



19 March 2011

# Tight binding parameters for charge transport along DNA

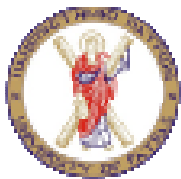
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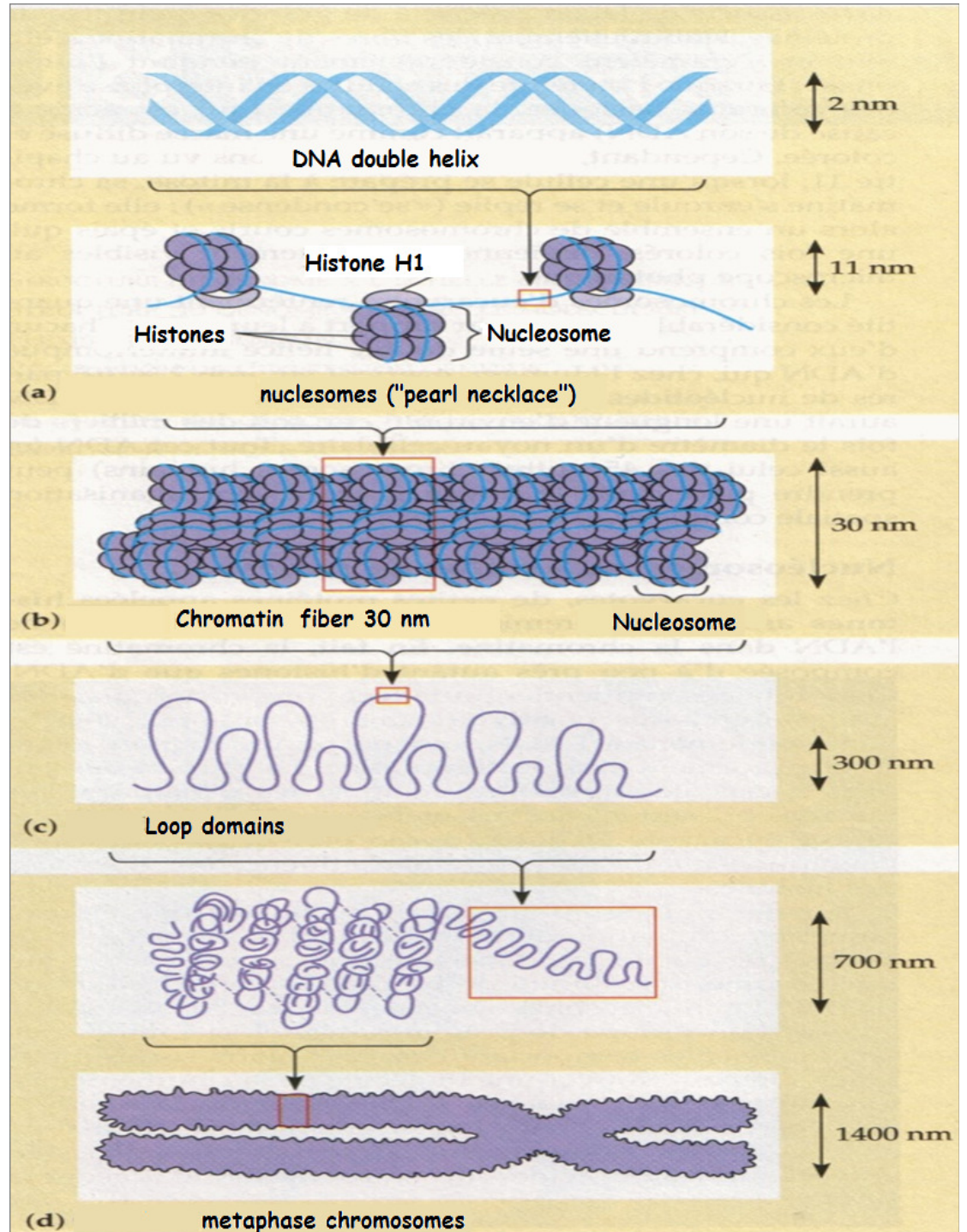


