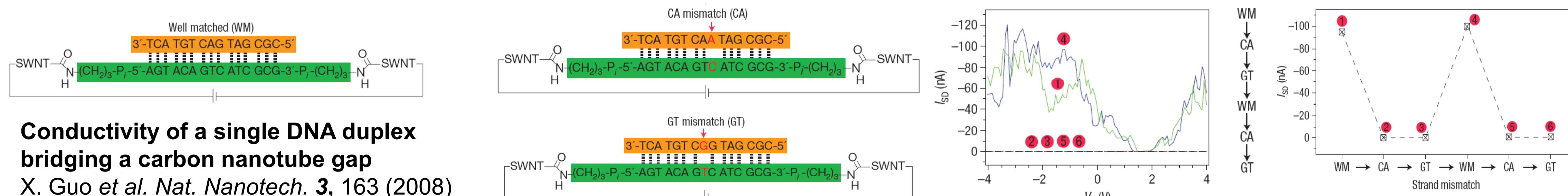
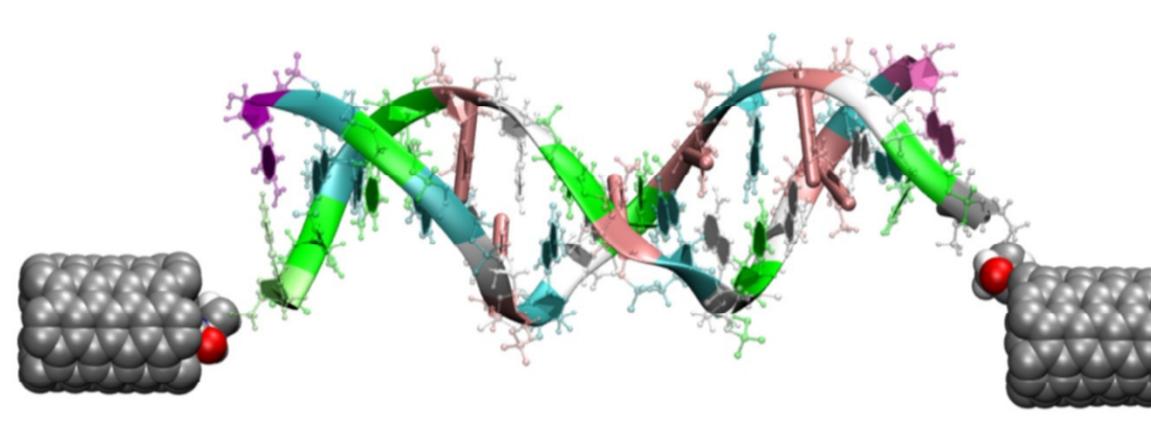


