

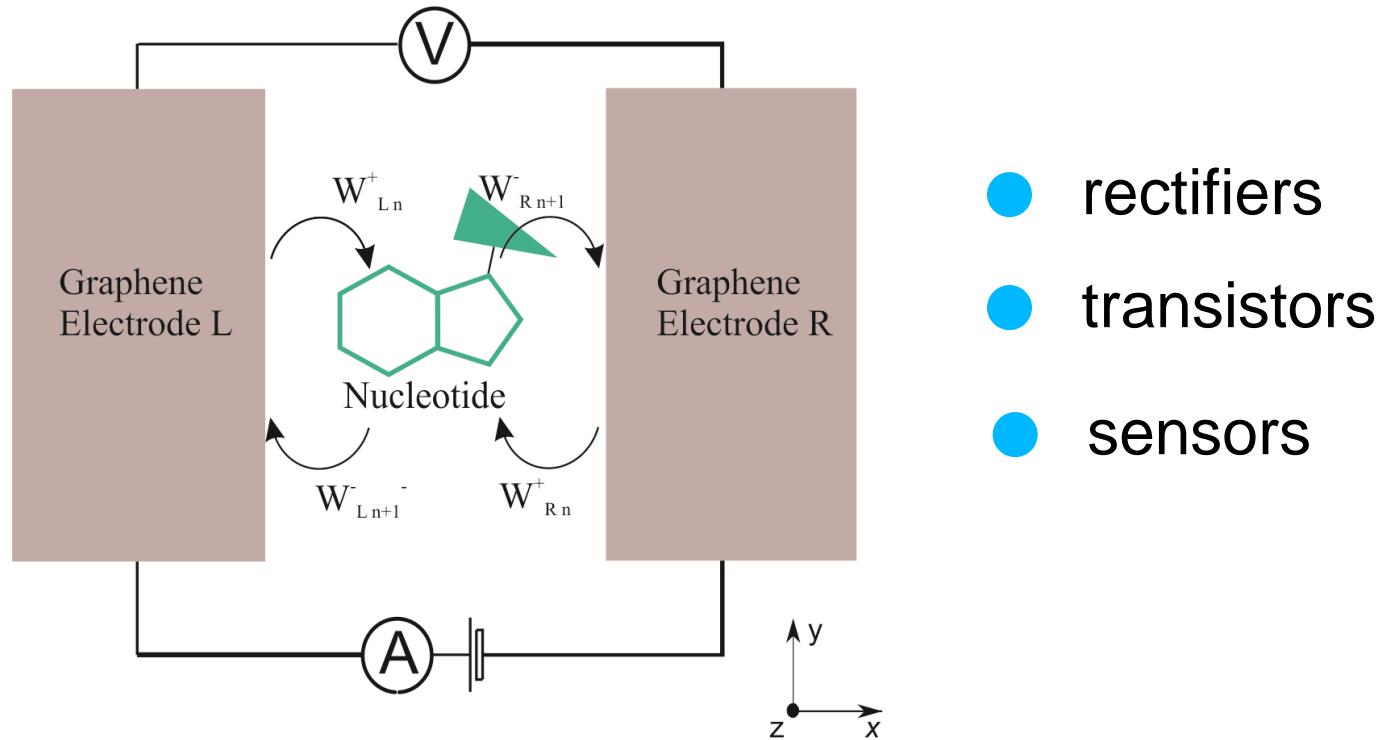


Bogoliubov Laboratory of Theoretical Physics
Joint Institute for Nuclear Research

Electron transport through graphene-DNA-graphene junction. DNA decoding

O.G. Isaeva, V.L. Katkov, V.A. Osipov

Molecular electronic circuit

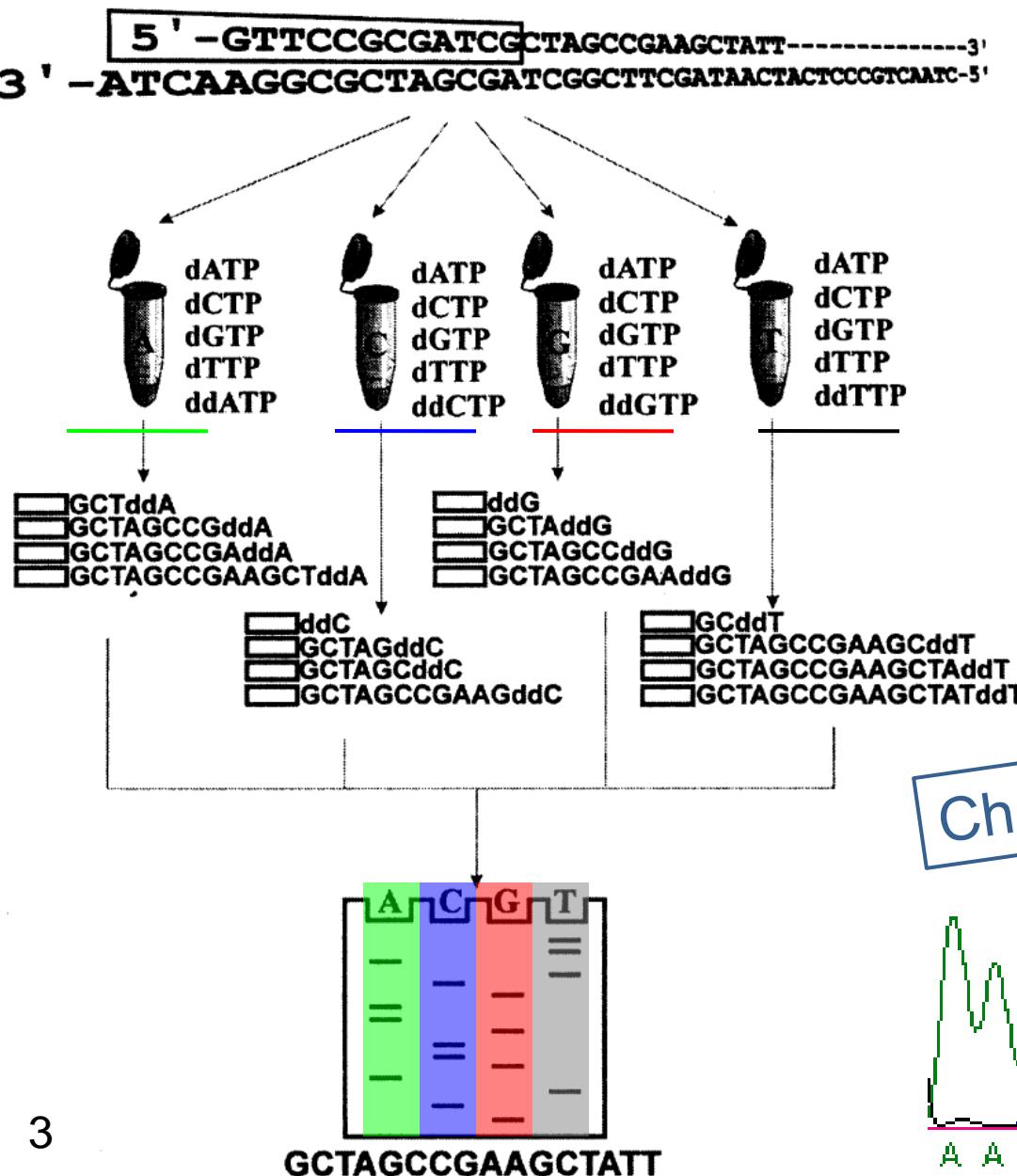
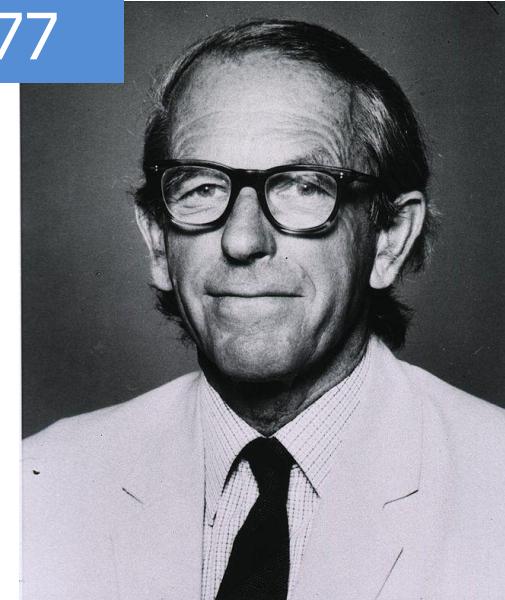