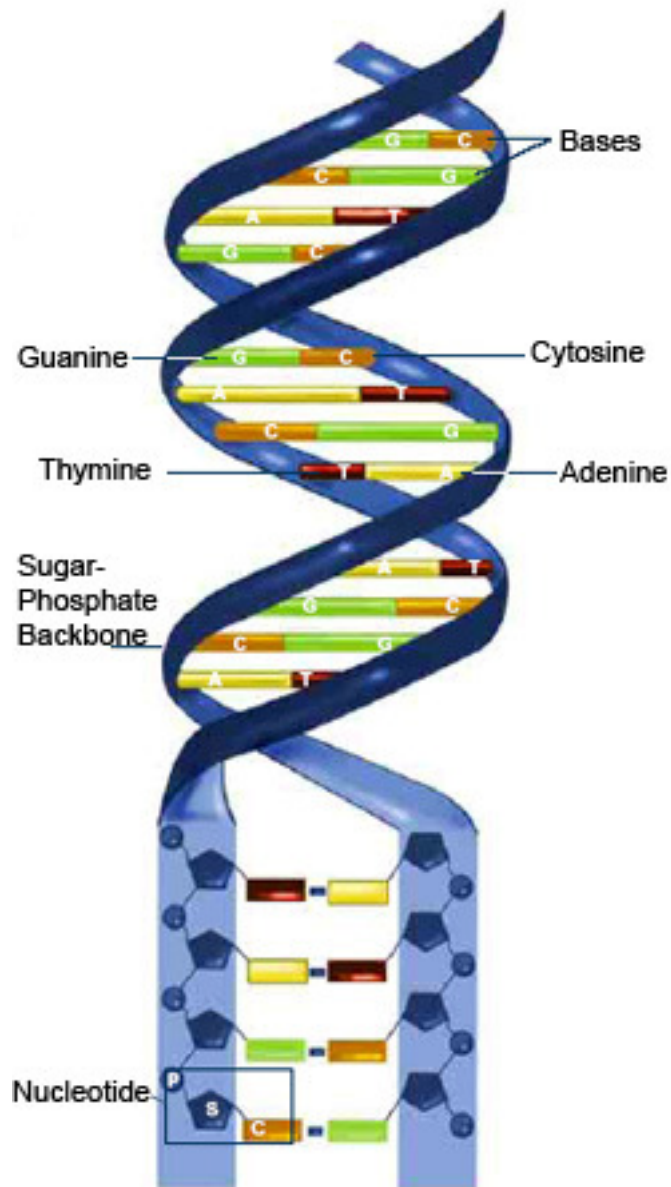
# From double helix to chromosomes

**Histones:** proteins which package and order DNA into structural units called nucleosomes.

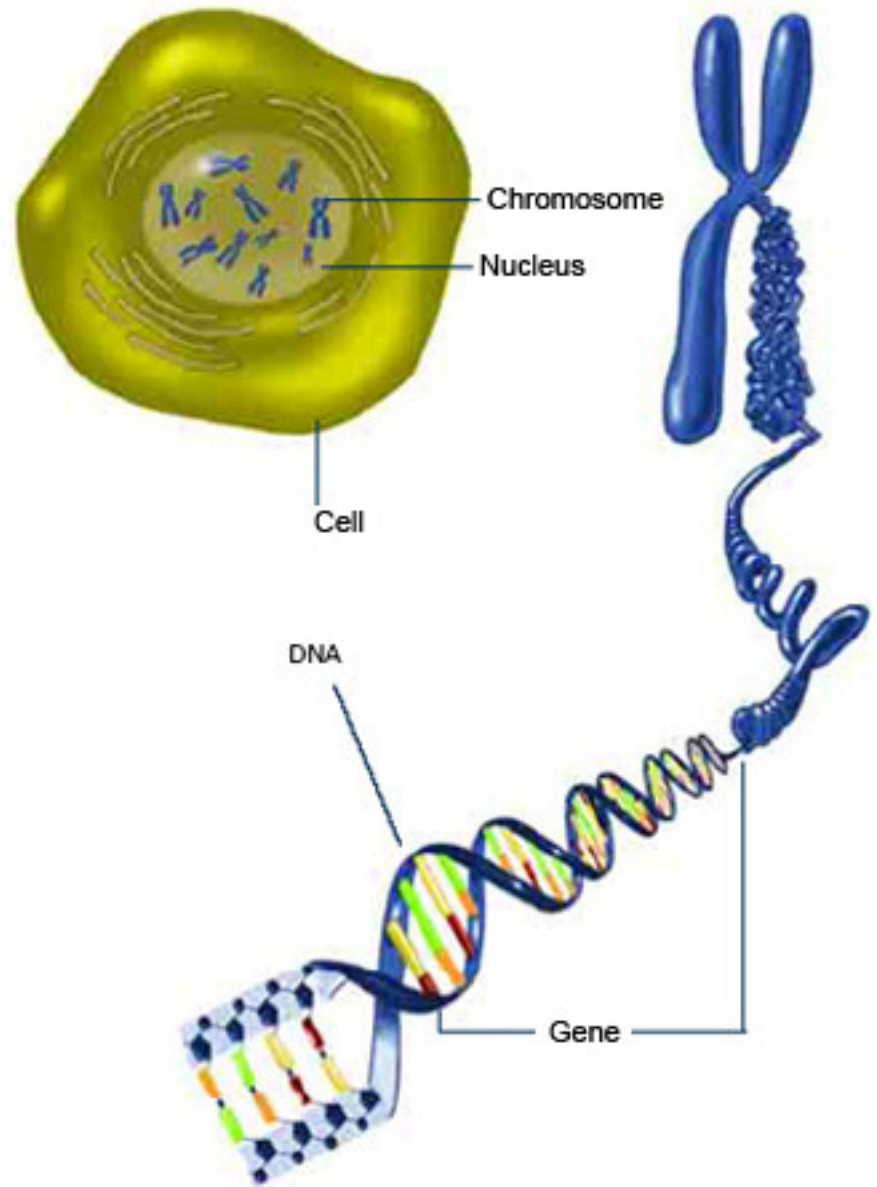
**Chromatin:** the combination of DNA, histone, and other proteins that make up chromosomes.

**Metaphase chromosome:** a chromosome in that stage of the cell cycle when it is most condensed and easiest to distinguish and so to study.



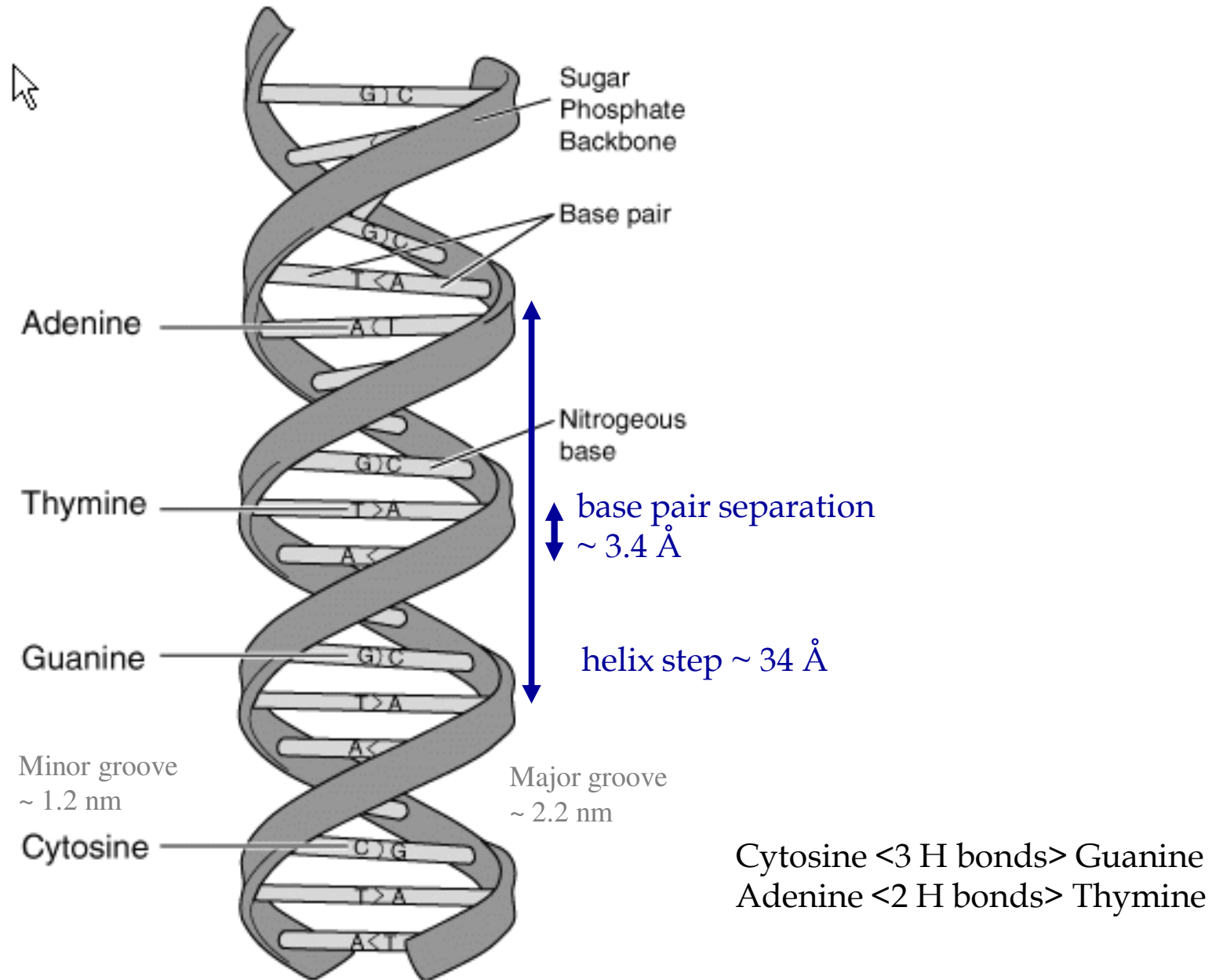


DNA: 2 long, twisted chains made up of nucleotides.  
 Nucleotide: base, sugar (deoxyribose), phosphate  
 Bases: adenine (A), thymine (T), cytosine (C), guanine (G)

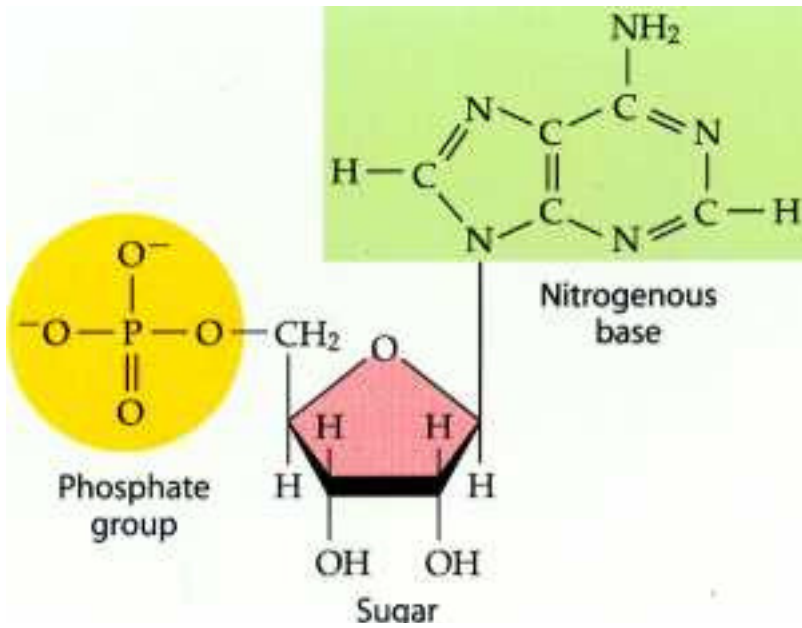


The long, stringy DNA that makes up genes is spooled within chromosomes inside the nucleus of a cell. (Note that a gene would actually be a much longer stretch of DNA than what is shown here.)

