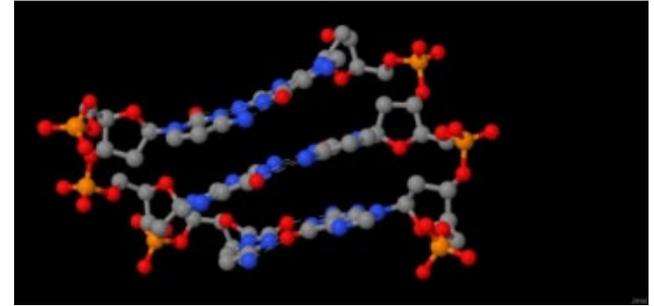




**EMN OPEN ACCESS WEEK**  
Energy Materials Nanotechnology  
September 22 – 25, 2014 Chengdu, China



## **Systematic study of carrier transfer in DNA polymers**

**monomer = a DNA base-pair**

**carrier = electron (through LUMOs) or hole (through HOMOs)**

**monomers, dimers, trimers, tetramers, polymers**

**Constantinos Simserides**

**National and Kapodistrian University of Athens, Faculty of Physics,  
Greece**



<http://www.phys.uoa.gr/>  
<http://users.uoa.gr/~csimseri>

[K. Lambropoulos, K. Kaklamanis, G. Georgiadis](#)

## Aim:

easily determine spatiotemporal evolution of electrons or holes  
along a  $N$  base-pair DNA segment

## Important for:

nanotechnology (molecular wires, nanocircuits)

biology (carcinogenesis, mutagenesis, damage, repair)

monomer = a DNA base-pair

systematic study of carrier transfer along

all possible dimers, all possible trimers, and

characteristic polymers, including segments taken from experiments

## Physical quantities defined:

Periodic cases (period  $T$ ):

maximum transfer percentage  $p$ ,    pure maximum transfer rate  $p / T$

All cases (charge transfer distance  $d$ ):

pure mean transfer rate  $k = \frac{\langle |A_N(t)|^2 \rangle}{t_{Nmean}}$ ,    speed  $u = k d$

Introduction to DNA

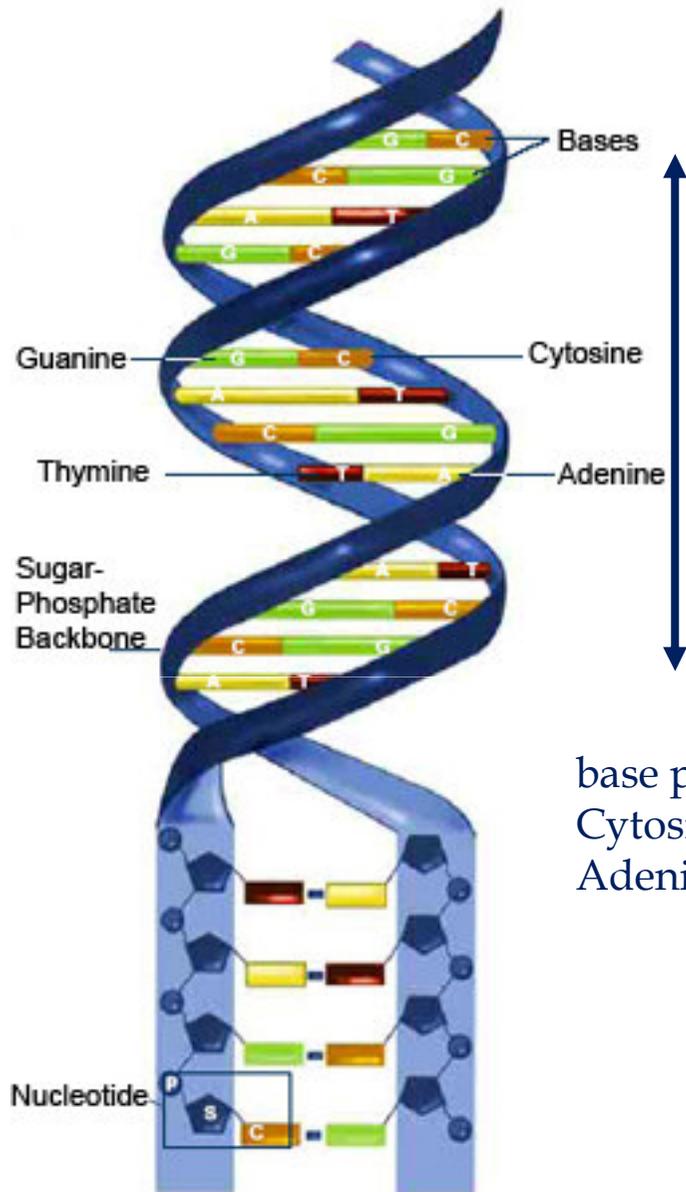
Charge transfer in DNA

Results for dimers

Results for trimers

Greater sequences

# Introduction to DNA



base pair separation  
 $\sim 3.4 \text{ \AA}$

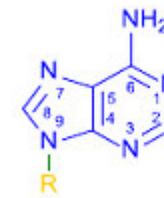
helix step  $\sim 34 \text{ \AA}$

base pairs:

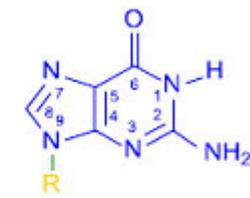
Cytosine  $\langle 3 \text{ H bonds} \rangle$  Guanine

Adenine  $\langle 2 \text{ H bonds} \rangle$  Thymine

## Purines

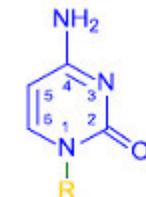


Adenine

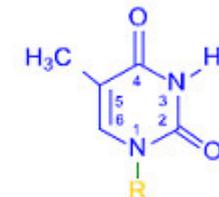


Guanine

## Pyrimidines



Cytosine



Thymine

# Charge transfer in DNA

# From Schrödinger equation to a Tight-Binding System of Differential Equations

## Description at the base-pair level

Starting from the time-dependent Schrödinger equation:

$$i\hbar \frac{\partial \Psi_{H/L}^{DNA}}{\partial t} = \hat{H}^{DNA} \Psi_{H/L}^{DNA}$$

We analyze the DNA wavefunction into the bp wavefunctions:

$$\Psi_{H/L}^{DNA}(\mathbf{r}, t) = \sum_{\mu} A_{\mu}(t) \Psi_{H/L}^{bp(\mu)}(\mathbf{r})$$