Aviram A. and Ratner M.A. Chem.Phys.Lett. 29 277 (1974)

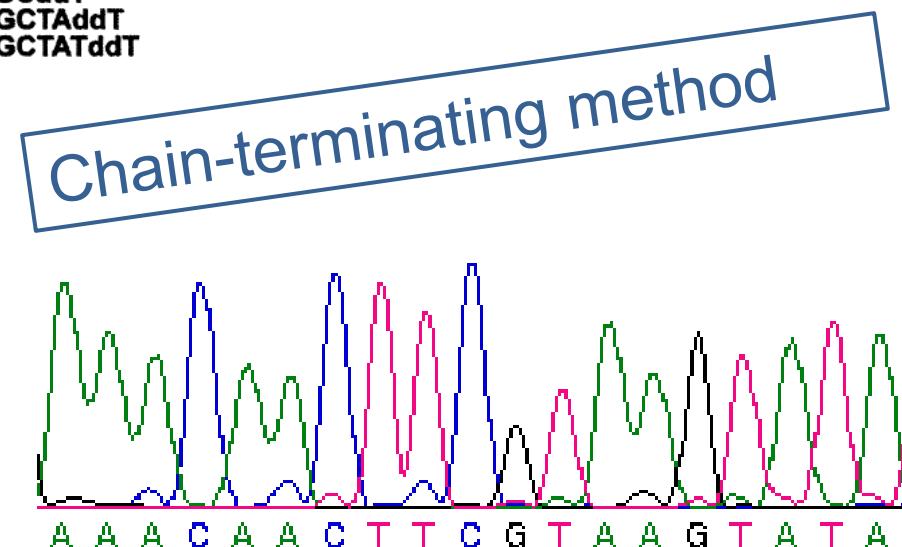
Sanger method

chemical elongation, electrophoresis

1977



Frederick Sanger
1918-2013





- cost of about 10 million USD;
- several months time;

Read-length

human genome

New trends in sequencing methods (in development):

- effective;
- rapid;
- low-cost

Nanopore concept;

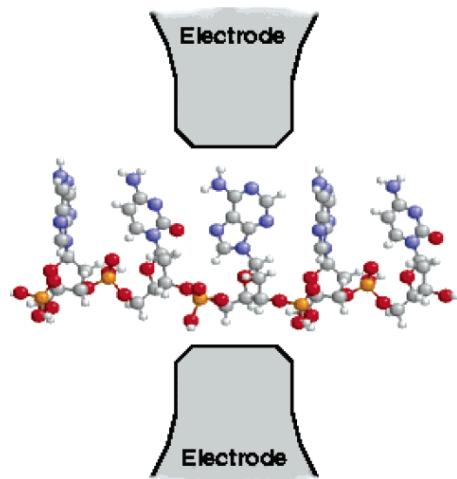
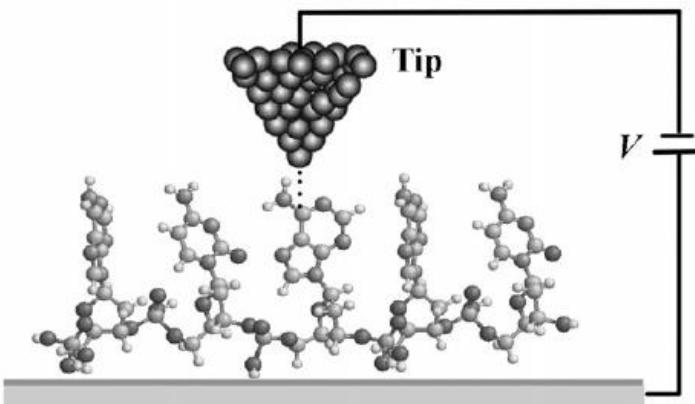
J. Kasianowicz et al., Proc. Natl. Acad. Sci. USA **93** (1996)

Transverse electronic current;

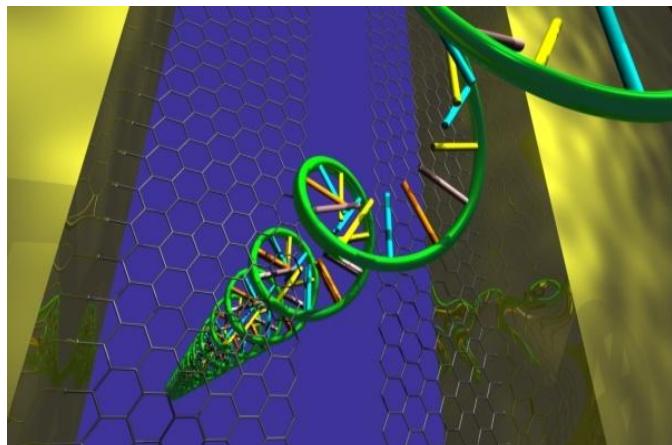
Zwolak M. and Di Ventra M. Nano Lett. **5** 421 (2005)

Transverse current for DNA decoding (physical approach)

M.S. Xu et al. *Perspectives from Physics, Chemistry and Biology*, 2007



Zwolak M. and Di Ventra M.
Nano Lett. 5 421 (2005)



H.W.C. Postma *NanoLett.* 10, 420 (2010)
Prasongkit J. et al *NanoLett.* 11, 1941
(2011)

L.A. Agapito, J. Gayles, Ch. Wolowiec
and N. Kiouassis. *Nanotechnology*, 23
135202 (2012)

Our study

1. The effect of band structure of graphene electrodes (mono, AA, AB) on the transport properties

V.L. Katkov, O.G. Isaeva, and V.A. Osipov, J. Phys.: Conf. Ser. 393 012026 (2012)

2. The role of both the Coulomb blockade and random positions of nucleotides in the gap for DNA decoding.

*O.G. Isaeva, V. L. Katkov, V. A. Osipov, **DNA sequencing through graphene nanogap: a model of sequential electron transport**, The European Physical Journal B 87, 272 (2014)*

RESONANT TUNNELING MODEL

$$I = \frac{2e}{\hbar} \int_{-\infty}^{+\infty} \frac{\Gamma_L(\varepsilon - \varepsilon_r - V/2)\Gamma_R(\varepsilon - \varepsilon_r + V/2)}{(\varepsilon - \varepsilon_r)^2 - (\Gamma(\varepsilon)/2)^2} (f_L(\varepsilon) - f_R(\varepsilon)) d\varepsilon$$

$$\Gamma(\varepsilon) = \Gamma_L(\varepsilon - \varepsilon_r - V/2) + \Gamma_R(\varepsilon - \varepsilon_r + V/2)$$

$$\Gamma_{L,R} = \hbar v \bar{D}_{L,R}$$

$$\bar{D}_{L,R} = P(\varepsilon) D_{L,R}$$

Channel density:

$$P(\varepsilon) = \frac{n_{L,R}(\varepsilon)}{N_{L,R}} = \frac{2a_0 \Delta p_y(\varepsilon)}{h}$$

a_0 is covalent bond length in graphene

Transmission probability:

$$D_{L,R} = \exp[-\lambda(d - d_0)]$$

$$\lambda = \frac{2\sqrt{2m\varphi}}{\hbar}$$

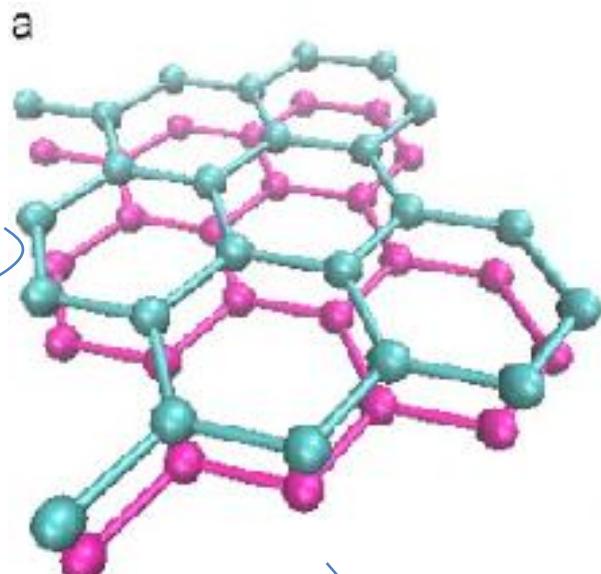
Attempt frequency:

$$v = \frac{\hbar}{2md_0^2 N}$$

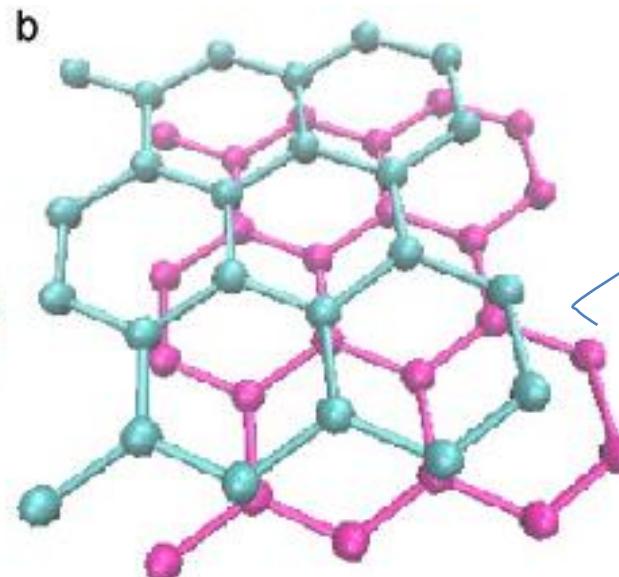
d_0 is covalent bond length in nucleotide