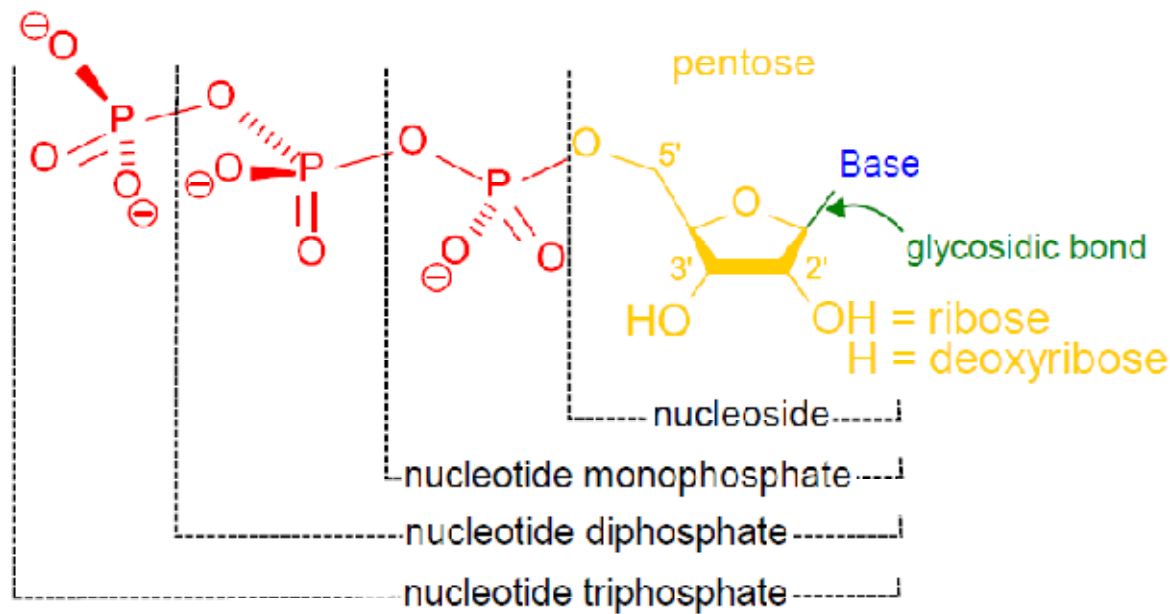
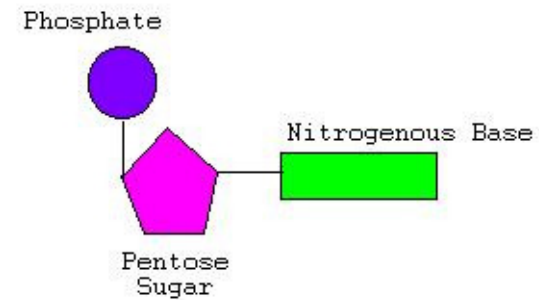
# deoxyribose nucleic acid



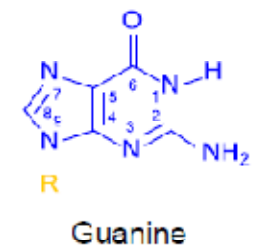
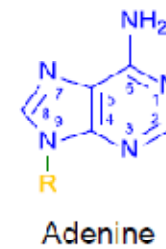




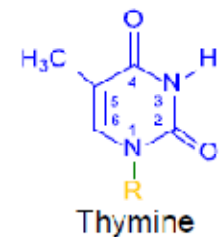
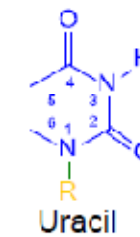
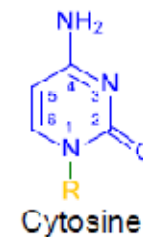
nucleotide



### Purines



### Pyrimidines



## Why study DNA electronic & charge transfer properties?

### Nanotechnology:

- (self)-assembling nanocircuits
- nanodevices as a molecular wire

### Biology:

- carcinogenesis and mutagenesis  
e.g. hole migration to guanine - - - direct strand breaks occur preferentially at guanines
- long-range charge transfer along the DNA double helix  
may be crucial for DNA damage and repair

### “How much” does DNA conduct? Experiments cover a wide range of behavior:

- \* insulator
- \* semiconductor
- \* metallic-like
- \* **Polarons vs. gap!**

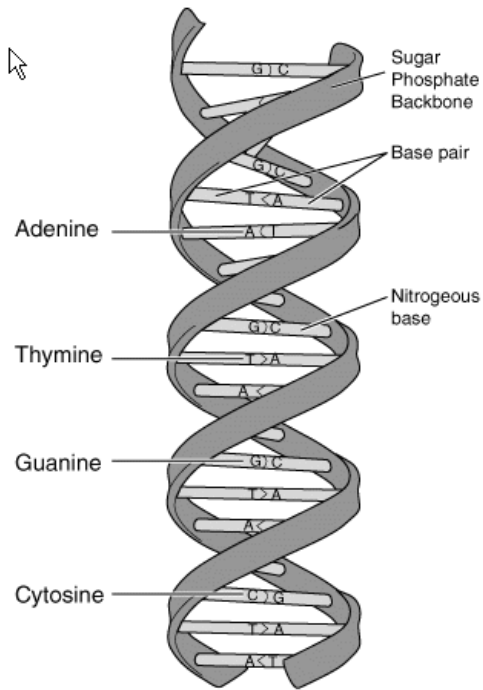
### Conductivity deviations due to external factors:

- the type of substrate
- the distance between the electrodes
- the contact material
- ...

### and intrinsic characteristics:

- local chemical environment due to solution used in preparation
- the hydrogen bonding
- the degree of stretching
- ...

