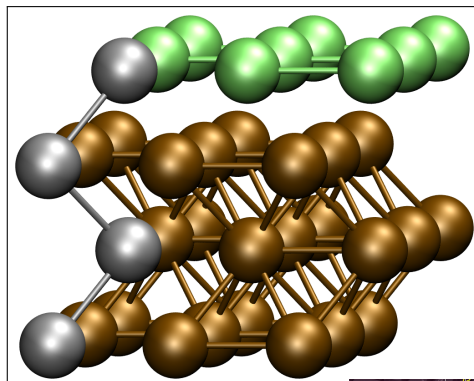
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# Contains the silver atoms:  
TS.HSFileLeft ../ELEC/siesta.TSHS  
TS.ReplicateLeftA1 3  
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# Do not use the green atoms:  
TS.NumUsedAtomsLeft 3
```



```
# Contains the silver atoms:  
TS.HSFileRight ../ELEC/siesta.TSHS  
TS.ReplicateRightA1 3  
TS.ReplicateRightA2 3  
# Do not use the green atoms:  
TS.NumUsedAtomsRight 3
```



FDF flags

- `SolutionMethod` `diagon/transiesta`
- `%block` `AtomicCoordinatesAndAtomicSpecies`
- `TS.HSFileLeft`
- `TS.ReplicateLeftA1/TS.ReplicateLeftA2`
- `TS.NumUsedAtomsLeft`
- `TS.HSFileRight`
- `TS.ReplicateRightA1/TS.ReplicateRightA2`
- `TS.NumUsedAtomsRight`

Doing TranSIESTA calculations:

- 1 `calculate electrodes (transiesta < elec.fdf | tee elec.out)`
- 2 `solve using (transiesta < chain.fdf | tee chain.out)`
- 3 `calculate transmission (tbtrans < chain.fdf | tee chain.tbtrans.out)`