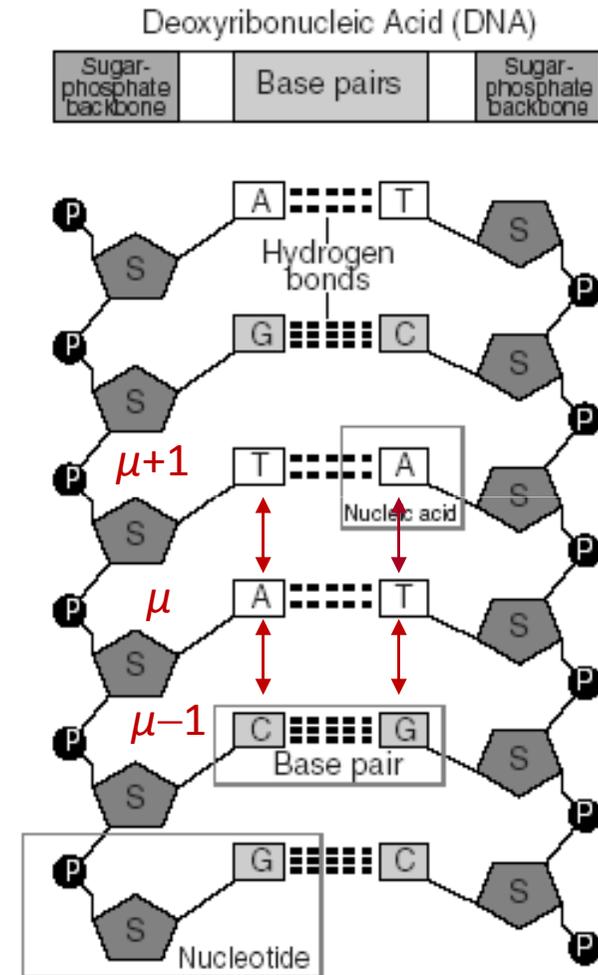
$|A_{\mu}(t)|^2$  probability to find the carrier at base-pair  $\mu$

we find that the time evolution of the coefficients  $A_{\mu}(t)$  obeys the following system of equations:

$$i\hbar \frac{dA_{\mu}}{dt} = E_{H/L}^{bp(\mu)} A_{\mu} + t_{H/L}^{bp(\mu, \mu-1)} A_{\mu-1} + t_{H/L}^{bp(\mu, \mu+1)} A_{\mu+1}$$

$E_{H/L}^{bp}$  : on-site energies of the two possible base-pairs

$t_{H/L}^{bp}$  : hopping parameters for all possible combinations of successive base-pairs



## HOMO and LUMO on-site energies of the base-pairs

- Calculated by various authors
- Used for the solution of the tight-binding system of equations

$$i\hbar \frac{dA_\lambda}{dt} = E_{H/L}^{bp(\lambda)} A_\lambda + t_{H/L}^{bp(\lambda;\lambda-1)} A_{\lambda-1} + t_{H/L}^{bp(\lambda;\lambda+1)} A_{\lambda+1}$$

B-DNA base-pair	A-T	G-C	reference
$E_H^{bp}$	-8.3	-8.0	[4]
$E_L^{bp}$	-4.9	-4.5	[4]
$E_{\pi-\pi^*}$	3.4	3.5	[4]
$E_H^{bp}$ first pr.	-(7.8-8.2)	-(6.3-7.7)	[7-12]
$E_{\pi-\pi^*}$ first pr.	6.4	4.3-6.3	[12, 13]
$E_H^{bp}$ used	8.3	8.0	[4]
$E_L^{bp}$ used	-4.9	-4.5	[4]

All energies in eV

## Hopping parameters between successive base-pairs

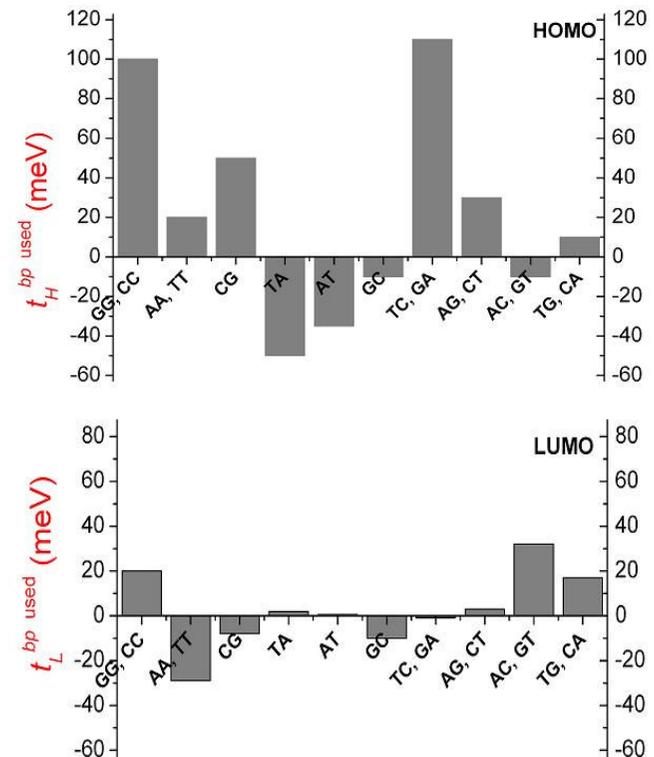
- Calculated by various authors
- Used for the solution of the tight-binding system of equations

$$i\hbar \frac{dA_\lambda}{dt} = E_{H/L}^{bp(\lambda)} A_\lambda + t_{H/L}^{bp(\lambda;\lambda-1)} A_{\lambda-1} + t_{H/L}^{bp(\lambda;\lambda+1)} A_{\lambda+1}$$

- Successive base-pairs  $\Leftrightarrow$  denoted by  $YX$   $\left\{ \begin{array}{l} \lambda \quad Y - Y_{compl} \\ \lambda' \quad X - X_{compl} \\ 3' \quad 5' \end{array} \right.$

Base-pair sequence	$t_H^{bp}$ [9]	$ t_H^{bp} $ [19]	$t_H^{bp}$ [8]	$t_H^{bp}$ [20]	$t_H^{bp}$ [21]	$t_H^{bp}$ [22]	$t_H^{bp}$ used	$t_L^{bp}$ [9]	$t_L^{bp}$ [8]	$t_L^{bp}$ used
AA, TT	-8	26	-25	8-17	19(19)	22	20	-29	35	-29
AT	20	55			47(74)	37	-35	0.5		0.5
AG, CT	-5	25	-50		35(51)	43	30	3	35	3
AC, GT	2	26			25(38)	20	-10	32		32
TA	47	50			32(68)	52	-50	2		2
TG, CA	-4	27			11(11)	25	10	17		17
TC, GA	-79	122	-160		71(108)	60	110	-1	35	-1
GG, CC	-62	93	-140	75	72(101)	63	100	20	35	20
GC	1	22			20(32)	22	-10	-10		-10
CG	-44	78			51(84)	74	50	-8		-8

All hopping parameters in meV



## General solution of the tight-binding system of equations

To solve the system:

$$i\hbar \frac{dA_\lambda}{dt} = E_{H/L}^{bp(\lambda)} A_\lambda + t_{H/L}^{bp(\lambda;\lambda-1)} A_{\lambda-1} + t_{H/L}^{bp(\lambda;\lambda+1)} A_{\lambda+1}$$

we define the vector matrix  $\mathbf{x}(t) = \begin{bmatrix} A_1(t) \\ A_2(t) \\ \vdots \\ A_N(t) \end{bmatrix}$

Therefore:

$$\dot{\mathbf{x}}(t) = \tilde{\mathcal{A}}\mathbf{x}(t), \quad \tilde{\mathcal{A}} = -\frac{i}{\hbar} \begin{bmatrix} E_{H/L}^{bp(1)} & t_{H/L}^{bp(1;2)} & 0 & \cdots & 0 & 0 & 0 \\ t_{H/L}^{bp(2;1)} & E_{H/L}^{bp(2)} & t_{H/L}^{bp(2;3)} & \cdots & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & \cdots & t_{H/L}^{bp(N-1;N-2)} & E_{H/L}^{bp(N-1)} & t_{H/L}^{bp(N-1;N)} \\ 0 & 0 & 0 & \cdots & 0 & t_{H/L}^{bp(N;N-1)} & E_{H/L}^{bp(N)} \end{bmatrix}$$