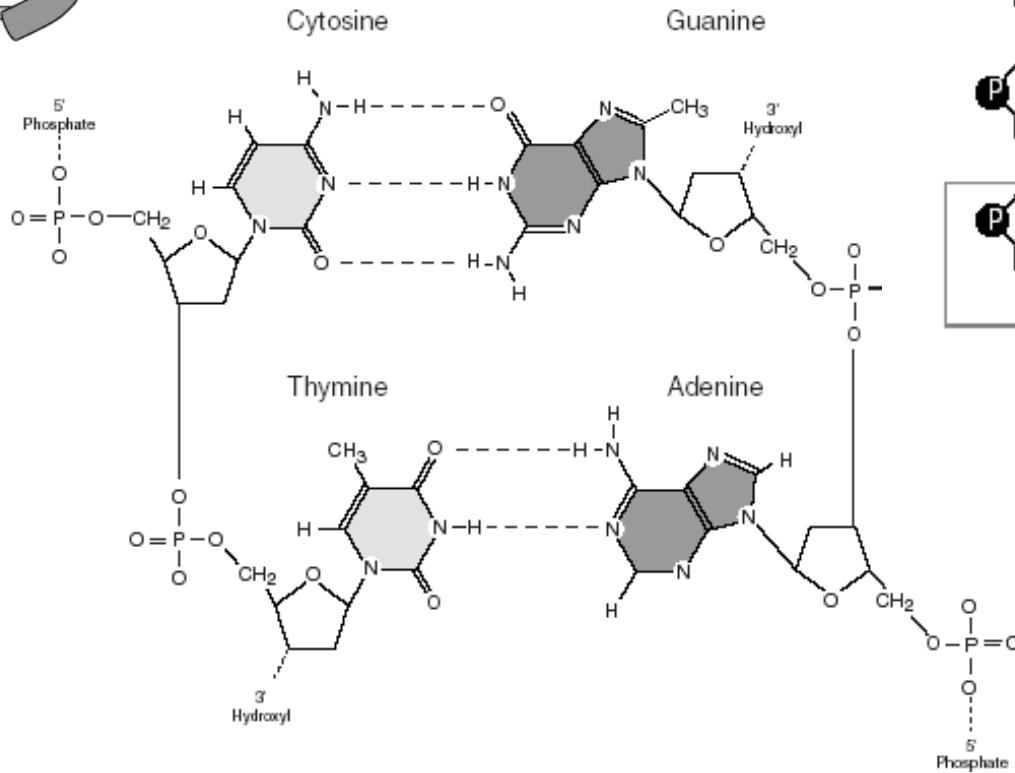
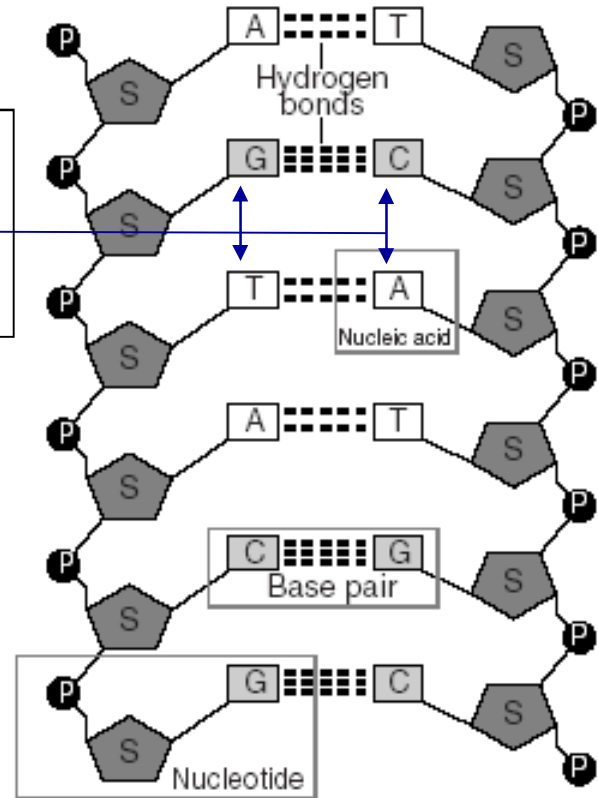
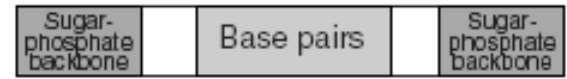
# DNA



overlap of  $\pi$  molecular orbitals  
(made up by  $p_z$  atomic orbitals).

No covalent bond here.

## Deoxyribonucleic Acid (DNA)



- A.  $\pi$  molecular structure of planar organic molecules  
     $\supset$  DNA bases: adenine (A), thymine (T), guanine (G), cytosine(C)

Linear Combination of Atomic Orbitals (LCAO):  $p_z$  electrons + novel parametrization  
occupied molecular orbitals ( $\pi$ )  
unoccupied molecular orbitals ( $\pi^*$ )

Highest Occupied Molecular Orbital (HOMO) used by holes  
Lowest Unoccupied Molecular Orbital (LUMO) used by electrons  
HOMO-LUMO gap ( $\pi$ - $\pi^*$ )

- B. HOMO and LUMO of base-pairs (A-T, G-C)  
    Linear Combination of Molecular Orbitals

- C. Tight-binding hopping parameters  
    1. Description at the base-pair level  
    2. Description at the single-base level

Relevant Publications

- L. G. D. Hawke, G. Kalosakas, C. Simserides, Eur. Phys. J. E **32**, 291 (2010)  
L. G. D. Hawke, G. Kalosakas, C. Simserides, Mol. Phys. **107**, 1755 (2009)  
L. G. D. Hawke, C. Simserides, G. Kalosakas, Mater. Sci. Eng. B **165**, 266 (2009)



# A. $\pi$ molecular structure of planar organic molecules

$sp^2$  hybridization

LCAO with  $p_z$  atomic orbitals

$\pi, \pi^*$  molecular orbitals

$$\Psi^b(\mathbf{r}) = \sum_{i=1}^N c_i p_z^i(\mathbf{r})$$

$$H^b \Psi^b(\mathbf{r}) = E^b \Psi^b(\mathbf{r})$$

$$\int p_z^{j*}(\vec{r}) p_z^i(\vec{r}) d^3r = \delta_{ji}$$

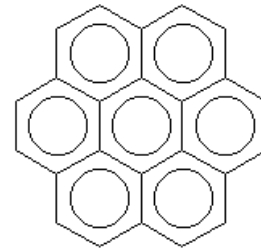
$$\sum_{i=1}^N [(H_{ji}^b - E^b \delta_{ji}) c_i] = 0, \quad j = 1, 2, \dots, N.$$

For the diagonalization we need  $H_{ij}$ .

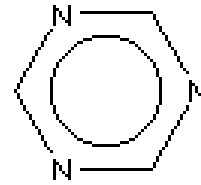
$$H_{ji}^b = \int d^3r p_z^{j*}(\mathbf{r}) H^b p_z^i(\mathbf{r})$$

Diagonalizing  $\rightarrow N$  molecular orbitals and their energies

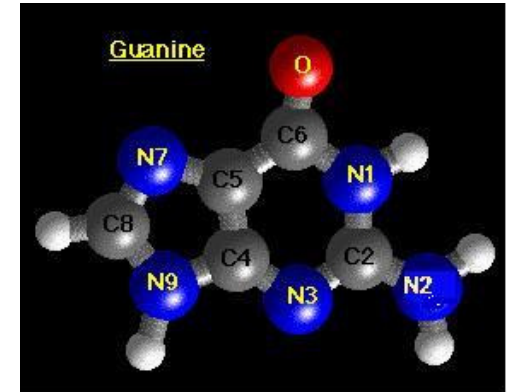
Successively fill them by 2 electrons each, until to accommodate all available  $p_z$  electrons.



coronene



1,3,5-triazine



Diagonal matrix elements,  $H_{ii}$ :

$$\varepsilon_C = -6.7 \text{ eV} \quad \varepsilon_O = -11.8 \text{ eV}$$

$$\varepsilon_{N_2} = -7.9 \text{ eV} \quad \varepsilon_{N_3} = -10.9 \text{ eV}$$

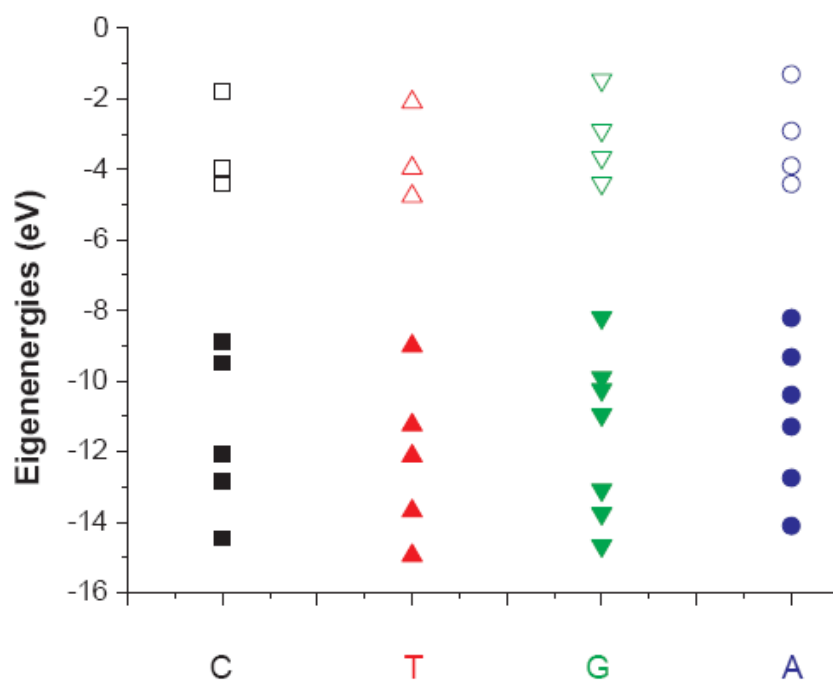
Non-diagonal matrix elements,  
atoms not  $sp^2$ -bonded,  $H_{ij} = 0$ .