**Motivation:**

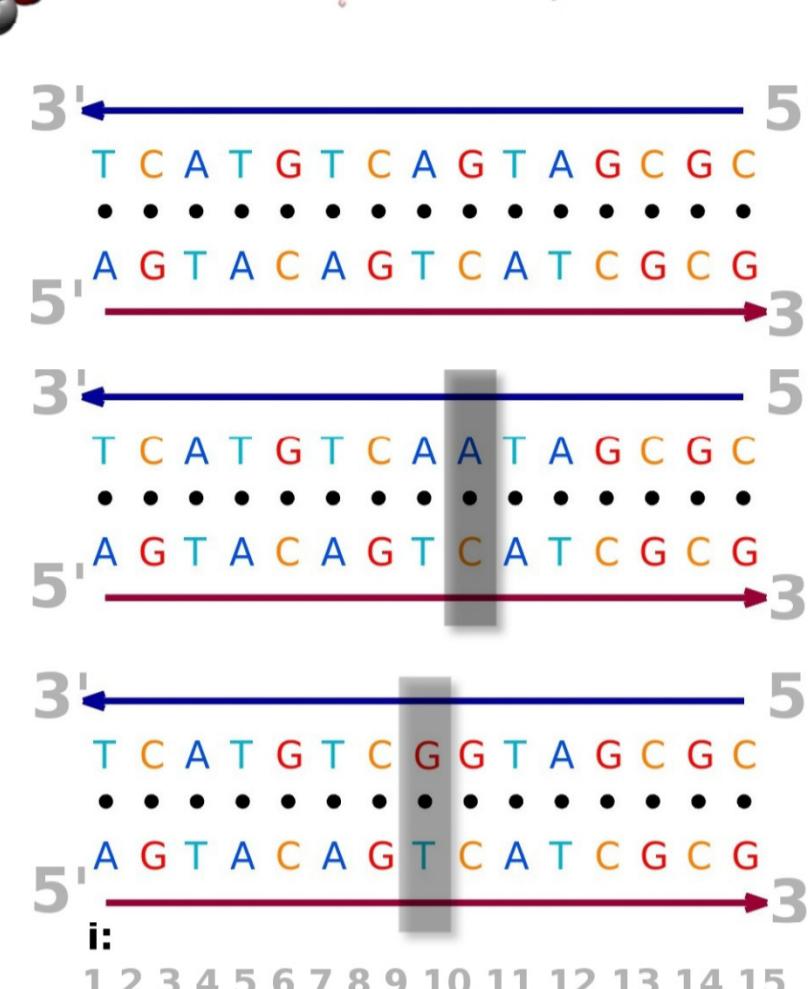
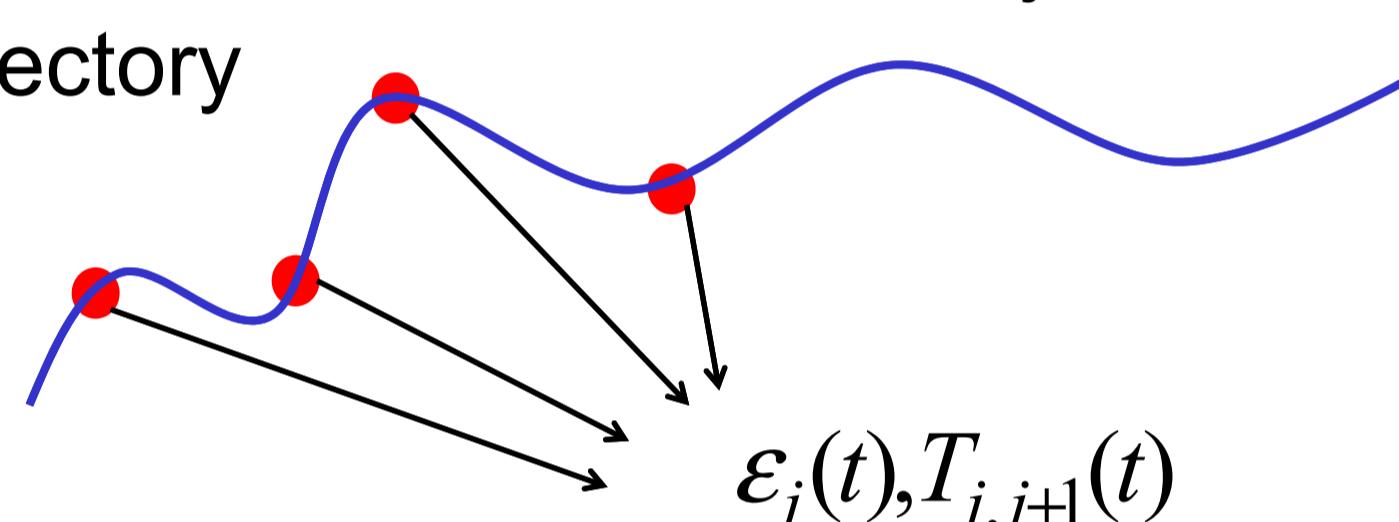
- Electrical detection of point mutations in DNA possible?
- Develop effective approach to combine dynamics and transport


**Simulation strategy: Molecular dynamics (MD) coupled to electronic structure calculations**
**MD simulation set-up:**

- AMBER10 package, NVT thermostat, 0.5 fs time step
- AMBER99 force field used for the  $sp^2$  carbon atoms of the CNT
- 70,000 atoms, TIP3P water box  $70 \times 70 \times 120 \text{ \AA}^3$ , 28  $\text{Na}^+$  ions neutralize the simulation box.