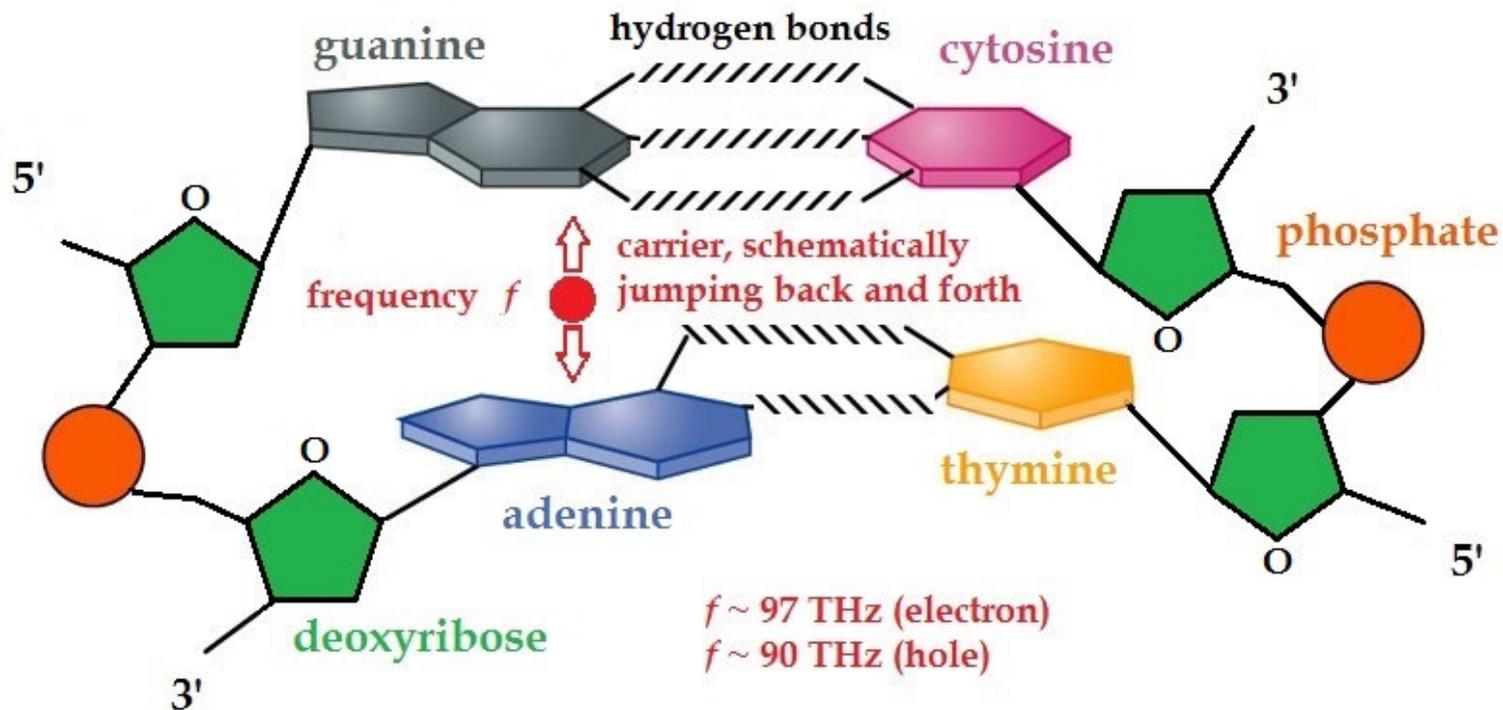
eigenvalue method, the general solution is:

$$\mathbf{x}(t) = \sum_{k=1}^N c_k \mathbf{v}_k e^{-\frac{i}{\hbar} \lambda_k t}$$

$\mathbf{v}_k$ : normalized (linearly independent) eigenvectors

$\lambda_k$ : eigenvalues.

# Results for dimers

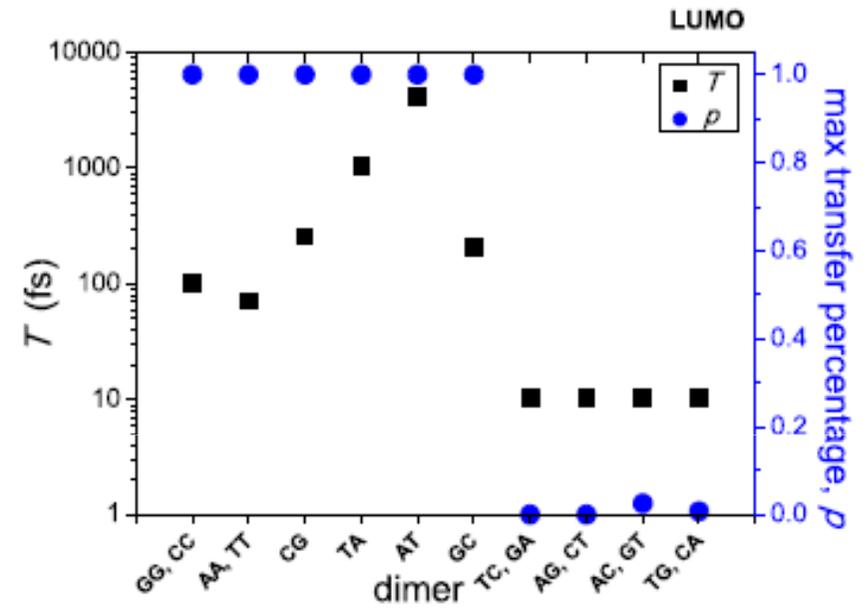
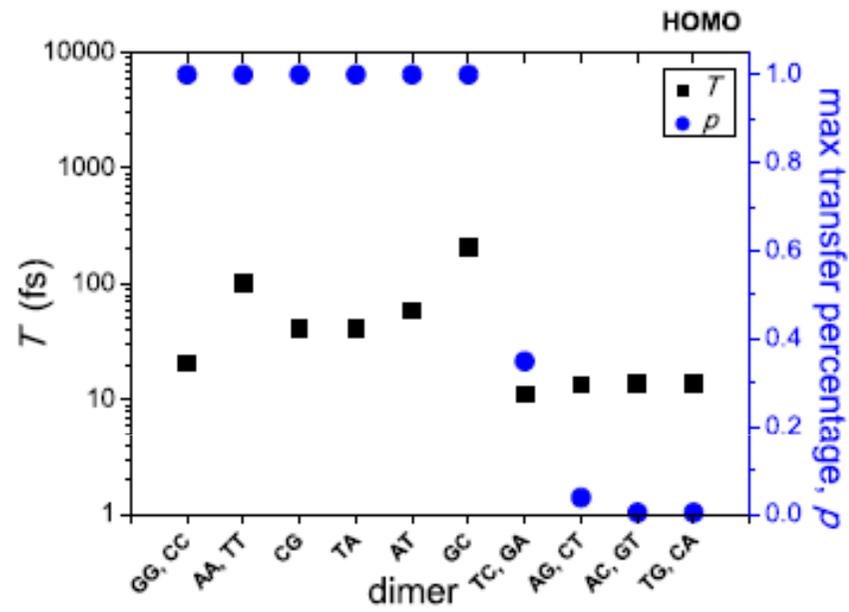