Non-diagonal neighboring matrix elements,  
atoms  $sp^2$ -bonded, Harrison's expression:

$$H_{ij} = V_{pp\pi} = -0.63 \frac{\hbar^2}{md_{ij}^2}$$

## results for DNA bases

all energies in eV



DNA base	Adenine	Thymine	Guanine	Cytosine
atoms in $\pi$ bonds	10	8	11	8
$p_z$ electrons	12	10	14	10
$E_H^b (isol.)$	-8.2	-9.0	-8.2	-8.9
$E_L^b (isol.)$	-4.4	-4.8	-4.4	-4.4
$E_{\pi-\pi^*}$	3.8	4.2	3.8	4.5
$IE^{\text{exp}}$	8.4-8.5	9.0-9.2	8.2-8.3	8.9
$E_{\pi-\pi^*}^{\text{exp}}$	4.5-4.8	4.6-4.7	4.3-4.5	4.5-4.7
$IE^{\text{first pr.}}$	8.2-8.6	9.1-9.7	7.8-8.3	8.9-9.4
$E_{\pi-\pi^*}^{\text{first pr.}}$	4.5-5.3	4.9-5.3	4.4-5.3	4.2-4.7
$E_H^b$ (in B-DNA)	-8.3	-9.0	-8.0	-8.8
$E_L^b$ (in B-DNA)	-4.4	-4.9	-4.5	-4.3

## B. HOMO and LUMO of B-DNA base-pairs (A-T, G-C)

### Linear Combination of Molecular Orbitals

$$\Psi_{H/L}^{bp}(\mathbf{r}) = C_1 \Psi_{H/L}^{b(1)}(\mathbf{r}) + C_2 \Psi_{H/L}^{b(2)}(\mathbf{r})$$

$$H^{bp} \Psi_{H/L}^{bp}(\mathbf{r}) = E_{H/L}^{bp} \Psi_{H/L}^{bp}(\mathbf{r}) \quad \dots \text{we must solve:}$$

$$\begin{aligned} E_{H/L}^{b(1)} C_1 + t_{H/L} C_2 &= E_{H/L}^{bp} C_1 \\ t_{H/L}^* C_1 + E_{H/L}^{b(2)} C_2 &= E_{H/L}^{bp} C_2 \end{aligned}$$

$$\int d^3r \Psi_{H/L}^{b(m)*} H^{bp} \Psi_{H/L}^{b(m)} \approx \int d^3r \bar{\Psi}_{H/L}^{b(m)*} H^b \Psi_{H/L}^{b(m)} = E_{H/L}^{b(m)}, \text{ for } m=1 \text{ or } 2$$

$t_{H/L}$  = overlap integral, the hopping parameter for hole (H) / electron (L) transfer between the two bases of the base-pair

$$t_{H/L} = \sum_{i=1}^{N_1} \sum_{j=1}^{N_2} c_{i(1)}^{H/L*} c_{j(2)}^{H/L} V_{ij} \quad t_{H/L} = t_{H/L}^*$$

$$V_{ij} = \int d^3r p_z^{i(1)*}(\mathbf{r}) H^{bp} p_z^{j(2)}(\mathbf{r})$$

overlap integral, the hopping parameter between  $p_z$  orbitals belonging to different bases of the base pair

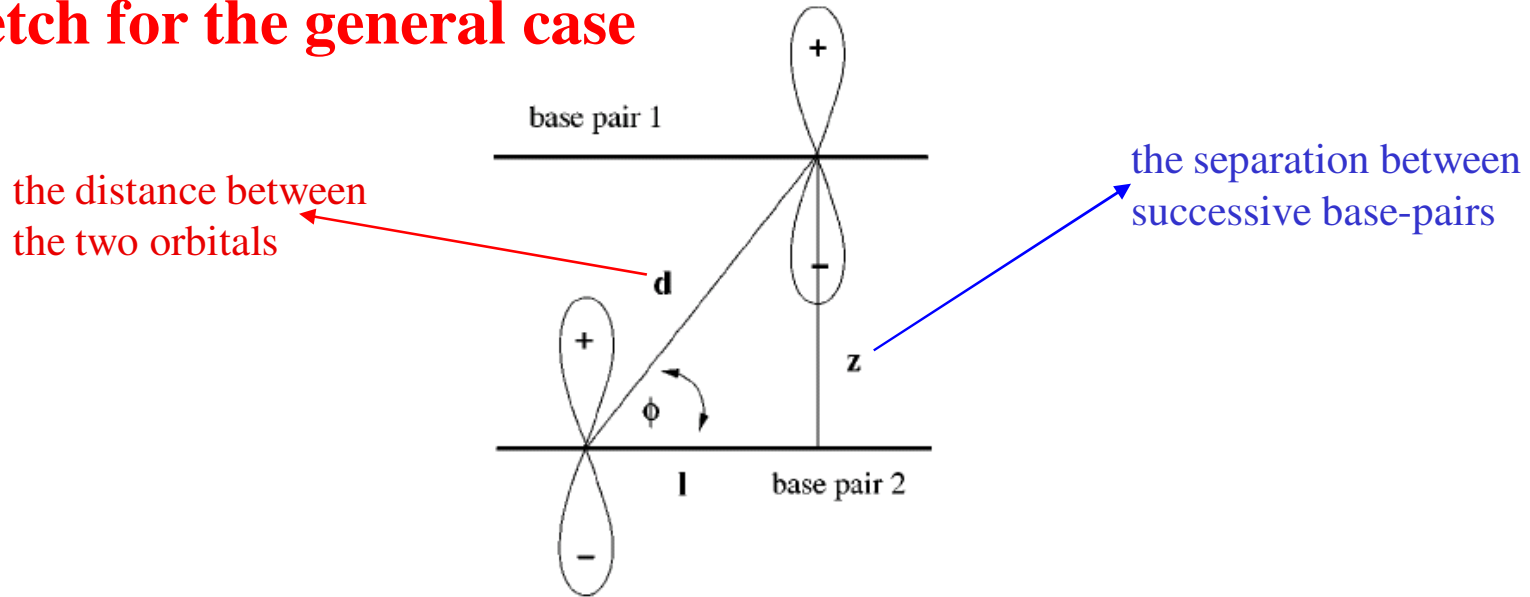
equivalently

$$\Psi_{H/L}^{bp}(\mathbf{r}) = \sum_{i=1}^N C_i^{H/L} p_z^i(\mathbf{r})$$

$V_{ij}$  are given by the Slater-Koster expression

$$V_{ij} = V_{pp\sigma} \sin^2 \phi + V_{pp\pi} \cos^2 \phi$$

## Sketch for the general case



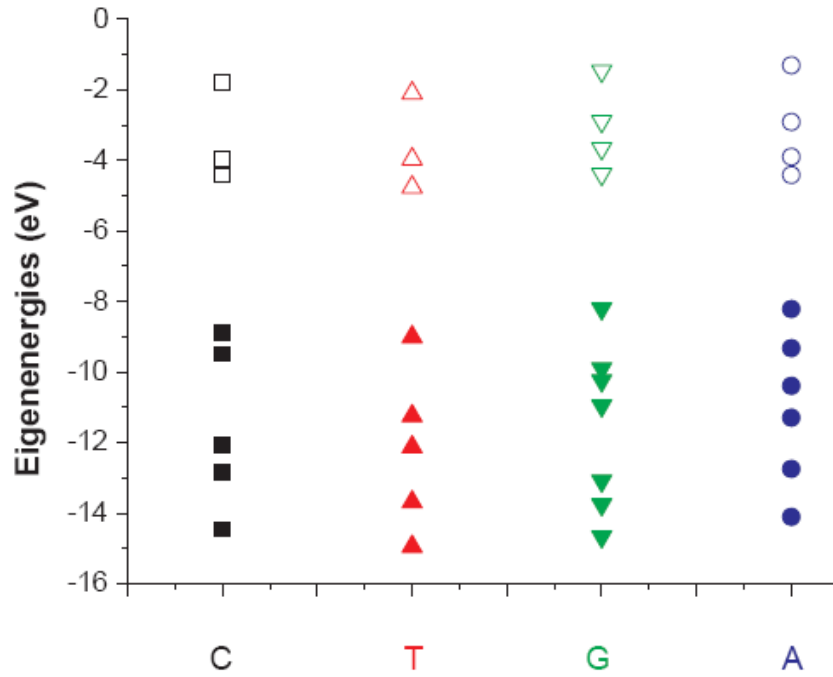
$V_{pp\pi}$  and  $V_{pp\sigma}$  for interatomic distances of the order of covalent bonds e.g.  $V_{pp\pi} = -0.63 \frac{\hbar^2}{md^2}$