Graphene bilayer

AA bilayer



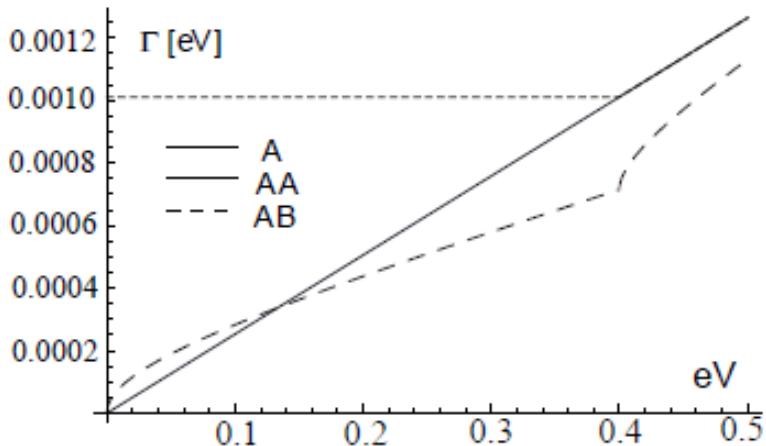
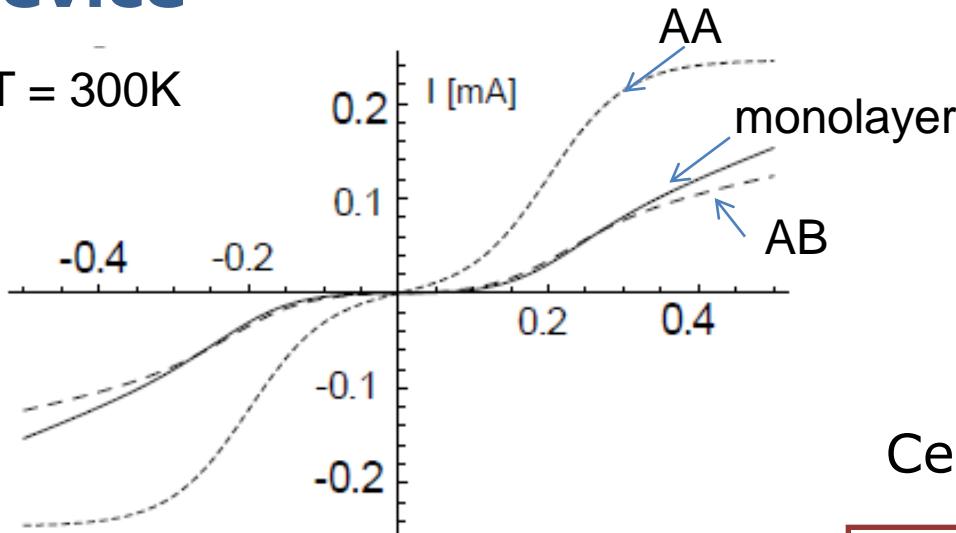
AB bilayer