**10 unique dimers, 6 made of identical monomers**

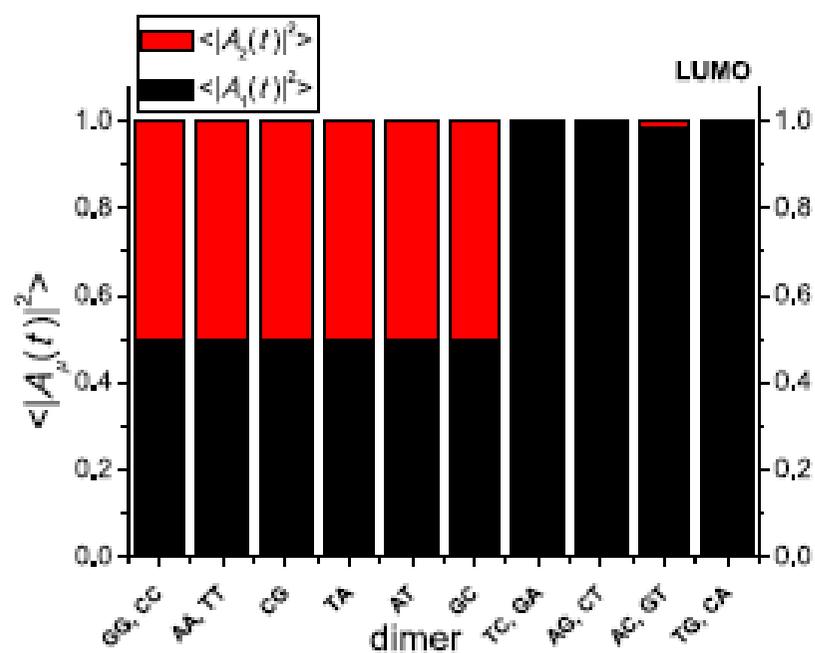
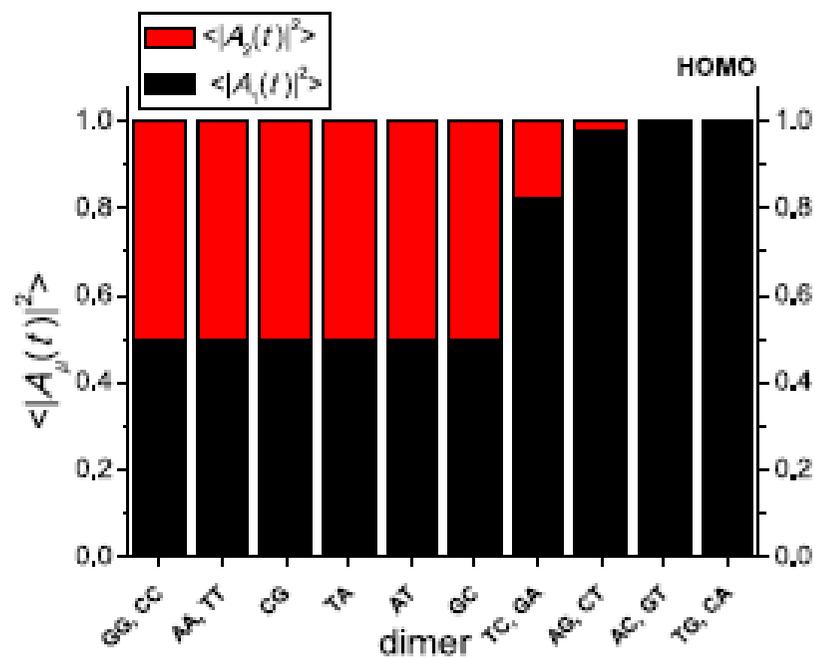
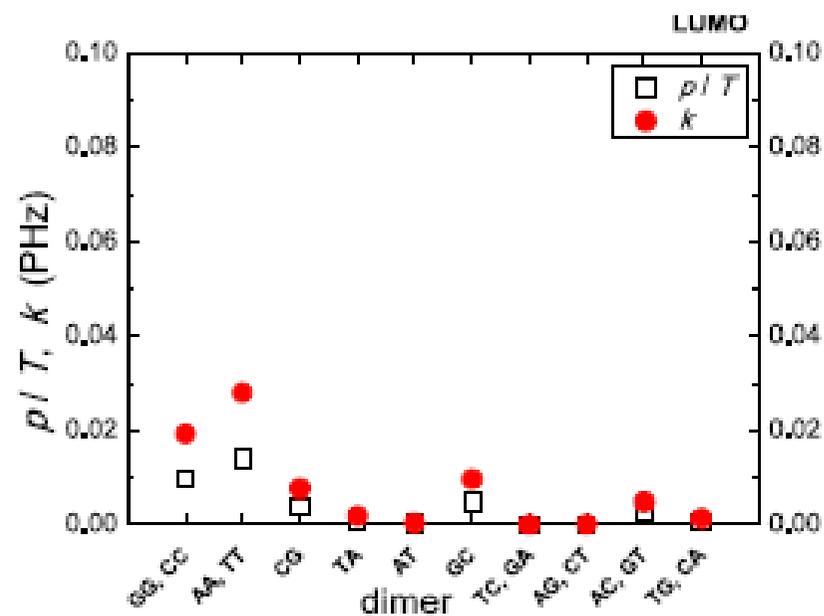
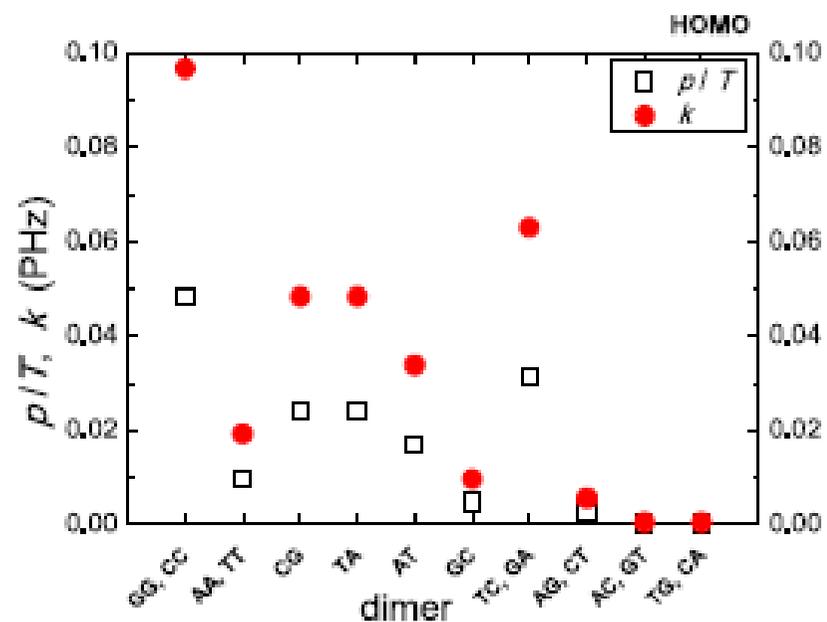
**periodic carrier transfer in all cases**