$V_{pp\pi}$  and  $V_{pp\sigma}$  for greater distances e.g.  $V_{pp\pi} = Ae^{-\beta(d-d_0)}$

For the intra-base-pair hopping parameters  $\phi = 0$  and only  $V_{pp\pi}$  survives.

## results for DNA bases

all energies in eV



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atoms in $\pi$ bonds	10	8	11	8
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all energies in eV

## results for B-DNA base-pairs

B-DNA base-pair	A-T	G-C
$E_H^{bp}$	-8.3	-8.0
$E_L^{bp}$	-4.9	-4.5
$E_{\pi-\pi^*}$	3.4	3.5
$E_H^{bp \text{ first pr.}}$	-(7.8-8.2)	-(6.3-7.7)
$E_{\pi-\pi^*}^{\text{first pr.}}$	6.4	4.3-6.3

### intra-base-pair hopping parameters

Base-pair	$t_H^b$	$t_H^b$	$t_L^b$	$t_L^b$
		[86]		[86]
A-T	-12	26	-9	34
G-C	-12	5	16	63

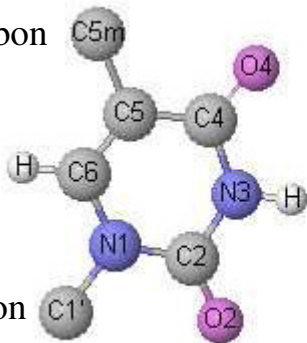
all hopping parameters in meV



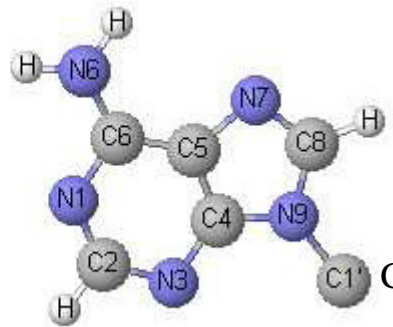
# Geometrical structure and atomic occupation probabilities A, T, A-T

C5m thymine's methyl carbon

thymine



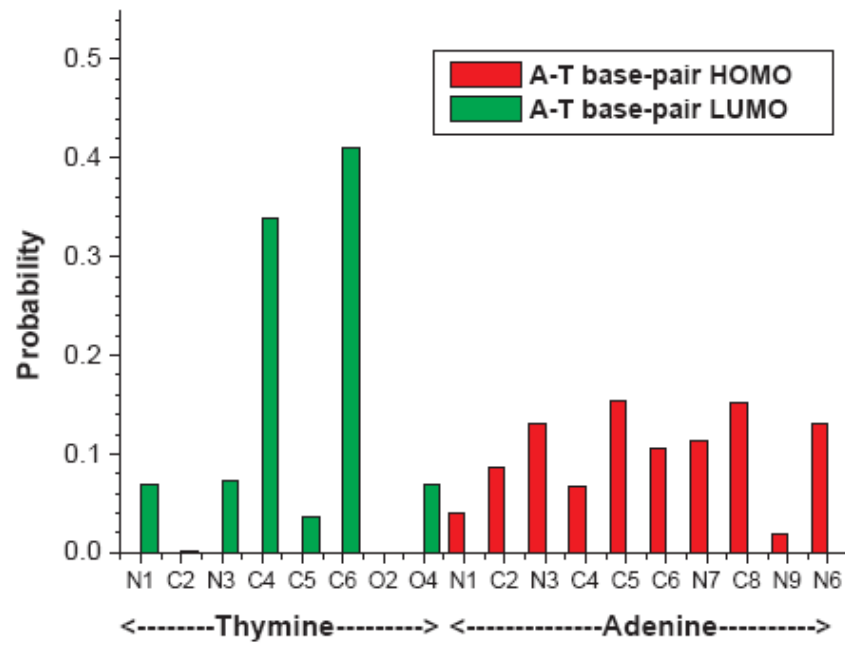
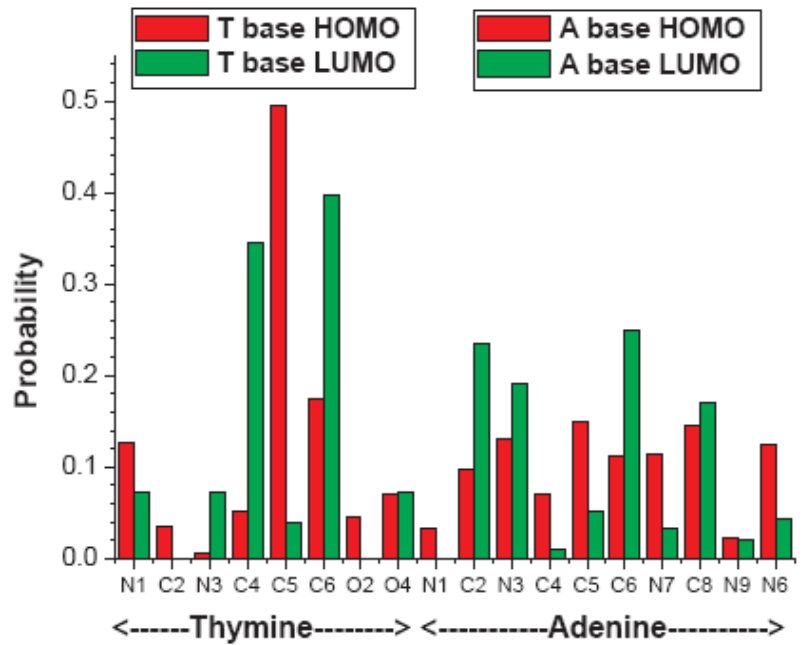
C1' deoxyribose carbon