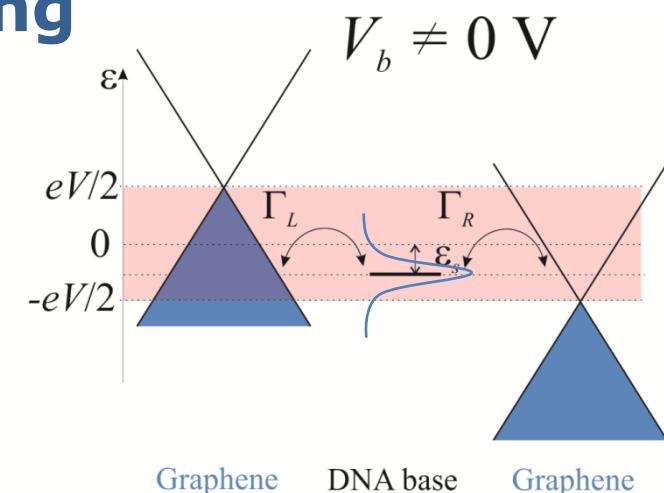
«zig-zag» edge

Results for part one: I-V characteristics of tunneling device

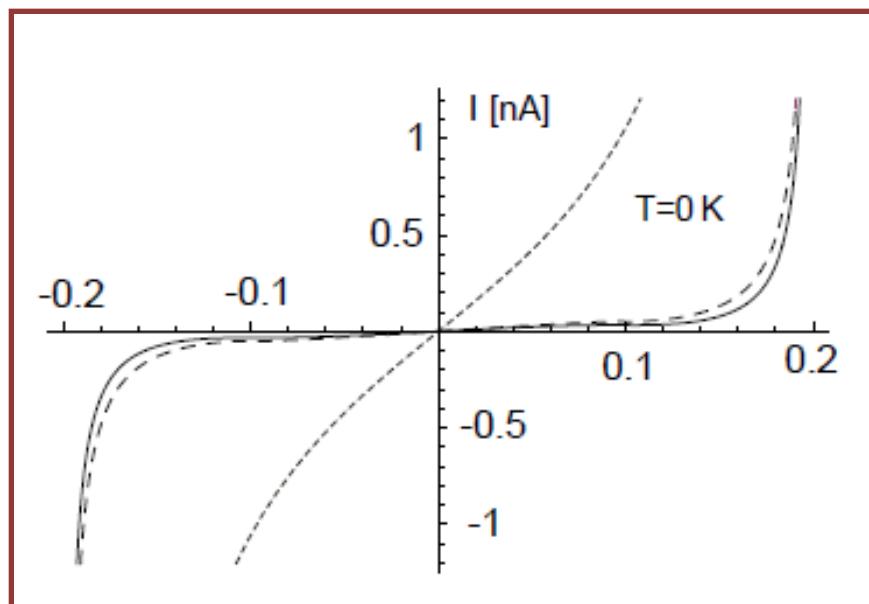
$T = 300\text{K}$



Energy dependence of $\Gamma(\varepsilon)$



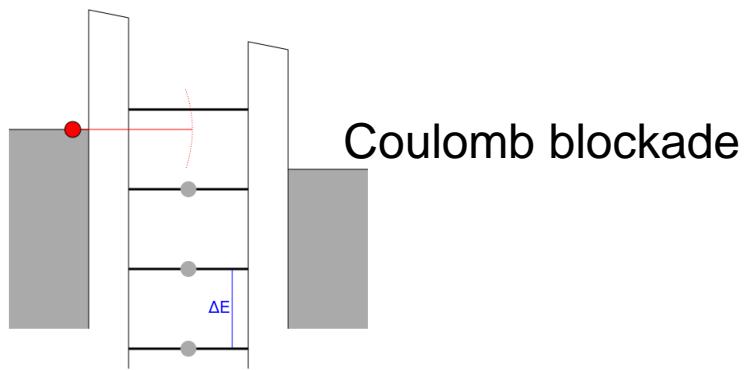
Central part of I-V characteristic



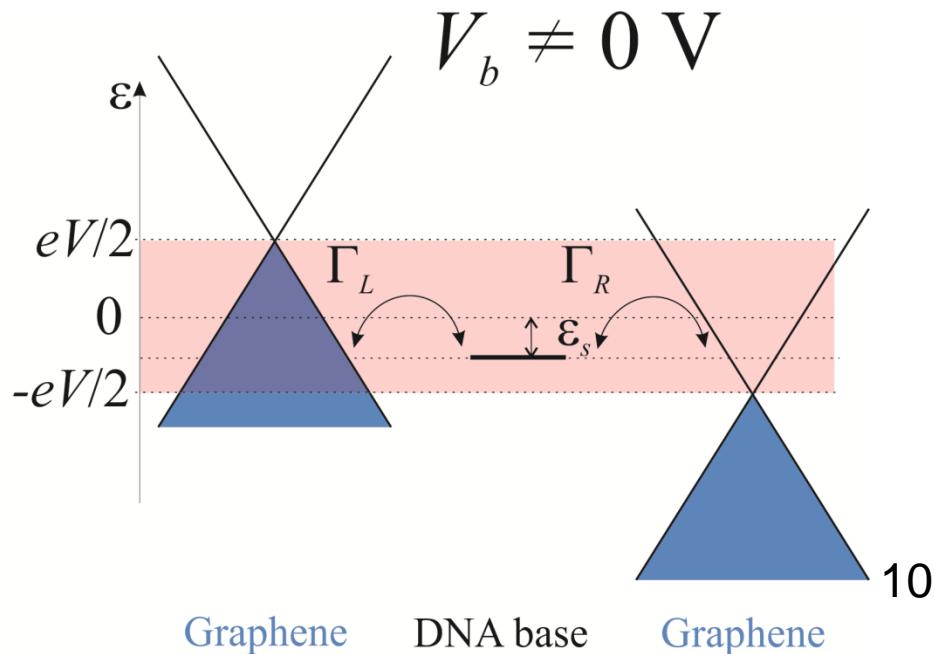
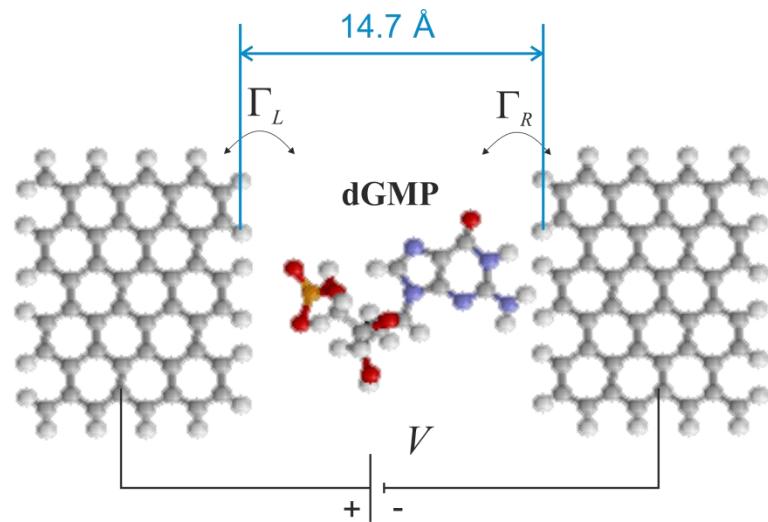
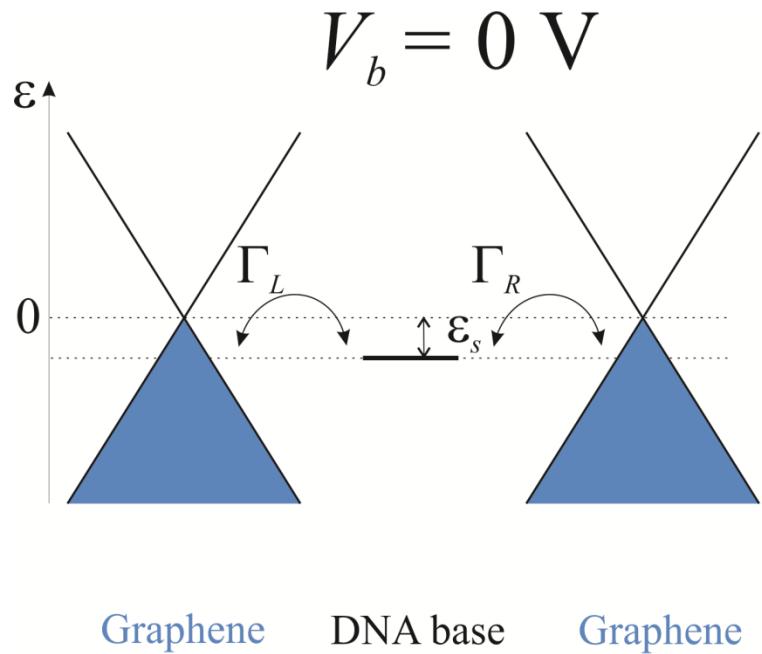
CONCLUSION (for part 1)

Our analysis shows that at the same bias voltage AA graphene bilayer electrodes provide a higher current in comparison with both graphene monolayer and AB bilayer. The use of electrodes on the base of AA graphene bilayer is expected to be much more productive for DNA decoding.

The role of both the Coulomb blockade and random positions of nucleotides in the gap for DNA decoding



$$\hbar\Gamma_{n \rightarrow n \pm 1} \ll |E_n - E_{n \pm 1}|$$



SEQUENTIAL TUNNELING MODEL

Charge states:

$$\begin{array}{l} 1. n = +2e \\ n = +1e \\ n = 0e \end{array}$$

$$\begin{array}{l} 2. n = +1e \\ n = 0e \\ n = -1e \end{array}$$

$$\begin{array}{l} 3. n = 0 \\ n = -1e \\ n = -2e \end{array}$$

Current is calculated by solving a master equation connecting the different charge states $n = 0$ to 2 of the molecule

$$I(V) = \frac{2e}{\hbar} \frac{W_{L0}^+ W_1^- W_2^- + W_0^+ W_2^- [W_{L1}^+ - W_{L1}^-] - W_0^+ W_1^+ W_{L2}^-}{W_1^- W_2^- + 2W_0^+ W_2^- + W_0^+ W_1^+}$$

$$W_n^\pm = W_{Ln}^\pm + W_{Rn}^\pm$$



$$W_{L(R)}^+(n) = f(E_{L(R), El \rightarrow M}) \Gamma_{L(R)};$$

$$W_{L(R)}^-(n) = (1 - f(E_{L(R), M \rightarrow El})) \Gamma_{L(R)}.$$

Elastic tunneling process:

$$E_{L(R) El \rightarrow M} = -\varepsilon_s + U(n+1) - U(n) \mp V/2$$

$$E_{L(R) M \rightarrow El} = -\varepsilon_s + U(n) - U(n-1) \mp V/2$$

$$f(E_{L(R), El \rightarrow M}) = \frac{1}{e^{E_{L(R), El \rightarrow M}/k_B T} + 1}$$

$$U(n) = \frac{n^2 e^2}{2C_{eff}}$$

charging energy of the molecule

Γ_L and Γ_R are tunneling rates.

The Fermi golden rule is used

$$\Gamma_{L,R} = 2\pi \sum_{k_x} \sum_{k_y} |T_{L,R}(k_x, k_y)|^2 \delta(E(k_x, k_y) - \varepsilon),$$

$$E(k_x, k_y) = \pm V_F \hbar |\mathbf{k}|$$

Tight-binding approach

$$V_{ij} = V_{pp\pi} = A \exp[-\beta(d - d_0)],$$

$$T_{L,R} = \sum_{i=1}^{N_g} \sum_{j=1}^{N_{A,G,C,T}} C_i^{L(R)} C_j V_{ij}^{L(R)} = \vec{C}^{L(R)} \hat{V}^{L(R)} \vec{C} \quad A = -0.63 \frac{\hbar^2}{m d_0^2}, \quad \beta = 2/d_0,$$