**Electronic structure calculation:**

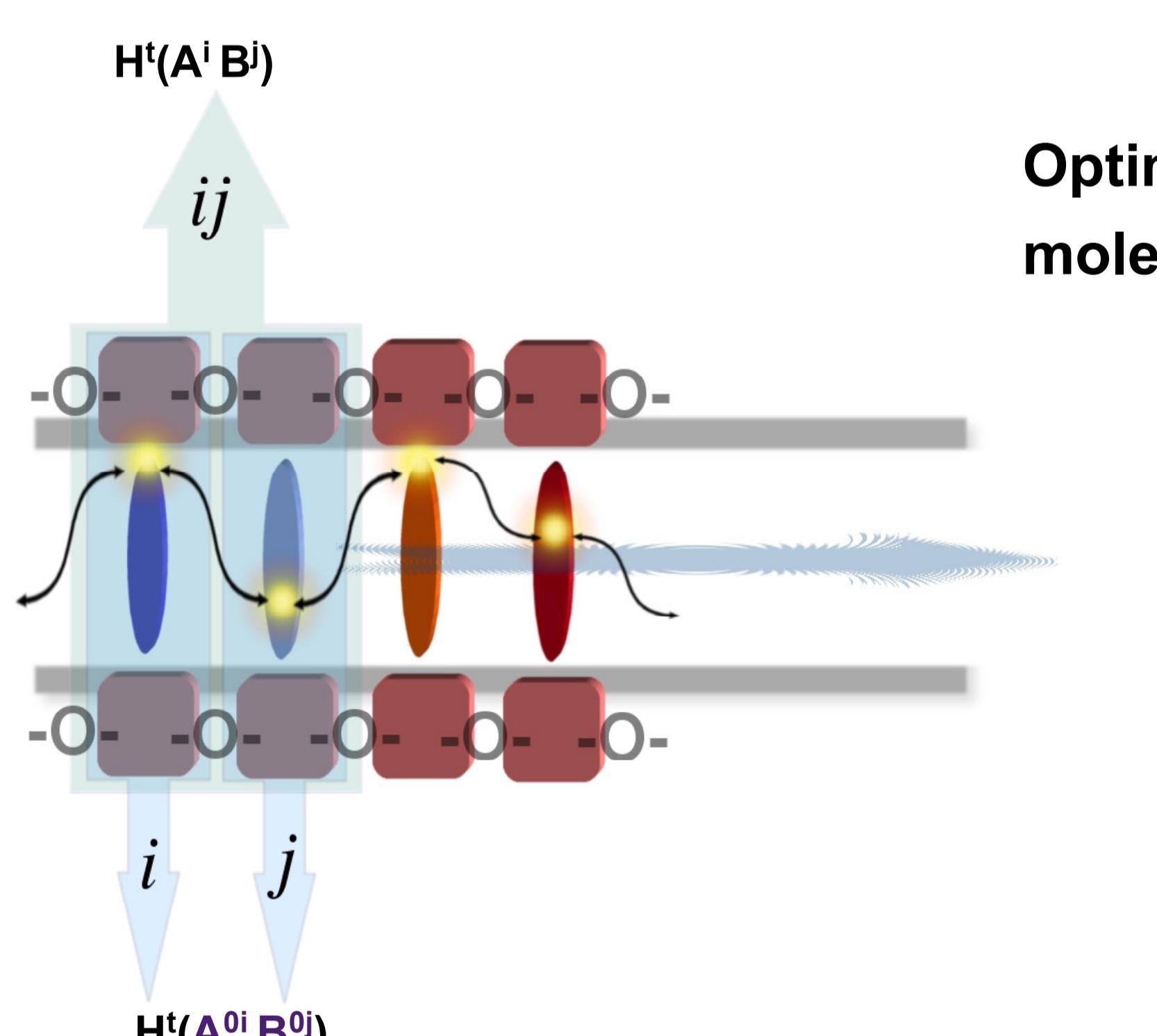
- Use QM/MM approach in **Amber10** package
- QM method: semi-empirical Hamiltonian (**AM1**)
- **Fragment molecular orbital** method is used to obtain effective on-site energies  $\epsilon_i(t)$  and inter-fragment transfer integrals  $T_{ij}(t)$  along the MD trajectory



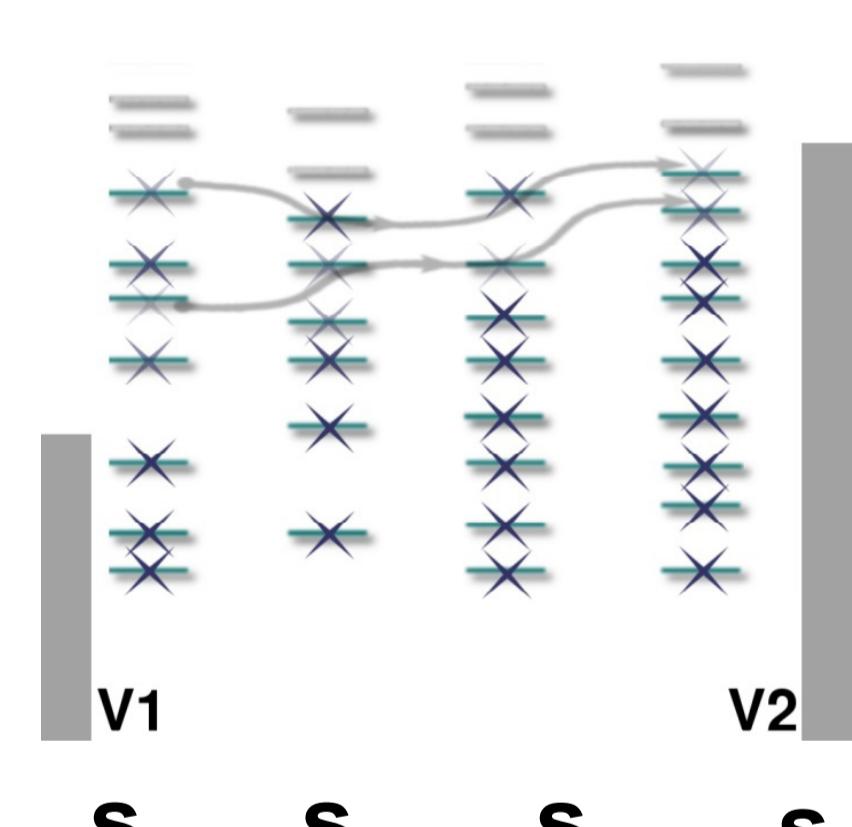
Snapshot of the CNT-DNA system (upper panel), the well-matched sequence and the sequences with mismatches

**Fragment Molecular Orbitals (FMO) technique<sup>1</sup>**

- $H(A^0 B^0)$ : Fock matrix for isolated fragments (nucleotides pairs)  $A^0$  and  $B^0$
- $H(AB)$ : Fock matrix for fragments  $AB$  embedded in the simulation box



Optimal transport pathway (relevant molecular orbital subspace)