**(equations, details . . . in our articles)**

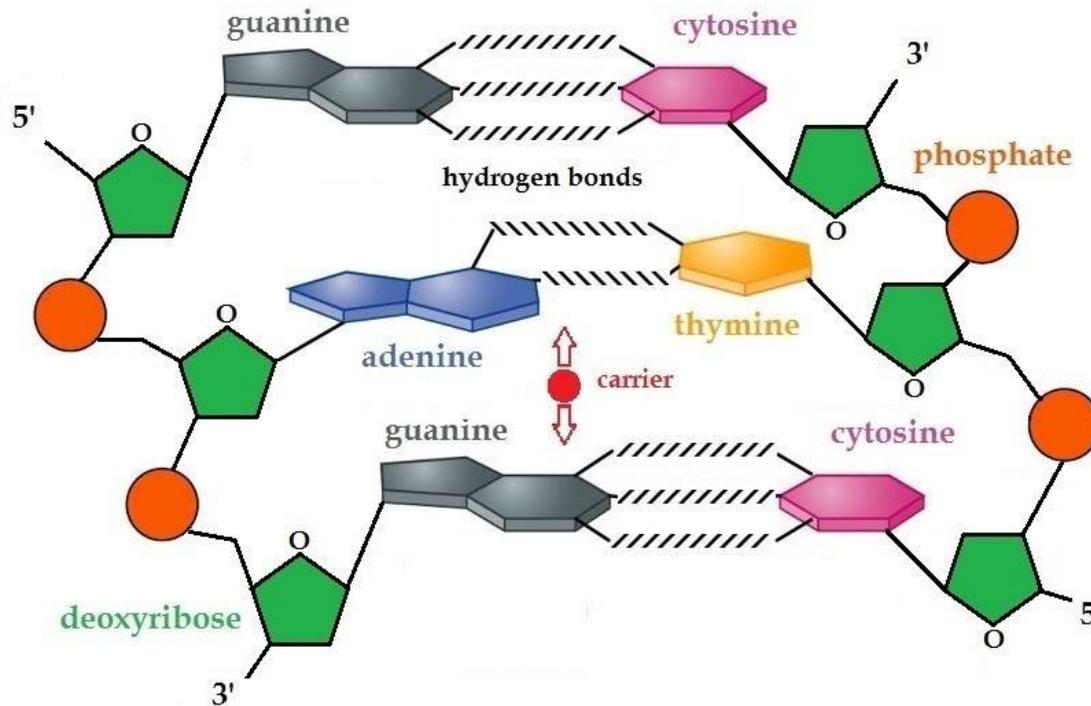
# Periodic carrier transfer in base-pair dimers



## Periodic carrier transfer in base-pair dimers



# Results for trimers



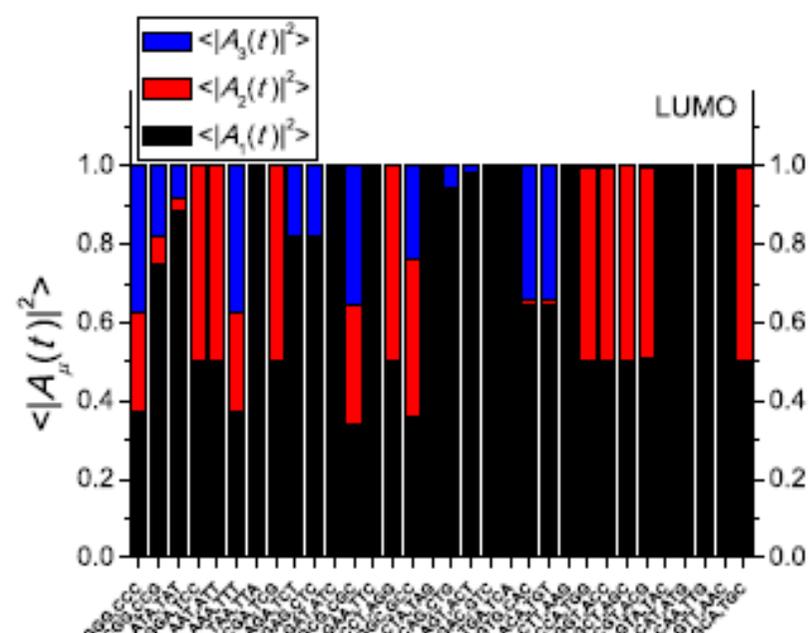
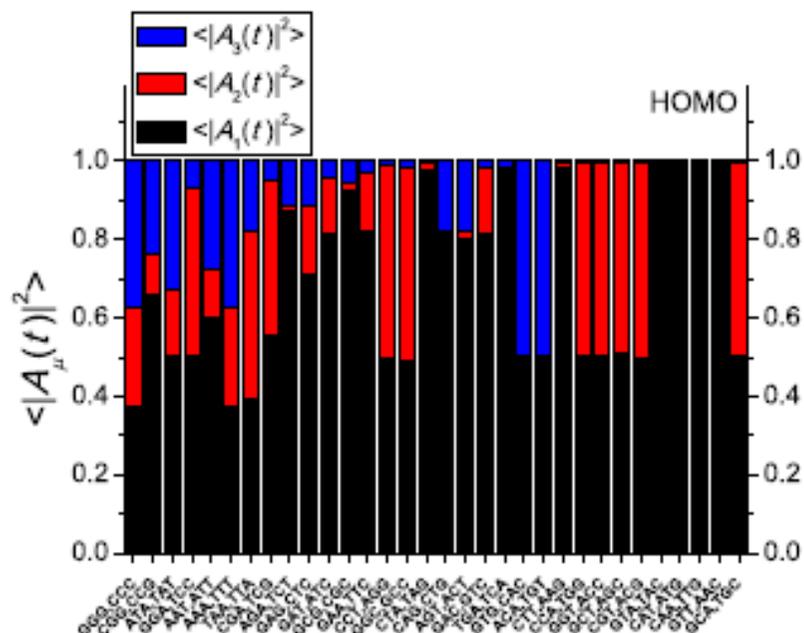
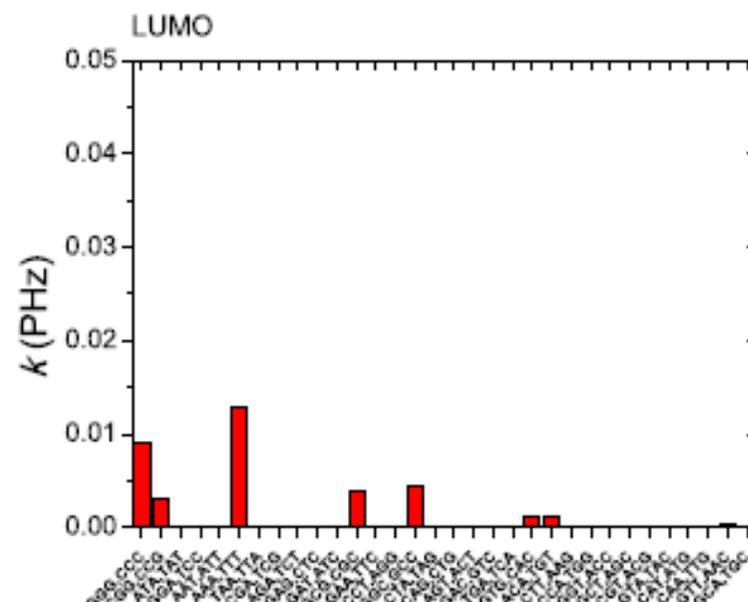
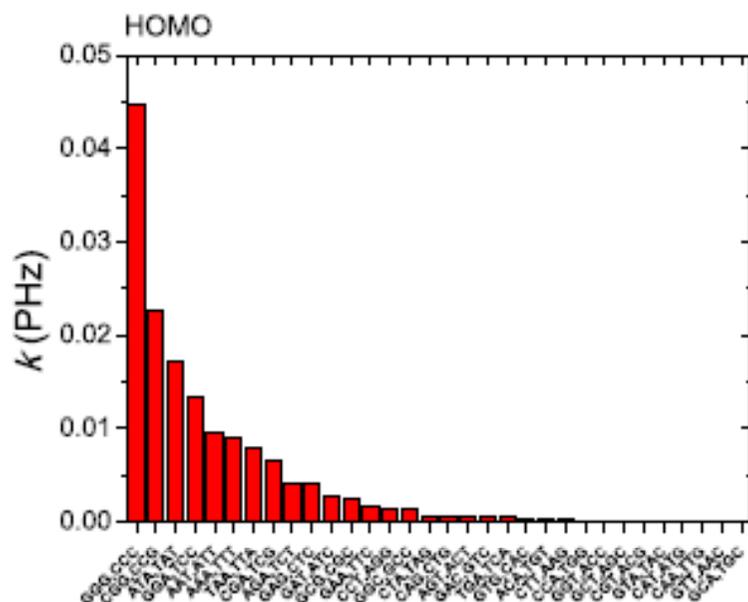
**32 unique trimers, 8 made of identical monomers**