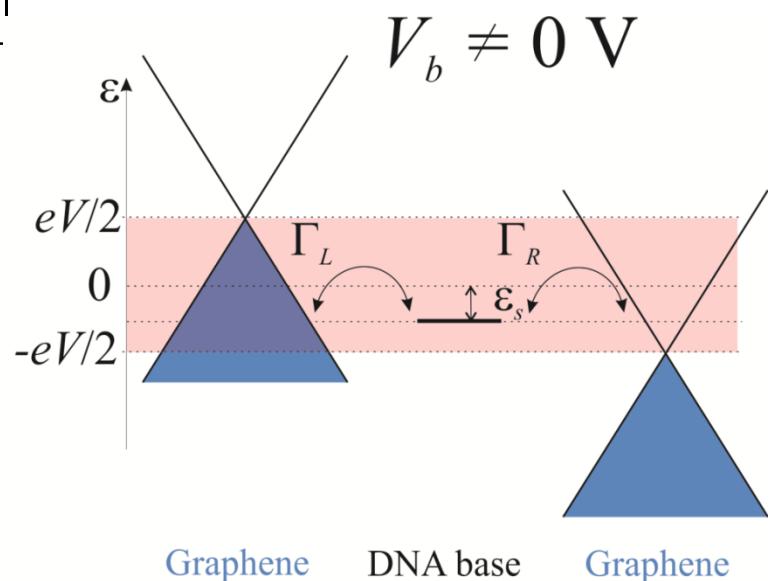
Tunneling rates

$$\Gamma_L(\varepsilon) = \frac{9a_0^2\sqrt{3}}{4\hbar^2 v_F^2} \left[\left(\sum_{i=1}^{N_g/2} S_{2i-1}^L \right)^2 + \left(\sum_{i=1}^{N_g/2} S_{2i}^L \right)^2 \right] |\varepsilon|$$

$$\Gamma_R(\varepsilon) = \frac{9a_0^2\sqrt{3}}{4\hbar^2 v_F^2} \left[\left(\sum_{i=1}^{N_g/2} S_{2i-1}^R \right)^2 + \left(\sum_{i=1}^{N_g/2} S_{2i}^R \right)^2 \right] |\varepsilon|$$

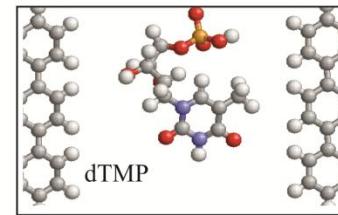
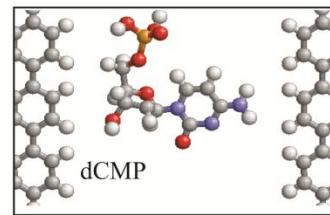
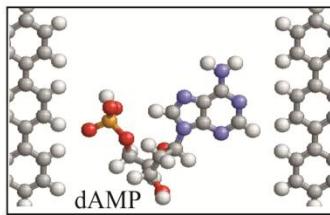
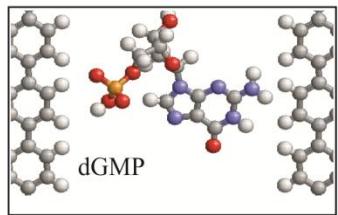
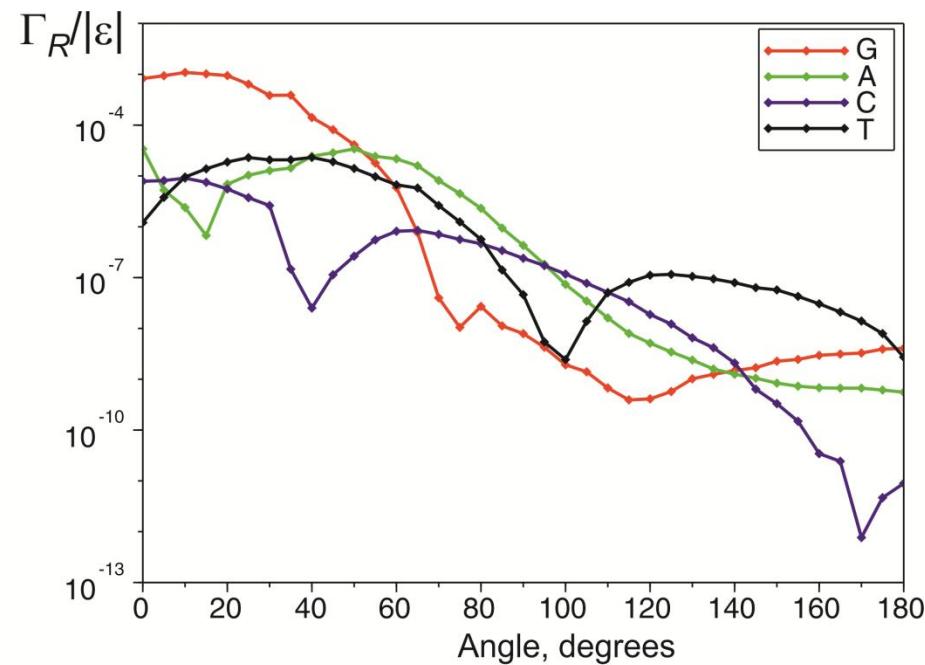
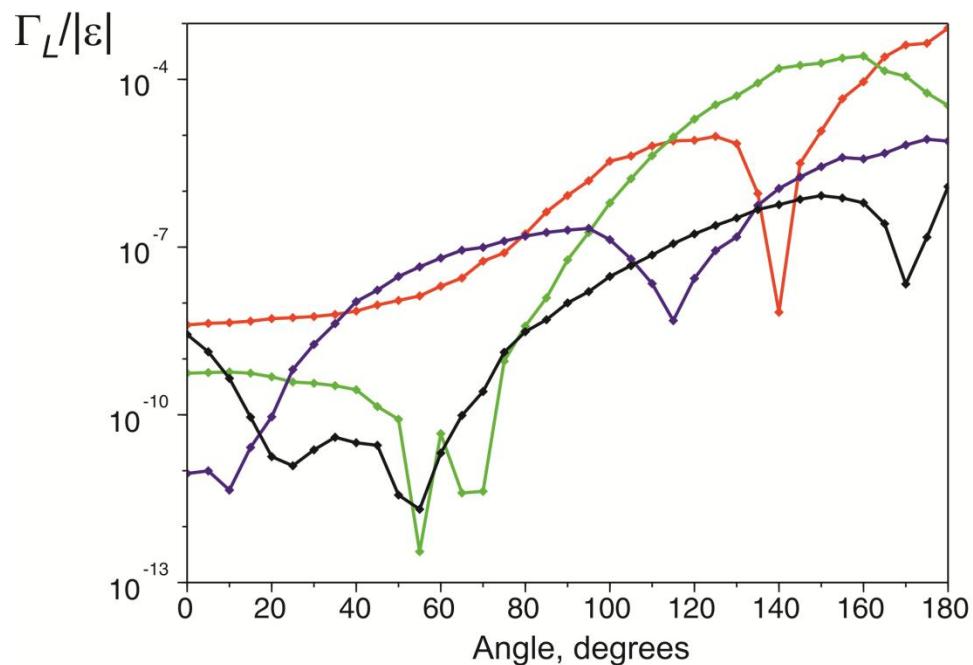
$$\vec{S}^{L(R)} = \hat{V}^{L(R)} \vec{C}$$