- Mapping onto effective Hamiltonian (linear chain) with time-dependent parameters

$$H_t = \sum_i \epsilon_i(t) c_i^+ c_i + \sum_{i,j} T'_{ij}(t) c_i^+ c_j$$

$$\epsilon_i(t) = \langle \Phi_i^{MO}(t) | H | \Phi_i^{MO}(t) \rangle$$

$$T'_{ij}(t) = \langle \Phi_{A^i}^{MO}(t) | H_{A^i B^j}(t) | \Phi_{B^j}^{MO}(t) \rangle$$

$$\Phi_i^{MO}(t) = \sum \mu C_i^\mu(t) \varphi_\mu^{AO}$$

$$T'_{ij}(t) = S_{AO}^{-1/2} T_{ij}(t) S_{AO}^{1/2}$$

**Transport properties:**

- Time-dependent transmission function  $T(E, t)$

$$T(E, t=t_j) = Tr [ \Gamma_R(E) G^r(E, t=t_j) \Gamma_L(E) G^a(E, t=t_j) ]$$

$$\Gamma_{R/L}(E) = i [ \Sigma_{R/L}^r(E) - \Sigma_{R/L}^a(E) ]$$

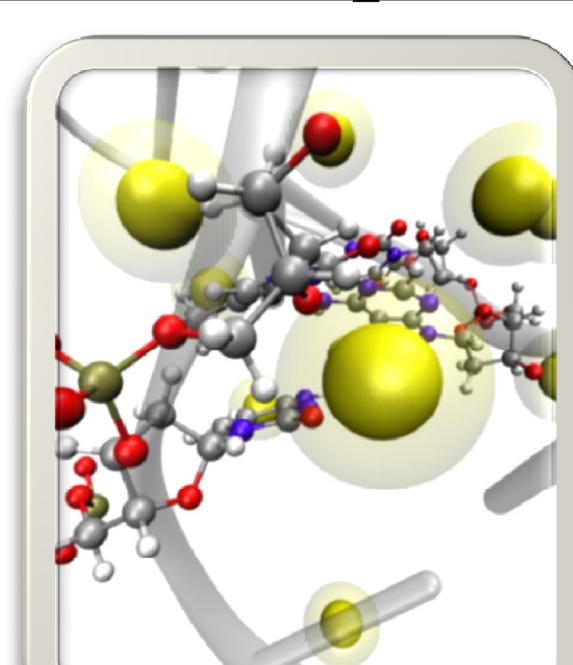
$$[G^r(E, t=t_j)]^{-1} = E - H(t=t_j) - \Sigma_L^r(E) - \Sigma_R^r(E)$$