**periodic carrier transfer for trimers of identical monomers**

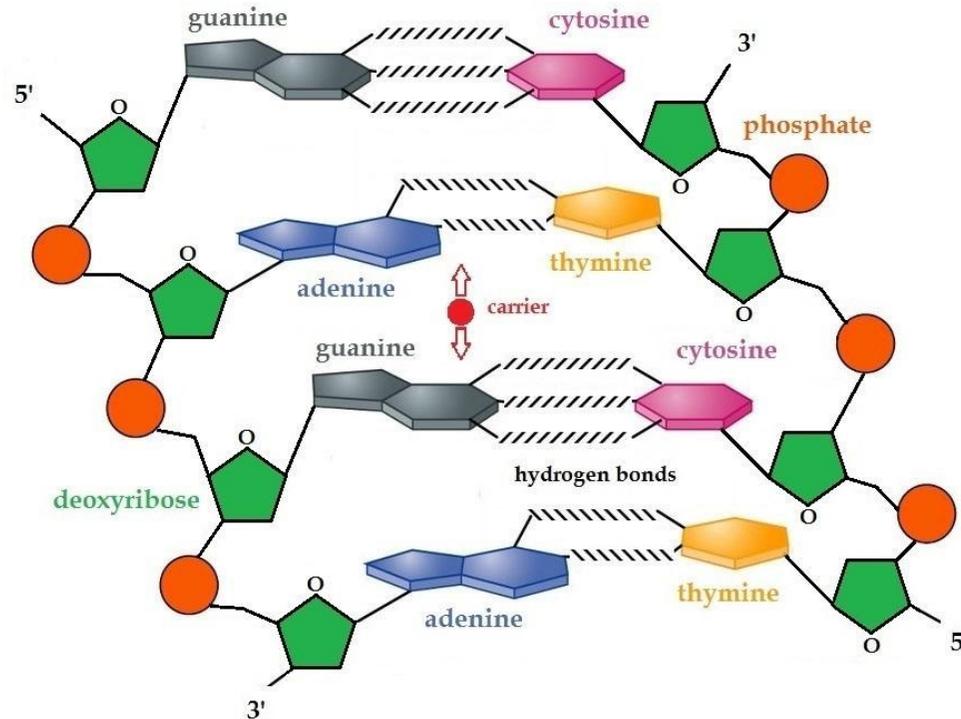
**for trimers of different monomers the carrier movement may be non periodic**

**(equations, details . . . in our articles)**

Pure mean transfer rate  $k$  &  $\langle |A_\mu(t)|^2 \rangle$  for all possible trimers.  
 Initially, we place the carrier in monomer 1.



# Greater sequences, polymers



e.g. there are 136 unique tetramers, 20 made of identical monomers

increasing the number of monomers above 3  
periodicity is (generally) lost

(equations, details . . . in our articles)

# Polymers

## pure mean transfer rate, $k$

Exponential fit       $k = k_0 \exp(-\beta d)$       inverse decay length  $\beta$

Power-law fit       $k = k_0' N^{-\eta}$       exponent  $\eta$

### *Computed values*

$\beta \approx 0.2 - 2 \text{ \AA}^{-1}$ ,       $k_0$  usually  $10^{-2}$ - $10^{-1}$  PHz, generally  $10^{-4}$ - $10$  PHz

$\eta \approx 1.7$ - $17$ ,       $k_0'$  usually  $10^{-2}$ - $10^{-1}$  PHz, generally  $10^{-4}$ - $10^3$  PHz