$$\varepsilon = -\varepsilon_s + \Delta U(n) \mp V/2$$



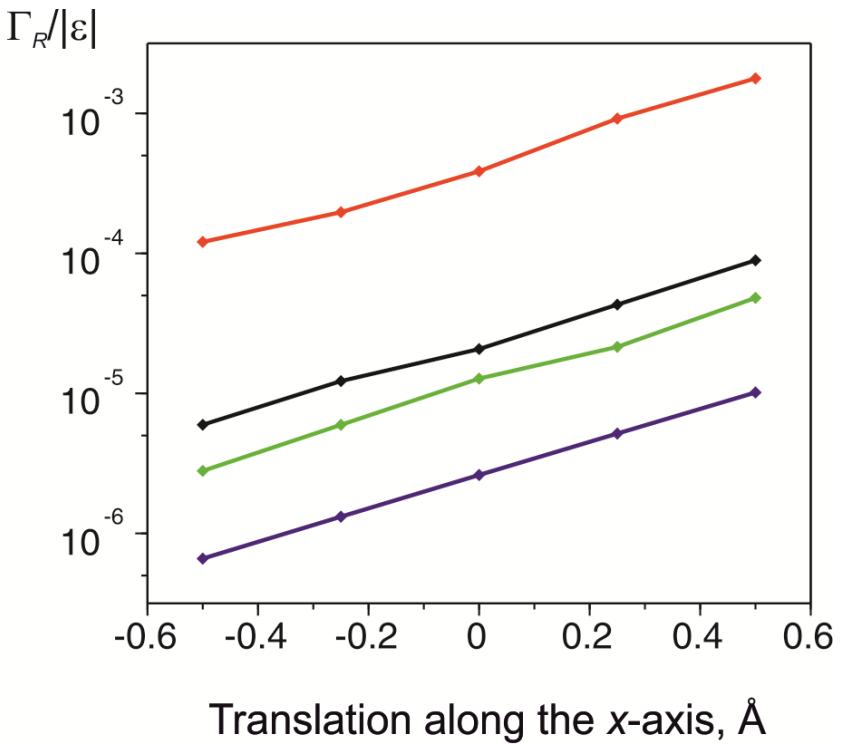
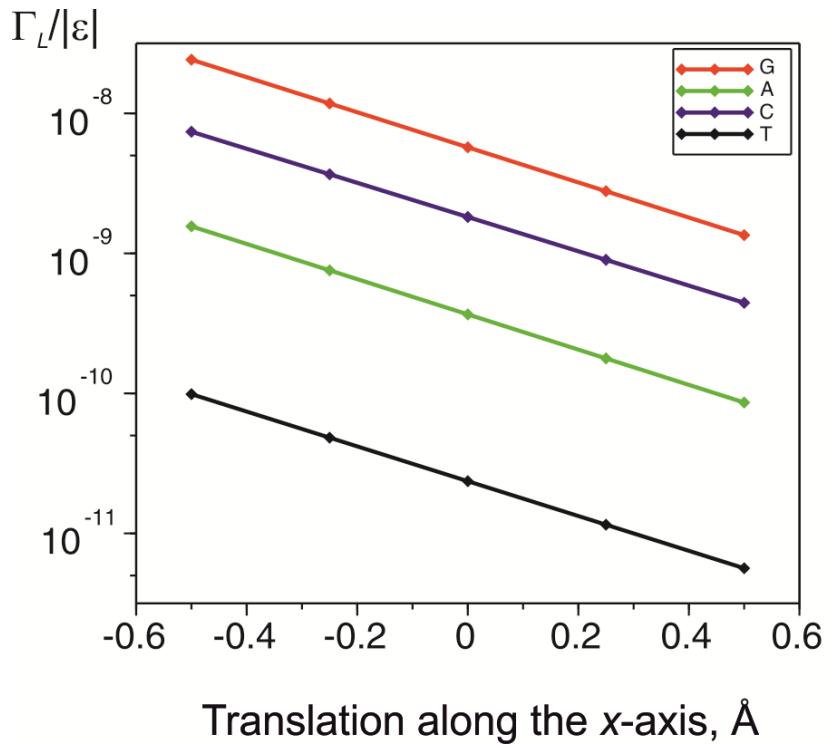
O.G. Isaeva, V. L. Katkov, V. A. Osipov, **DNA sequencing through graphene nanogap: a model of sequential electron transport**, The European Physical Journal B 87, 272 (2014)

Results



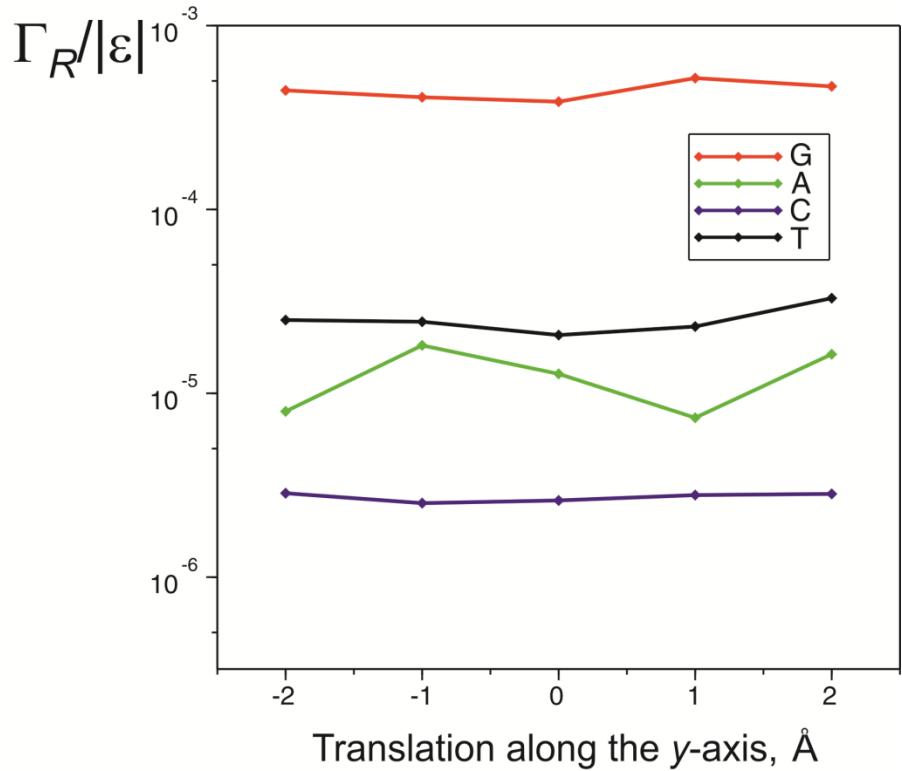
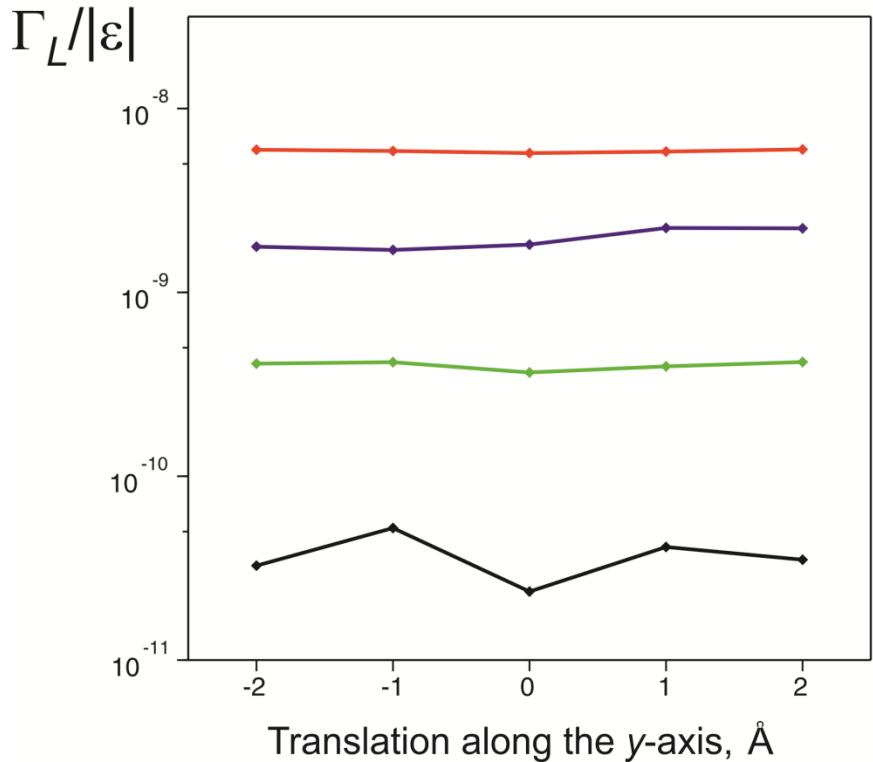
Angular dependences of $\Gamma_L/|\epsilon|$ (left) и $\Gamma_R/|\epsilon|$ (right) for dGMP (G), dAMP (A), dCMP (C), and dTMP (T). The pictures below show orientations corresponding to 0° .

Results



$\Gamma_L/|\varepsilon|$ (left) и $\Gamma_R/|\varepsilon|$ (right) as functions of a translation along the x-axis. Each nucleotide has fixed angular position 30°

Results



$\Gamma_L/|\varepsilon|$ (left) и $\Gamma_R/|\varepsilon|$ (right) as functions of a translation along the y-axis. Each nucleotide has fixed angular position 30°