Time-averaged transmission

$$T(E) = \frac{1}{t_{MD}} \sum_i T(E, t=t_i)$$

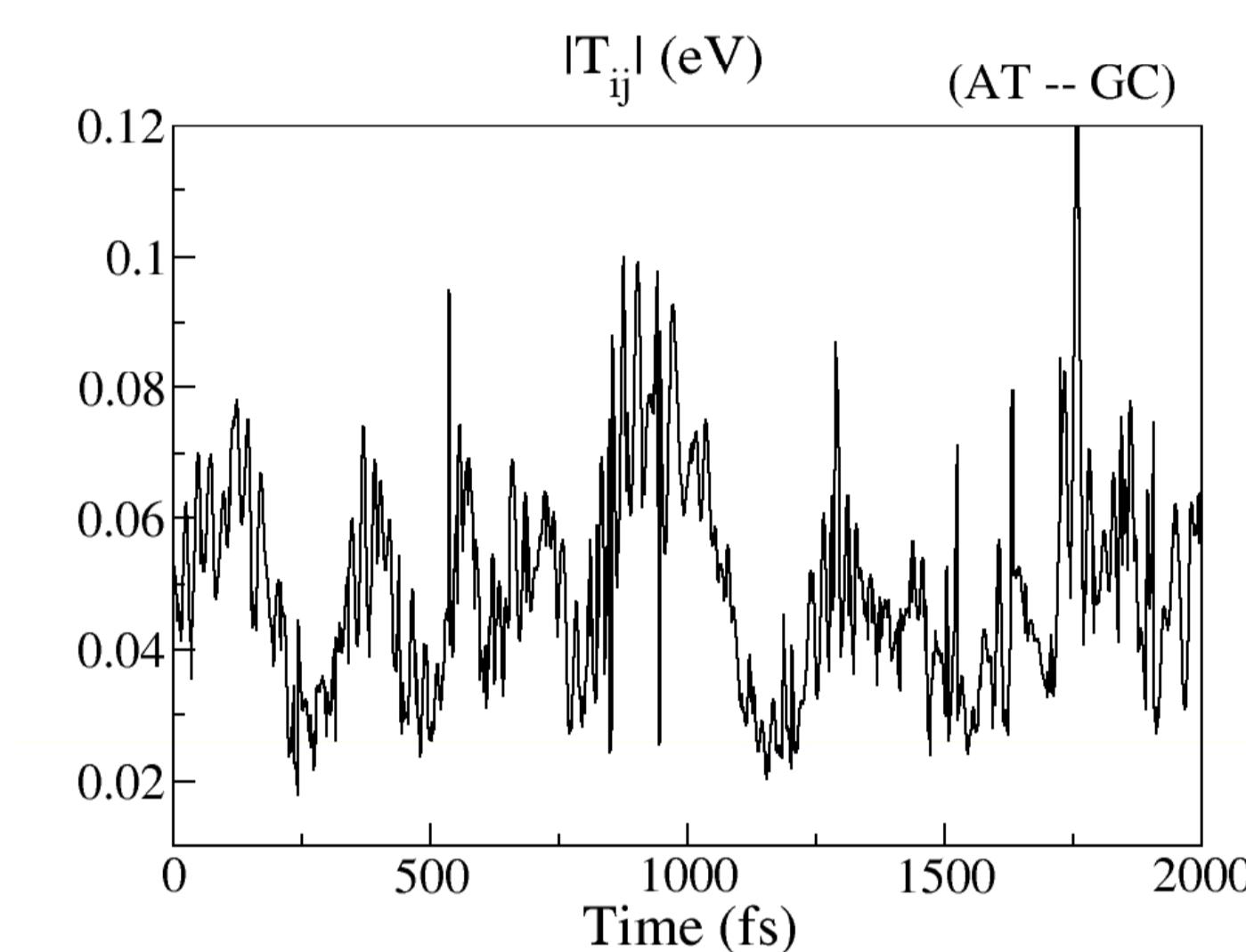
**References:**

1. Kitaura & Morokuma, J. Quantum Chem. **10**, 325 (1976); T. Kubas, et al., J. Phys. Chem. B **112**, 7937 (2008)
2. P. B. Woiczkowski, T. Kubas, R. Gutierrez, R. A. Caetano, G. Cuniberti, and M. Elstner, J. Chem. Phys. **130**, 215104 (2009)
3. R. Gutierrez, R. A. Caetano, B. P. Woiczkowski, T. Kubas, M. Elstner, and G. Cuniberti, Phys. Rev. Lett. **102**, 208102 (2009)

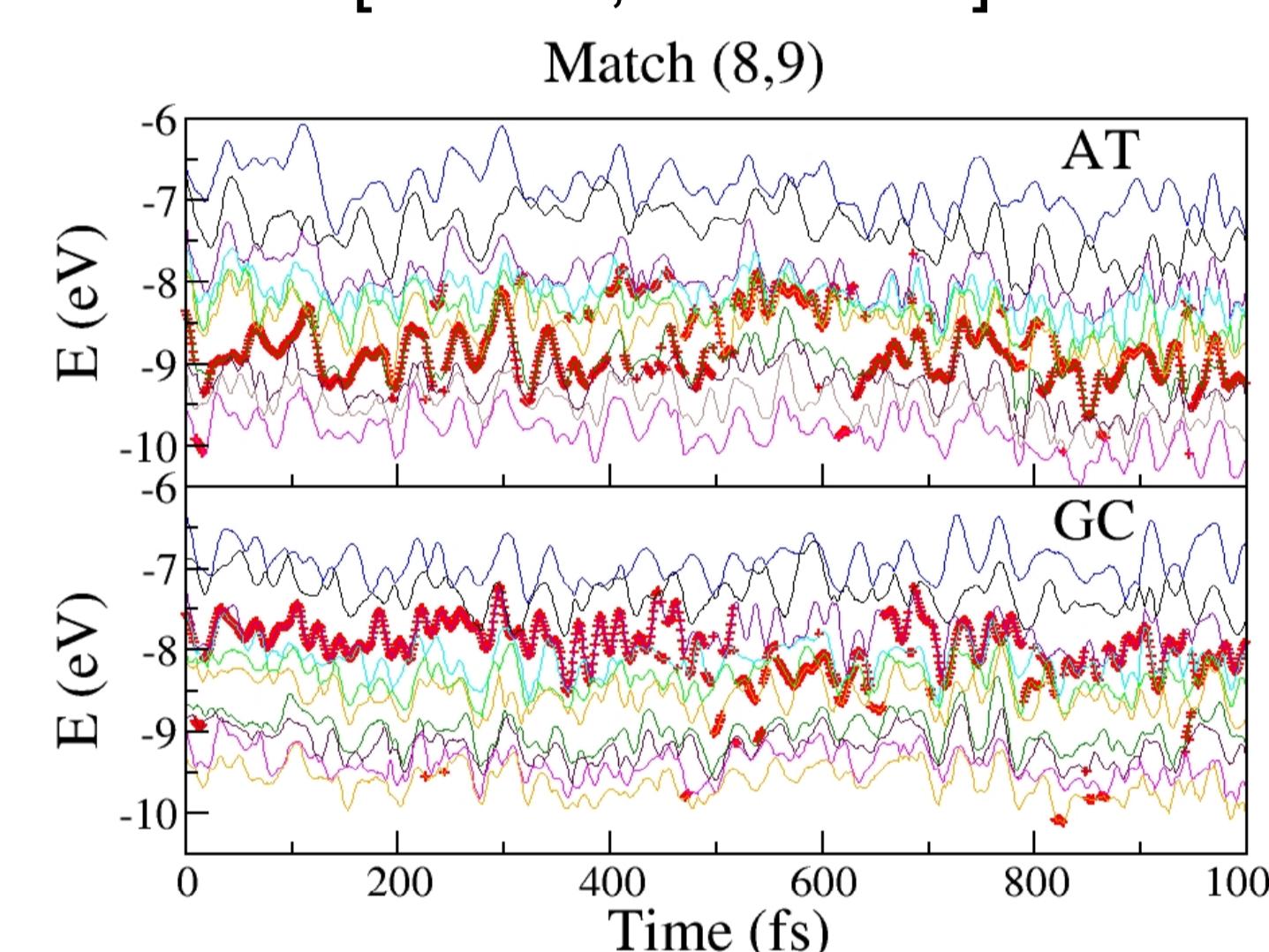

**Results: DNA coupled to CNT electrodes**
**Time-dependent e-structure and orbitals**

HOMO, HOMO-1 orbitals are mainly **localized on backbones**, hopping very small ( $\sim 1 \text{ meV}$ )  
→ relevant orbitals for hole transport **below the HOMO level**