**& probability to find the carrier at a particular monomer**  
 **$\langle |A_i(t)|^2 \rangle$**

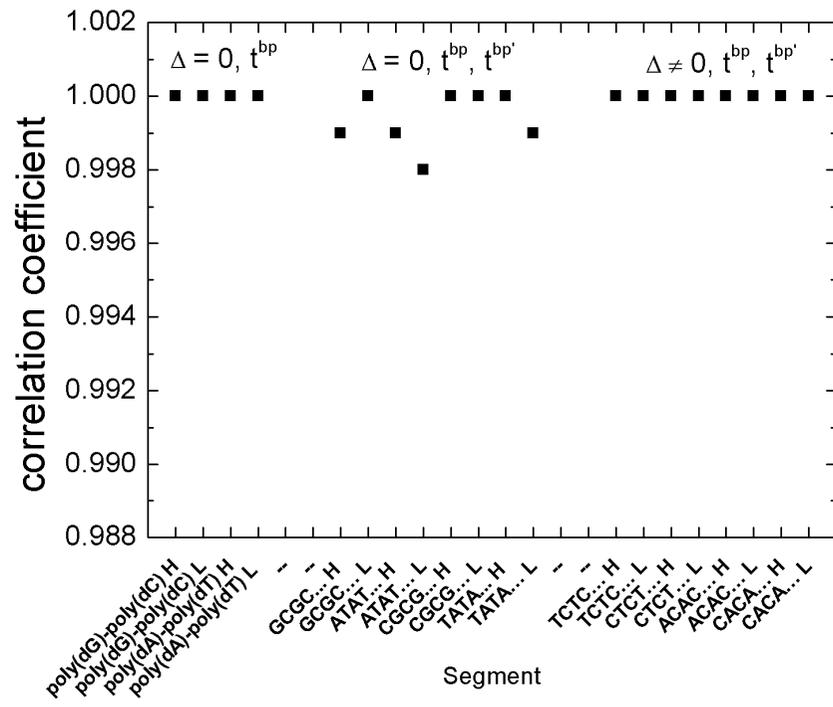
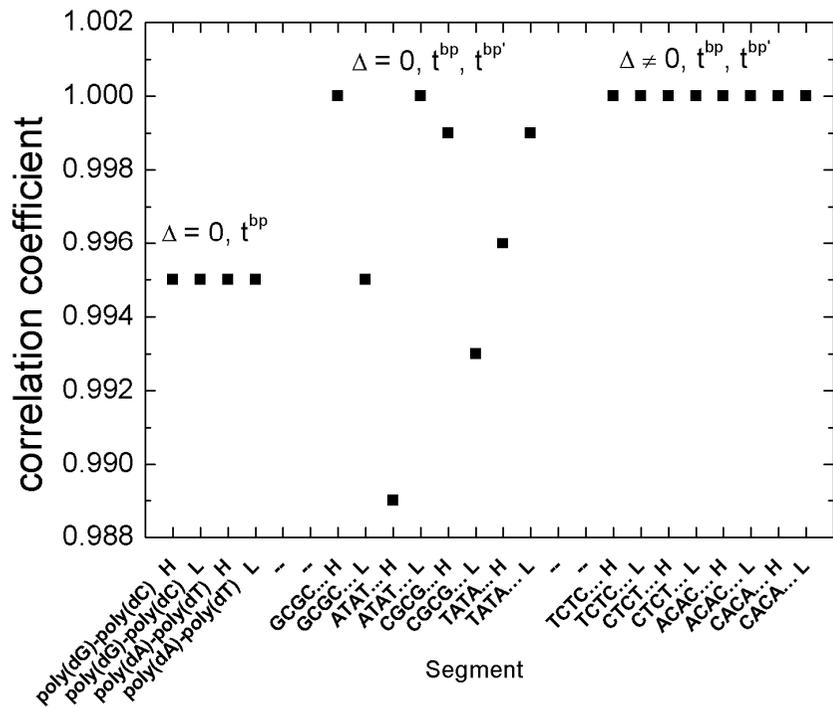
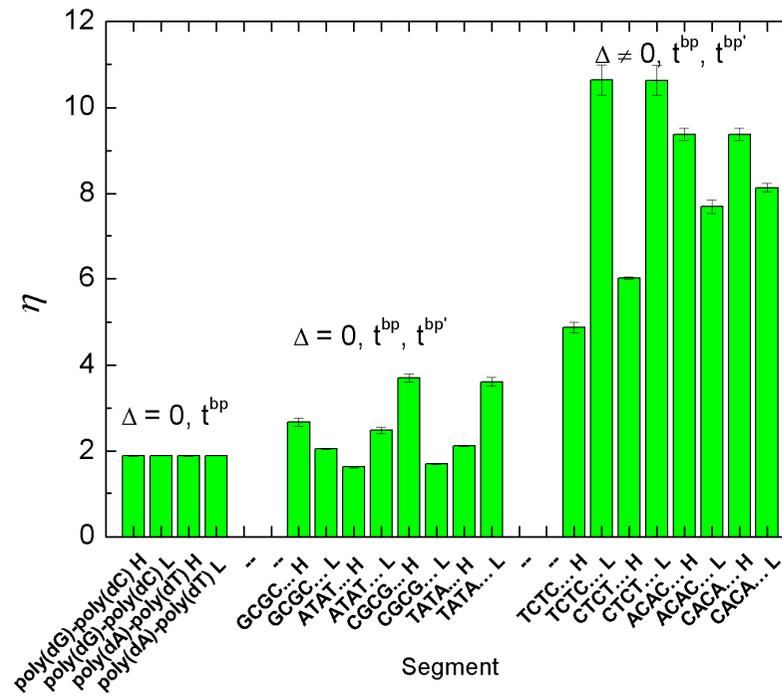
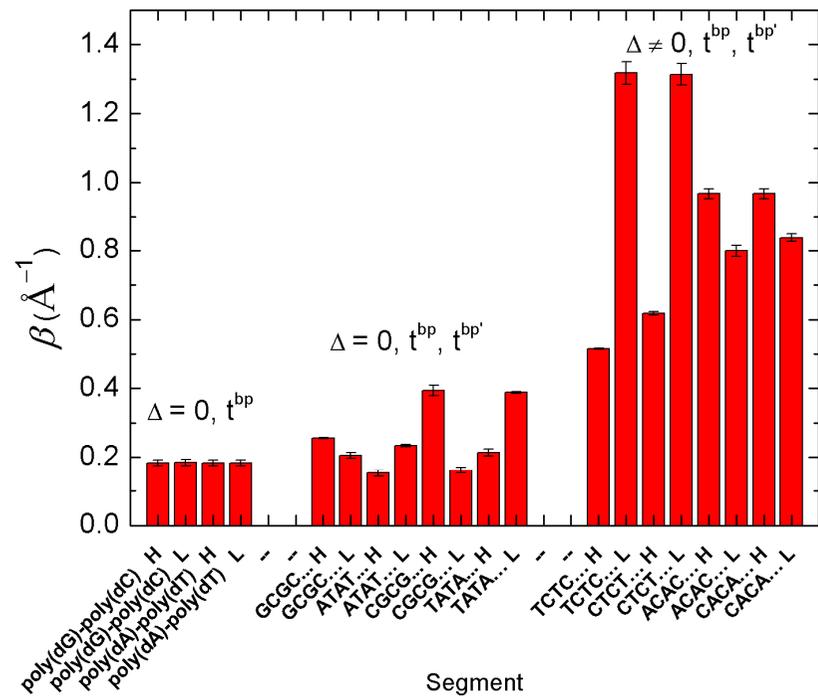
# Polymers transfer rates

**Table 3**Estimated  $k_0$  and  $\beta$  of the exponential fit  $k = k_0 \exp(-\beta d)$  for various DNA polymers.

DNA segment	$k_0$ (PHz)	$\beta$ ( $\text{\AA}^{-1}$ )	Correlation coefficient	H/L
poly(dG)–poly(dC)	$0.176 \pm 0.007$	$0.189 \pm 0.008$	0.988	H
poly(dG)–poly(dC)	$0.035 \pm 0.001$	$0.189 \pm 0.007$	0.989	L
poly(dA)–poly(dT)	$0.035 \pm 0.001$	$0.189 \pm 0.008$	0.988	H
poly(dA)–poly(dT)	$0.051 \pm 0.002$	$0.189 \pm 0.008$	0.989	L
GCGCGC...	$0.032 \pm 0.003$	$0.358 \pm 0.023$	0.988	H
ATATAT...	$0.057 \pm 0.002$	$0.168 \pm 0.008$	0.985	H
CGCGCG...	$0.932 \pm 0.234$	$0.871 \pm 0.074$	0.994	H
TATATA...	$0.110 \pm 0.006$	$0.251 \pm 0.012$	0.985	H
AGTGCCAAGCTTGCA [46]	$0.059 \pm 0.002$	$0.685 \pm 0.008$	1.000	H
AGTGCCAAGCTTGCA [46]	$(9.8 \pm 2.6) \times 10^{-5}$	$0.197 \pm 0.059$	0.808	L
TAGAGGTGTTATGA [49]	$4.306 \pm 5.001$	$1.321 \pm 0.342$	0.998	H
TAGAGGTGTTATGA [49]	$2.877 \pm 0.833$	$2.154 \pm 0.085$	1.000	L

**Table 4**Estimated  $k'_0$  and  $\eta$  of the power fit  $k = k'_0 N^{-\eta}$  for various DNA polymers.

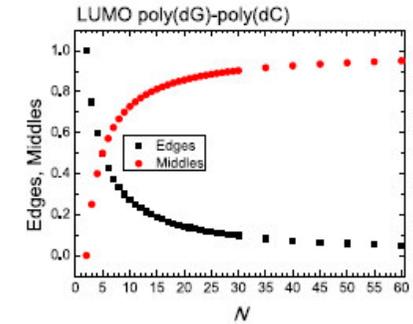
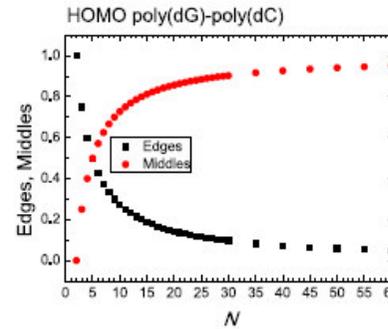
DNA segment	$k'_0$ (PHz)	$\eta$	Correlation coefficient	H/L
poly(dG)–poly(dC)	$0.359 \pm 0.001$	$1.893 \pm 0.002$	1.000	H
poly(dG)–poly(dC)	$0.072 \pm 0.000$	$1.895 \pm 0.002$	1.000	L
poly(dA)–poly(dT)	$0.072 \pm 0.000$	$1.892 \pm 0.002$	1.000	H
poly(dA)–poly(dT)	$0.104 \pm 0.000$	$1.893 \pm 0.002$	1.000	L
GCGCGC...	$0.087 \pm 0.008$	$3.176 \pm 0.127$	0.993	H
ATATAT...	$0.117 \pm 0.004$	$1.776 \pm 0.035$	0.994	H
CGCGCG...	$5.082 \pm 1.619$	$6.715 \pm 0.458$	0.994	H
TATATA...	$0.236 \pm 0.007$	$2.295 \pm 0.035$	0.997	H
AGTGCCAAGCTTGCA [46]	$1.383 \pm 0.826$	$4.487 \pm 0.487$	0.997	H
AGTGCCAAGCTTGCA [46]	$(2.2 \pm 1.0) \times 10^{-4}$	$2.176 \pm 0.543$	0.761	L
TAGAGGTGTTATGA [49]	$46.300 \pm 53.288$	$9.902 \pm 1.660$	0.998	H
TAGAGGTGTTATGA [49]	$203.457 \pm 99.552$	$16.708 \pm 0.706$	1.000	L