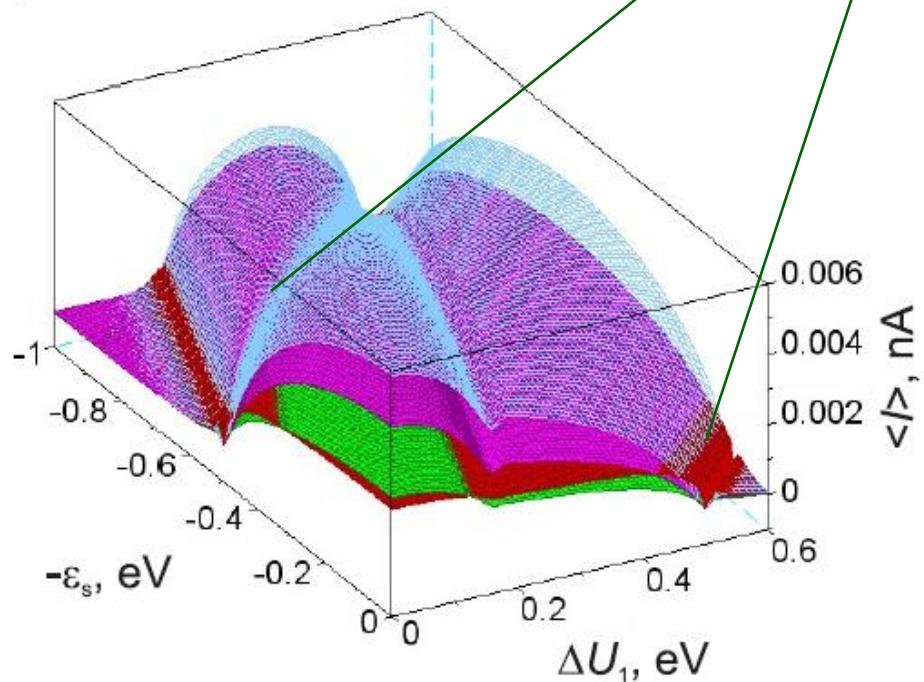
Bias voltage $V_b = 1\text{V}$,
Temperature = 300 K

17

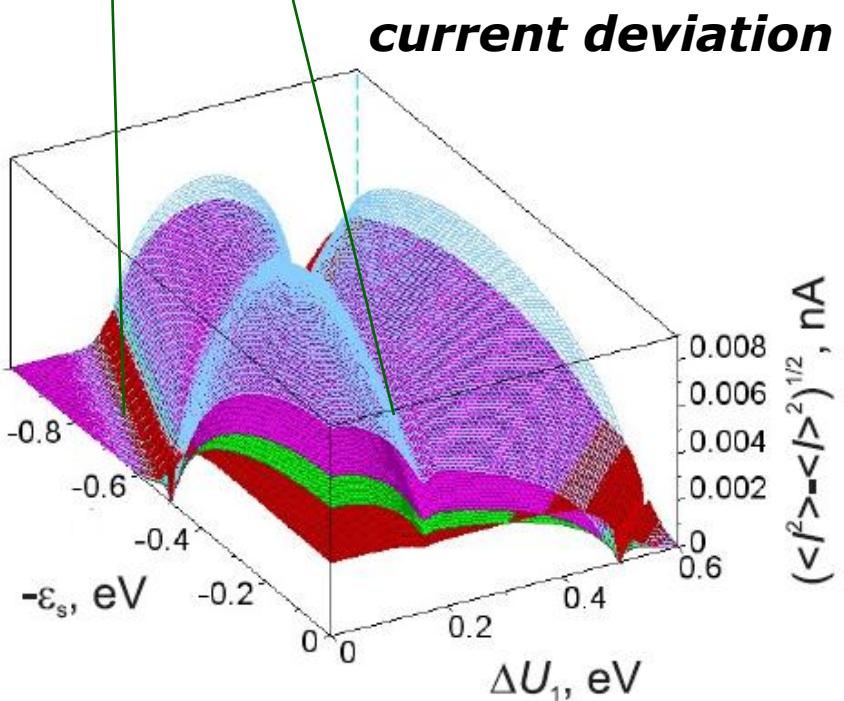
$$| -\varepsilon_s + U_1 | - V_b/2 = 0$$

$$| -\varepsilon_s + 3U_1 | - V_b/2 = 0$$

a) ***current***



b)



— dGMP

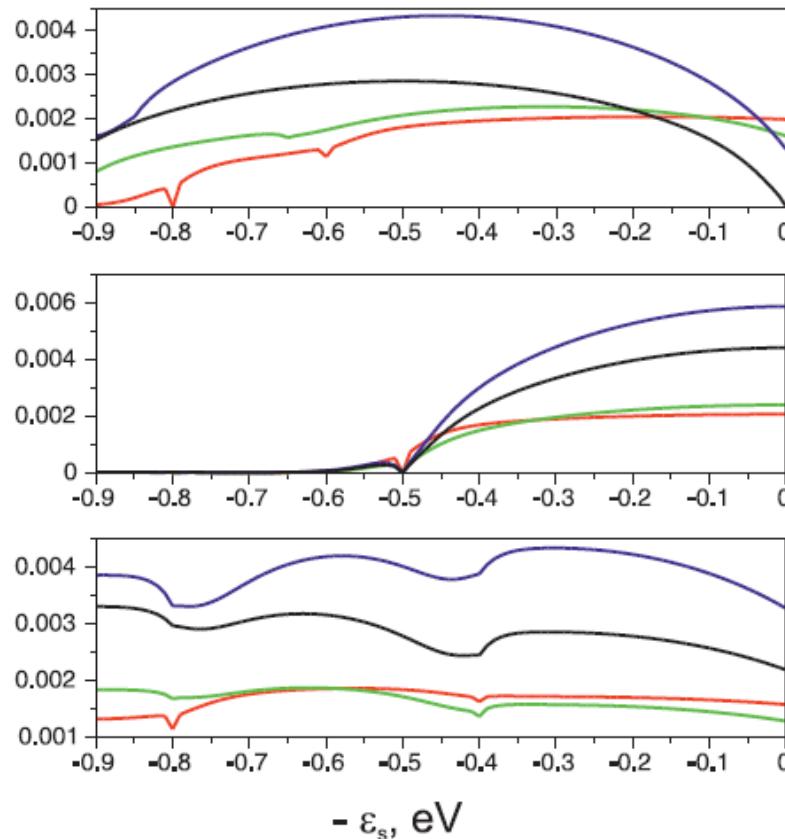
— dAMP

— dCMP

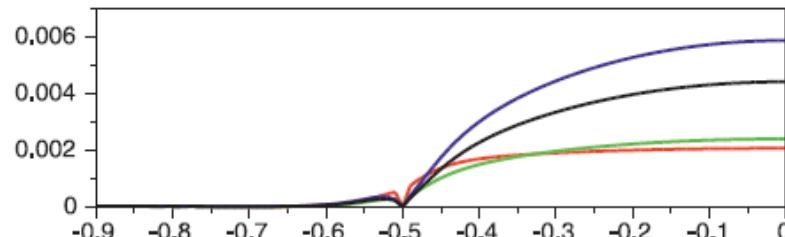
— dTMP

Bias voltage $V_b = 1\text{V}$,
Temperature = 300 K

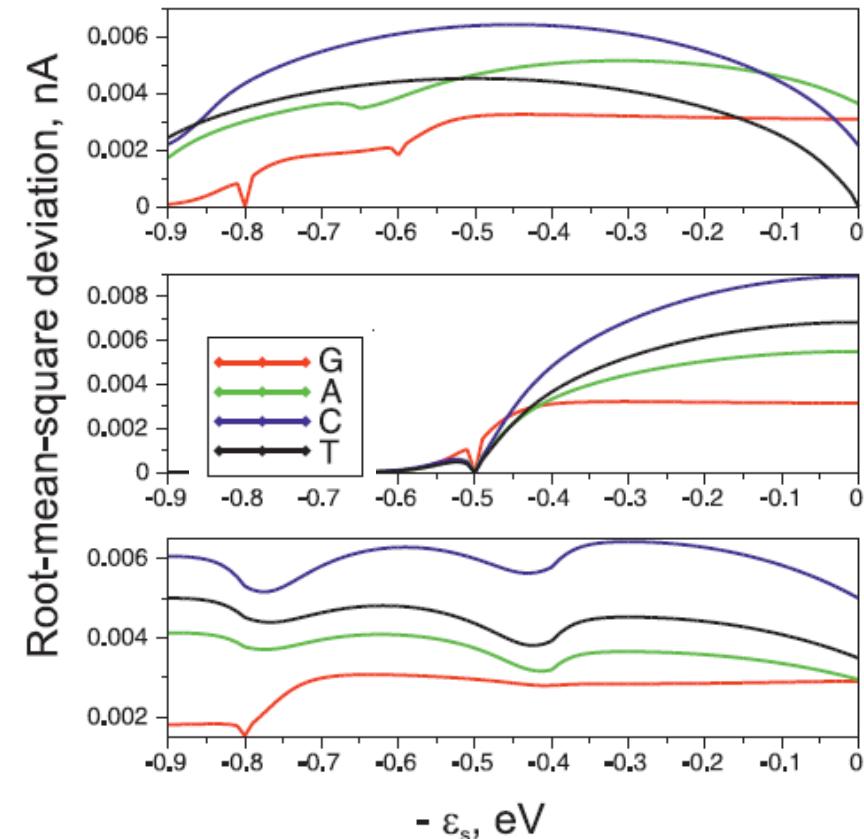
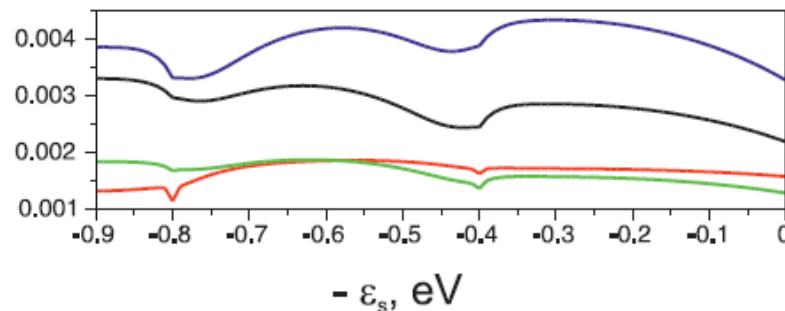
a)