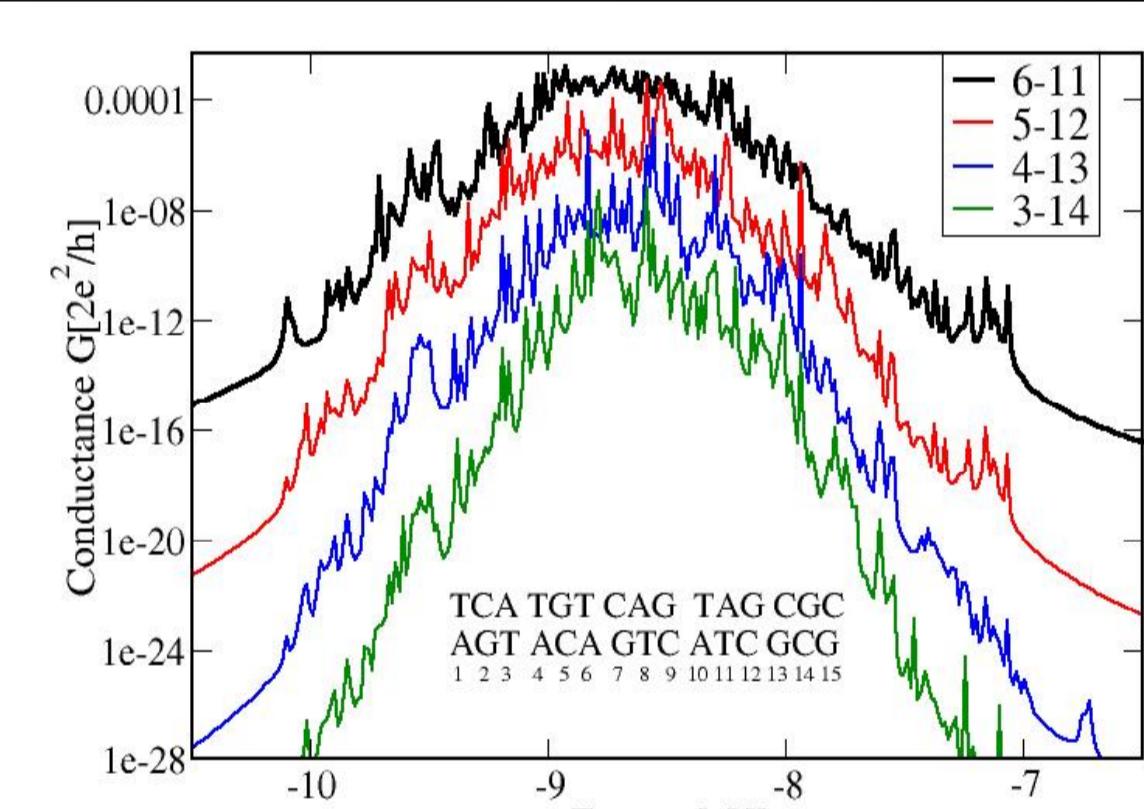
Effective hopping integral  $T_{ij}$  between the AT- and GC fragments