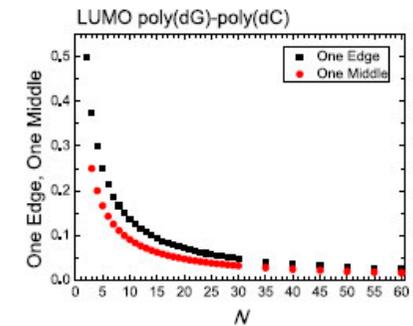
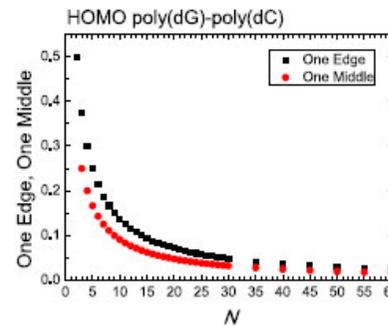
poly(dG)-  
poly(dC)

Edge Group = first and last monomer  
Middle Group = rest monomers

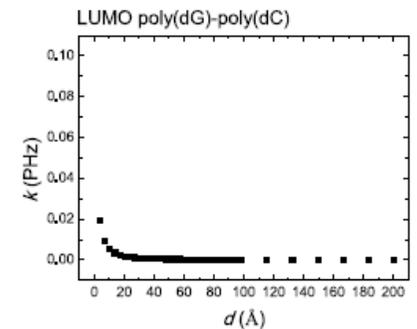
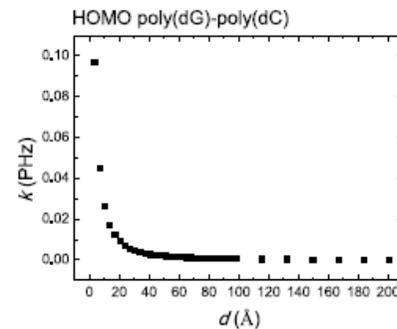
total probability  
at Edge Group & Middle Group



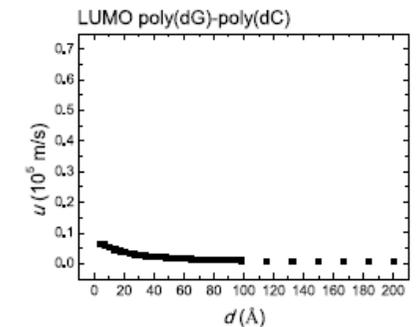
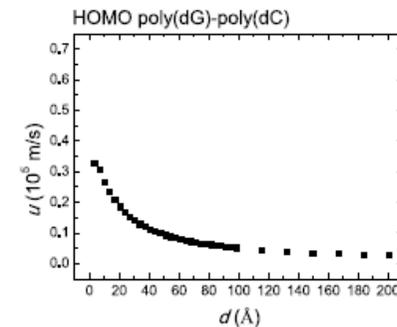
probability  
at each member of Groups



pure mean transfer rate  
 $k(d)$

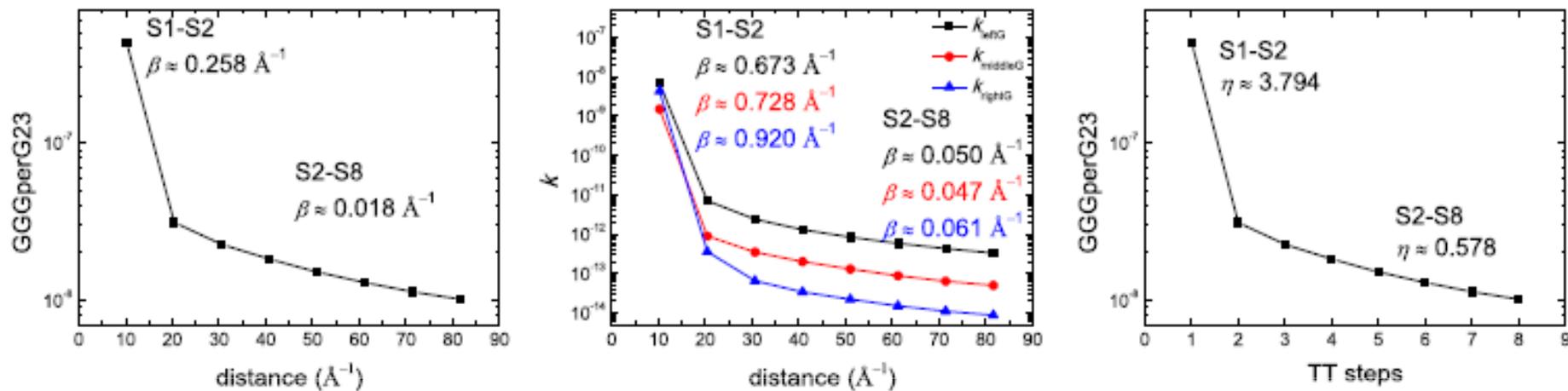


speed  
 $u = k d$



e.g. comparison with the experiment

[48] B. Giese, S. Wessely, M. Spormann, U. Lindemann, E. Meggers, M.E. Michel-Beyerle, *Angew. Chem. Int. Ed.* 38 (1999) 996



Hole transfer in ACGCACGTCGCATAATATTACG [bridge] GGGTATTATATTACGC.  
The [bridge] is made up of TT dimers separated by G monomers.

# Conclusions

A handy method to examine the charge transfer in DNA segments.

. . . illustrates the extent a specific DNA segment can serve as a medium for charge transfer.

The temporal and spatial evolution of electrons or holes along a  $N$  base-pair DNA segment can be determined, solving a system of  $N$  coupled differential equations.

As input one needs the relevant on-site energies of the base-pairs and the hopping parameters between successive base-pairs.

The method can be applied to any DNA segment.

# Conclusions

The method has been applied here (either for electrons or holes) to  
all possible dimers,  
all possible trimers,  
various polymers,  
experimentally relevant segments

The results were compared with results obtained by other workers.

Useful physical quantities defined & calculated

maximum transfer percentage	$p$	(periodic cases)
pure maximum transfer rate	$p/T$	(periodic cases)
pure mean transfer rate	$k$	(all cases)
speed of charge transfer	$u = kd$	(all cases)

where  $d$  is the charge transfer distance.

The end

Thank you !

### Related Work

[1] C. Simserides, Chemical Physics **440** (2014) 31

[2] K. Lambropoulos, K. Kaklamanis, G. Georgiadis, C. Simserides,  
Annalen der Physik (Berlin) **526** (2014) 249

[3] L.G.D. Hawke, G. Kalosakas, C. Simserides,  
Eur. Phys. J. E **32** (2010) 291; *ibid.***34** (2011) 118