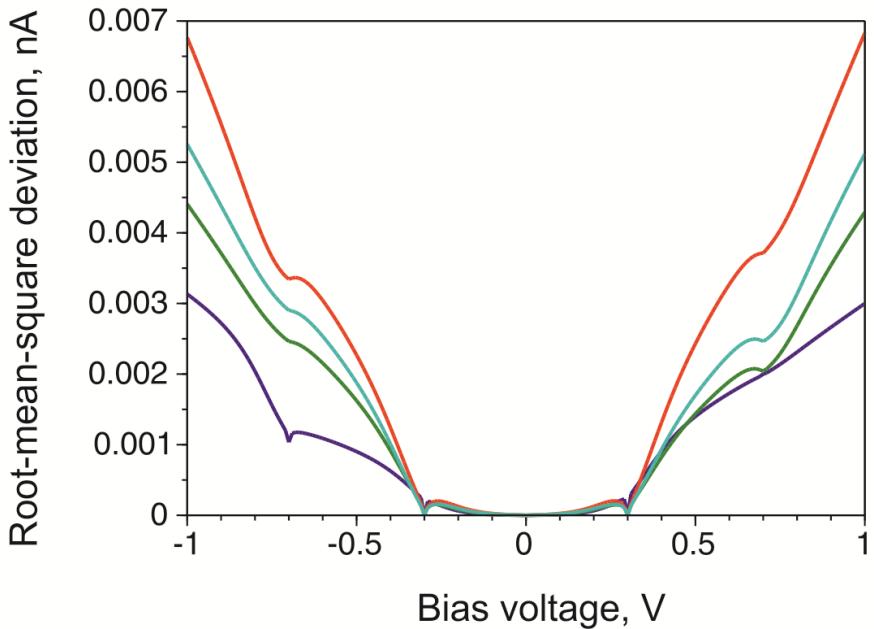
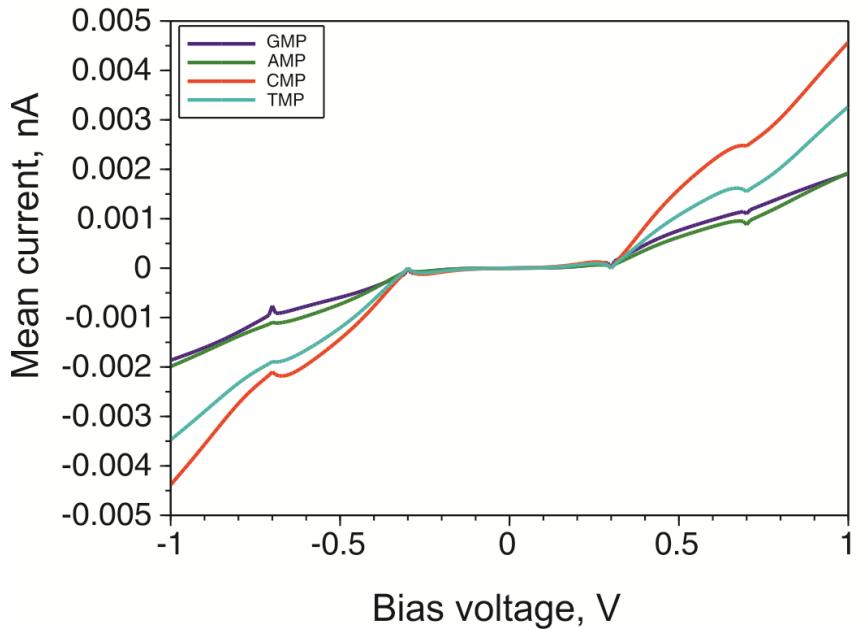
b)



c)



- a) $\Delta U_{1G} = 0.1 \text{ eV}$, $\Delta U_{1A} = 0.15 \text{ eV}$, $\Delta U_{1C} = 0.45 \text{ eV}$, $\Delta U_{1T} = 0.5 \text{ eV}$;
- b) $\Delta U_1 = 0 \text{ eV}$ (for each nucleotide);
- c) $\Delta U_1 = 0.3 \text{ eV}$ (for each nucleotide).



Mean I-V characteristics (left). rmsd vs voltage (right). Parameters for calculation: $\varepsilon_s = -0,4 \text{ eB}$, $\Delta U_1 = 0,25 \text{ eB}$, $T = 300 \text{ K}$

CONCLUSION (for part 2)

- Unique shape of each nucleotide provides a specific dispersion of tunnel currents so that combined measurements of the tunnel current and its root-mean-square deviation allow to facilitate the identification of nucleotides

O.G. Isaeva, V. L. Katkov, V. A. Osipov, DNA sequencing through graphene nanogap: a model of sequential electron transport, The European Physical Journal B 87, 272 (2014)

Thank you for attention

SEQUENTIAL TUNNELING MODEL

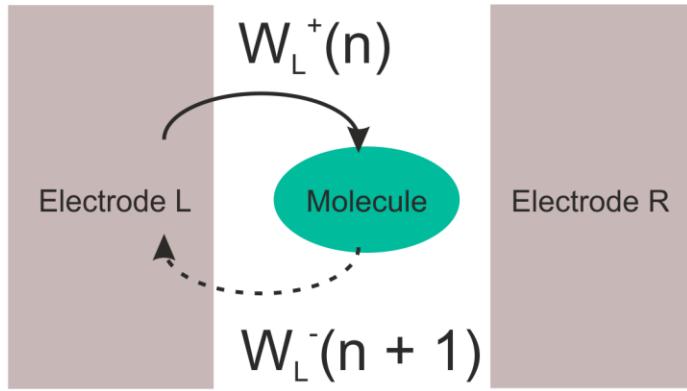
Charge states:

$$1. \begin{aligned} n &= +2e \\ n &= +1e \\ n &= 0e \end{aligned}$$

$$2. \begin{aligned} n &= +1e \\ n &= 0e \\ n &= -1e \end{aligned}$$

$$3. \begin{aligned} n &= 0 \\ n &= -1e \\ n &= -2e \end{aligned}$$

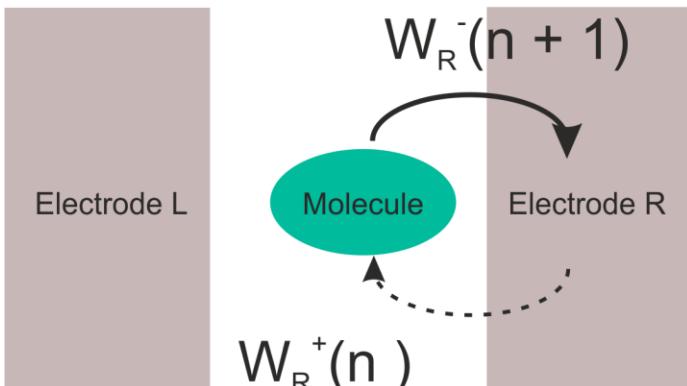
Current is calculated by solving a master equation connecting the different charge states $i = 0$ to 2 of the molecule



$$\frac{d\sigma(n)}{dt} = W^+(n-1)\sigma(n-1) + W^-(n+1)\sigma(n+1) - (W^+(n) + W^-(n))\sigma(n);$$

$$\sum_{i=0}^2 \sigma(n+i) = 1;$$

$$W^\pm = W_L^\pm + W_R^\pm$$



$$W^-(n+1)\sigma(n+1) = 2W^+(n)\sigma(n);$$

$$2W^-(n+2)\sigma(n+2) = W^+(n+1)\sigma(n+1)$$

$$I = -e \sum_{i=0}^2 \sigma(n+i)(W_L^+(n+i) - W_L^-(n+i))$$