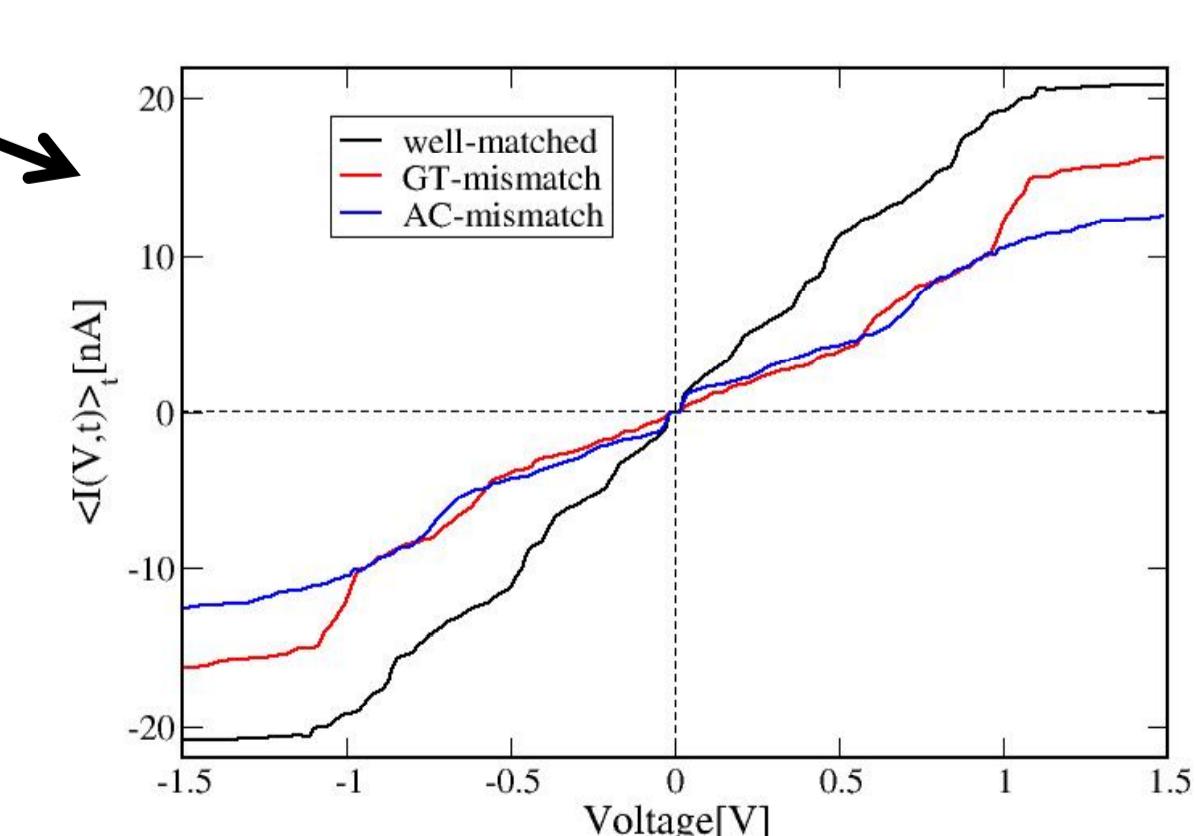
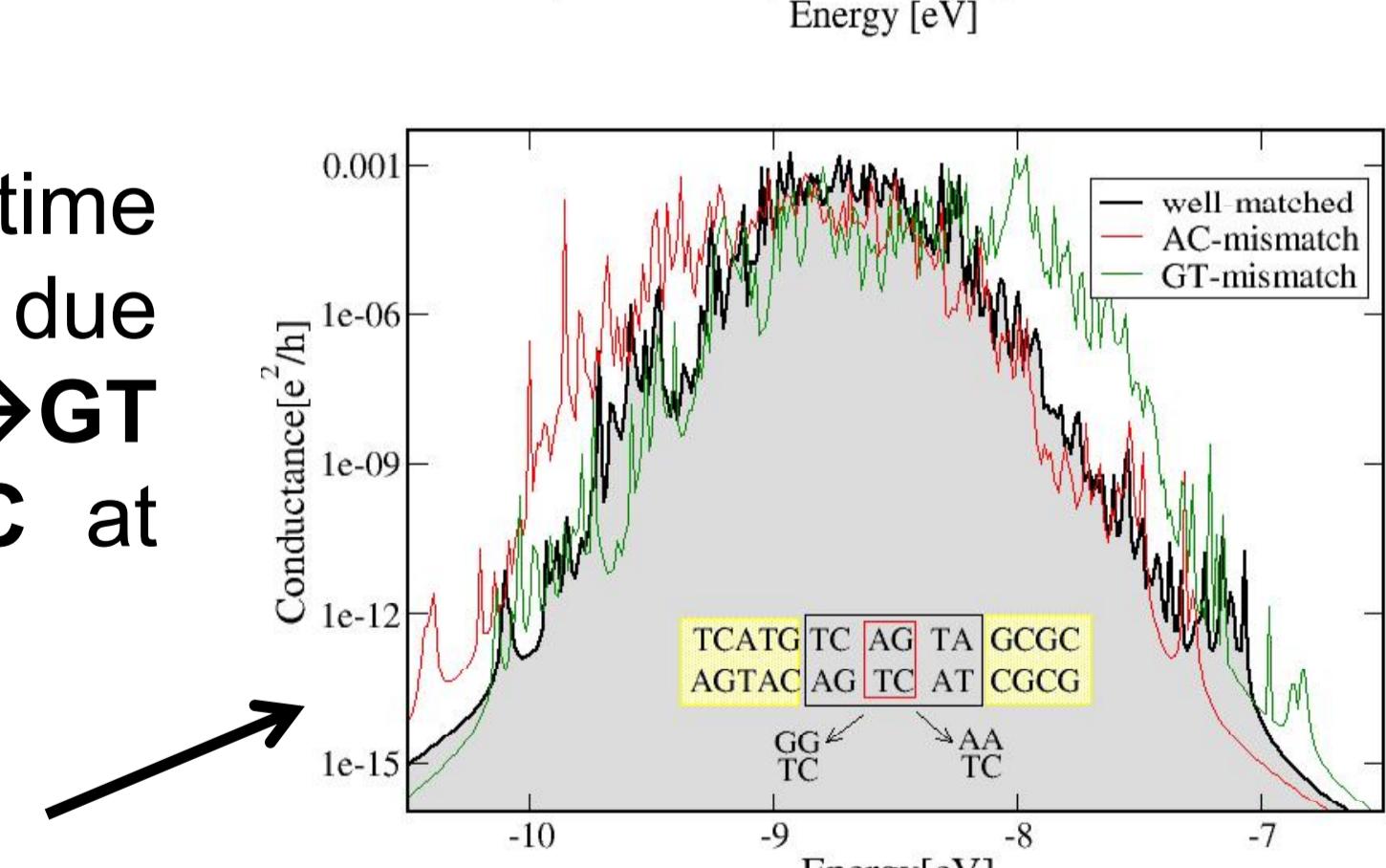
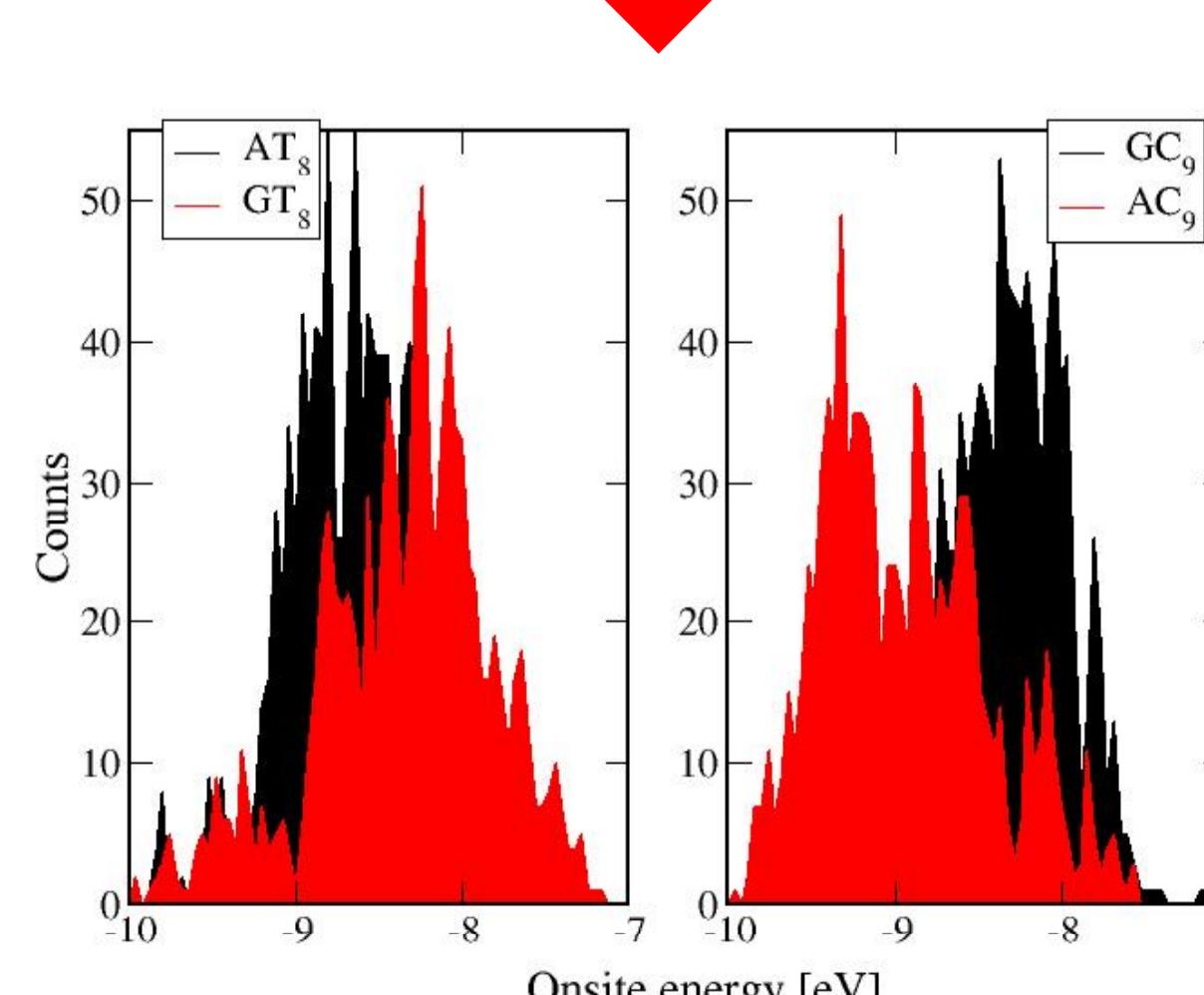
Effective onsite energy  $\epsilon_i$  time series at site 8 (AT base pair) and 9 (GC base pair) for the interval [HOMO, HOMO-10]


**Results: Charge transport**

Conductance calculations with an increasing number of sites around the base pair region where mismatches are introduced



Histograms drawn from the time series showing the energy shifts due to introducing a mismatch **AT → GT** at chain site 8 resp. **GC → AC** at chain site 9


**Conclusions and Outlook**

- Dynamical fluctuations included in efficient computational scheme
- Mapping of complex electronic structure onto effective model
- Differences between matched and mismatched sequences less dramatic than in experiment → improve e-structure methodology
- **Open:** Decoherence effects should be included (real-time charge propagation or coupling to dissipative environments)