adenine

C1' deoxyribose carbon

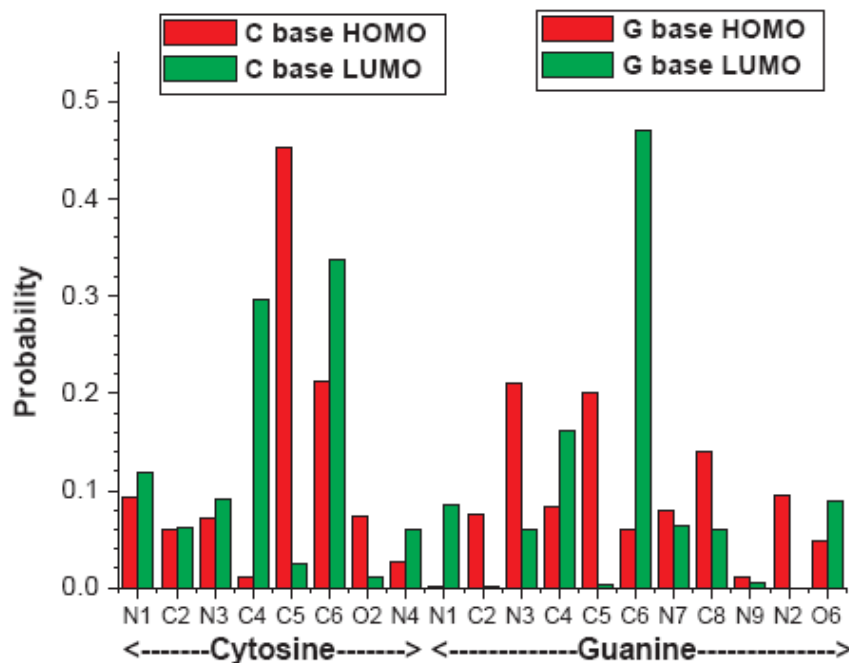
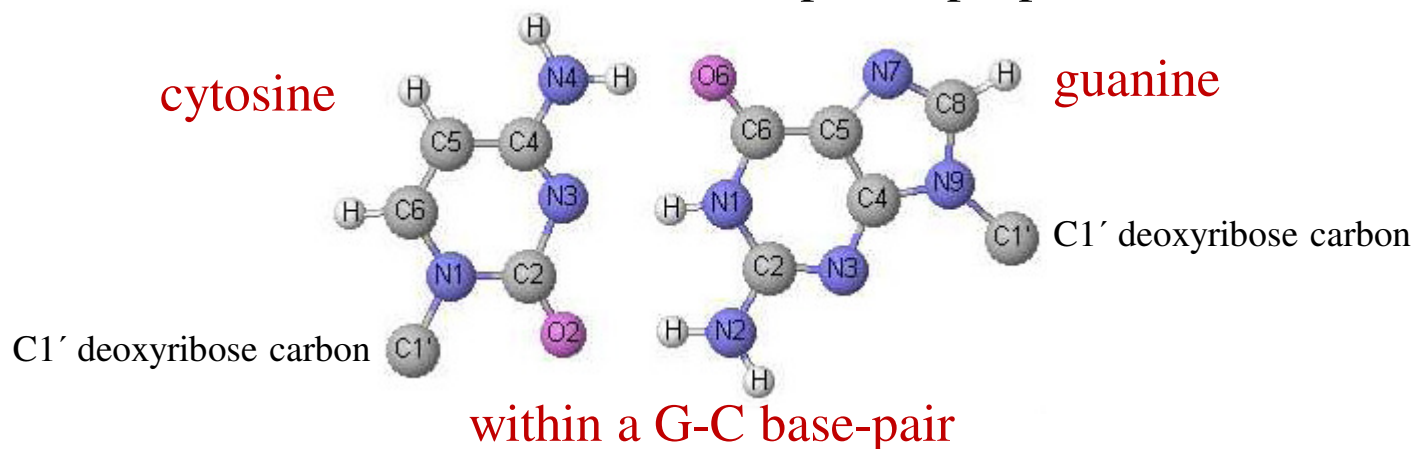
within an A-T base-pair



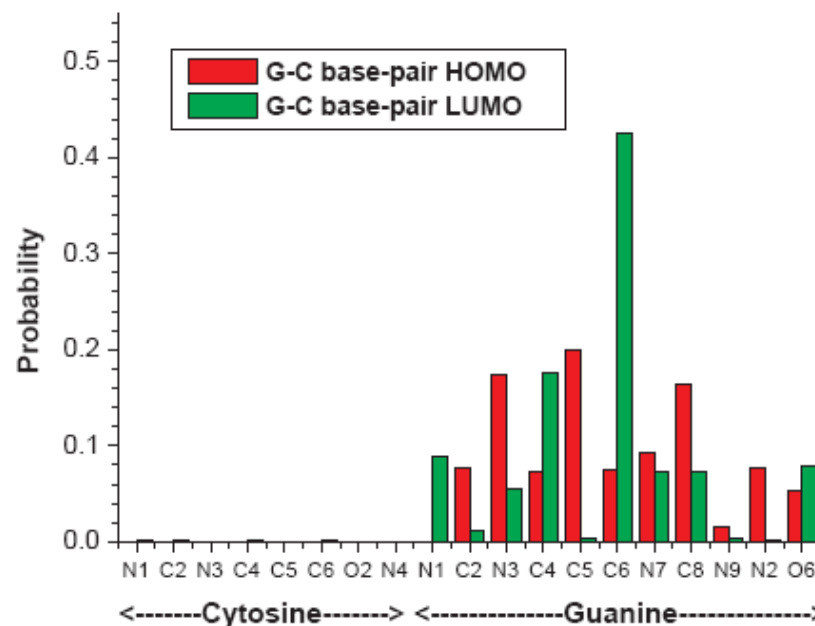
$|c_i|^2$   
HOMO & LUMO wavefunctions of isolated T and A bases

$|C_i|^2$   
HOMO & LUMO wavefunctions of A-T base-pair

# Geometrical structure and atomic occupation probabilities G, C, G-C



$|c_i|^2$   
HOMO & LUMO wavefunctions of  
isolated C and G bases



$|C_i|^2$   
HOMO & LUMO wavefunctions of  
G-C base-pair

## C. Tight-binding hopping parameters

### 1. Description at the base-pair level

**Aim:** calculate all tight binding parameters for charge transfer along B-DNA

**Assume:** holes (. . . HOMOs) or electrons (. . . LUMOs) can be transferred via the overlap of the  $\pi$ -molecular orbitals of the stacked base-pairs

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

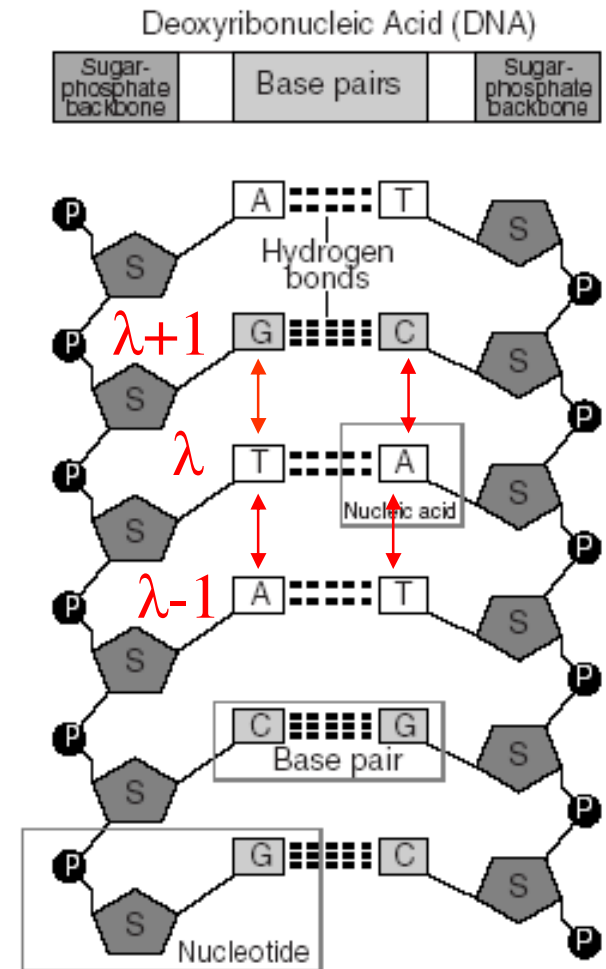
time dependent wavefunction of the whole DNA

$\lambda^{\text{th}}$  base-pair's HOMO/LUMO wavefunction

*Description at the base-pair level*

The time evolution of the coefficients  $A_{\lambda}(t)$  obeys the following system of equations:

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



## hopping parameters between successive base-pairs

$$t_{H/L}^{bp(\lambda; \lambda')} = \sum_{i=1}^{N_\lambda} \sum_{j=1}^{N_{\lambda'}} C_{i(\lambda)}^{H/L} * C_{j(\lambda')}^{H/L} V_{ij}$$

denoted by  $\Leftrightarrow YX$ 
↓
 $\lambda$ 

 $Y - Y_{compl}$ 
↑
 $\lambda'$ 

 $X - X_{compl}$ 
denoted by  $\Leftrightarrow X_{compl} Y_{compl}$

$5'$       $3'$   
 $3'$       $5'$

Base-pair sequence	$t_H^{bp}$	$ t_H^{bp} $ [83]	$t_H^{bp}$ [84]	$t_H^{bp}$ [4]	$t_L^{bp}$	$t_L^{bp}$ [84]	$t_L^{bp}$ [4]
AA, TT	-8	26	-70	$\approx -25$	-29	105	$\approx 35$
AT	20	50			0.5		
AG, CT	-5	122	-71	$\approx -50$	3	112	$\approx 35$
AC, GT	2	27			32		
TA	47	55			2		
TG, CA	-4	26			17		
TC, GA	-79	25	-187	$\approx -160$	-1	47	$\approx 35$
GG, CC	-62	93	-141	$\approx -140$	20	53	$\approx 35$
GC	1	78			-10		
CG	-44	22			-8		

all hopping parameters in meV

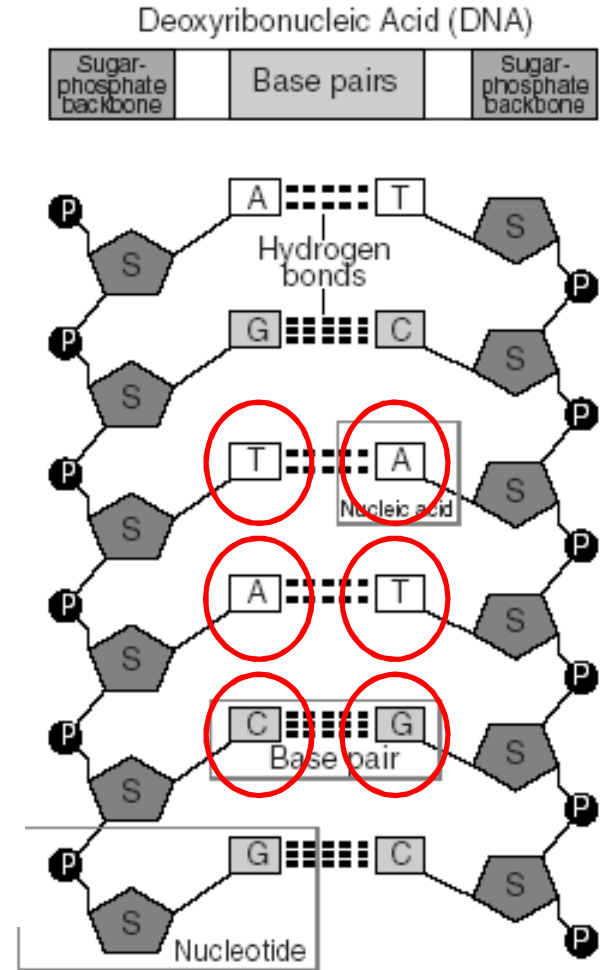
## C. Tight-binding hopping parameters

### 2. Description at the single-base level

$$\Psi_{H/L}^{\text{DNA}}(\mathbf{r}, t) = \sum_{\lambda} \left[ A_{\lambda}(t) \Psi_{H/L}^{\text{b}(\lambda,1)}(\mathbf{r}) + B_{\lambda}(t) \Psi_{H/L}^{\text{b}(\lambda,2)}(\mathbf{r}) \right]$$

$$i\hbar \frac{dA_{\lambda}}{dt} = E_{H/L}^{\text{b}(\lambda,1)} A_{\lambda} + t_{H/L}^{\text{b}(\lambda,1;\lambda,2)} B_{\lambda} + t_{H/L}^{\text{b}(\lambda,1;\lambda-1,1)} A_{\lambda-1} \\ + t_{H/L}^{\text{b}(\lambda,1;\lambda+1,1)} A_{\lambda+1} + t_{H/L}^{\text{b}(\lambda,1;\lambda-1,2)} B_{\lambda-1} \\ + t_{H/L}^{\text{b}(\lambda,1;\lambda+1,2)} B_{\lambda+1},$$

$$i\hbar \frac{dB_{\lambda}}{dt} = E_{H/L}^{\text{b}(\lambda,2)} B_{\lambda} + t_{H/L}^{\text{b}(\lambda,2;\lambda,1)} A_{\lambda} + t_{H/L}^{\text{b}(\lambda,2;\lambda-1,2)} B_{\lambda-1} \\ + t_{H/L}^{\text{b}(\lambda,2;\lambda+1,2)} B_{\lambda+1} + t_{H/L}^{\text{b}(\lambda,2;\lambda-1,1)} A_{\lambda-1} \\ + t_{H/L}^{\text{b}(\lambda,2;\lambda+1,1)} A_{\lambda+1}.$$





## C. Tight-binding hopping parameters

### 2. Description at the single-base level

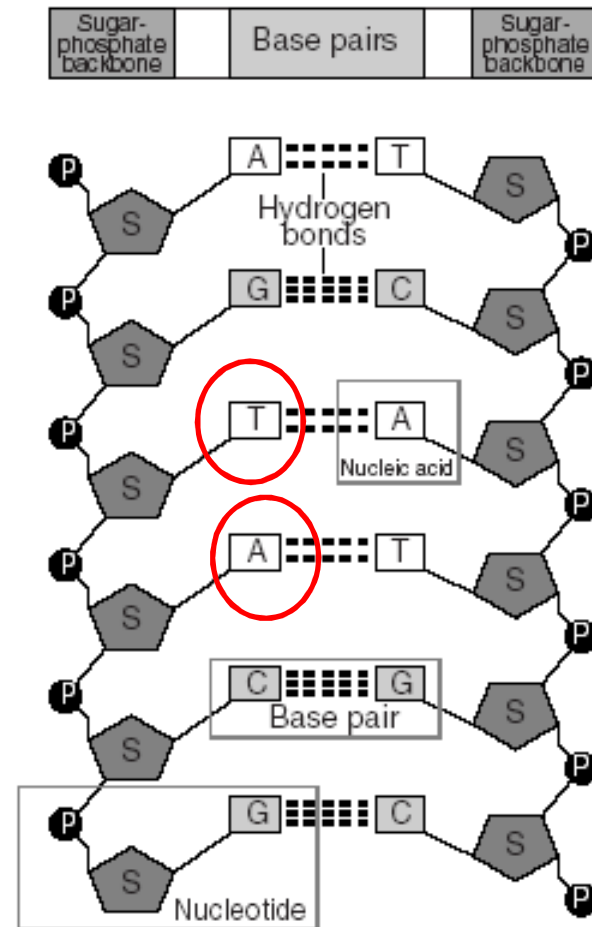
(2a) successive bases in the same strand

$$t_{H/L} = \sum_{i=1}^{N_1} \sum_{j=1}^{N_2} c_{i(1)}^{H/L} \star c_{j(2)}^{H/L} V_{ij}$$

$\begin{matrix} 5' & & 3' \\ \boxed{Y} & - & Y_{compl} \\ \boxed{X} & - & X_{compl} \end{matrix}$

Base sequence	$t_H^b$	$ t_H^b $ [87]	$ t_H^b $ [85]	$t_H^b$ [88]	$ t_H^b $ [89]	$t_H^b$ [86]	$t_L^b$	$t_L^b$ [86]
AA	-8	30	4	-4	8	21	16	25
AT	68	105		-63	28		7	
AG	-5	49	44	-10	37		1	
AC	68	61		42	30		-3	
TA	26	86		-31	64		-7	
TT	-117	158		72	93	-98	-30	-23
TG	28	85	61	18	70		-17	
TC	-86	76		-28	52		22	
GA	-79	89	36	-77	52		30	
GT	73	137	81	141	49		-32	
GG	-62	84	51	53	61	-114	20	20
GC	80	110		-114	57		43	
CA	5	29		-2	5		-12	
CT	-107	100		-55	33		63	
CG	-1	42		9	31		15	
CC	-66	41		22	26	-21	-47	-60

Deoxyribonucleic Acid (DNA)



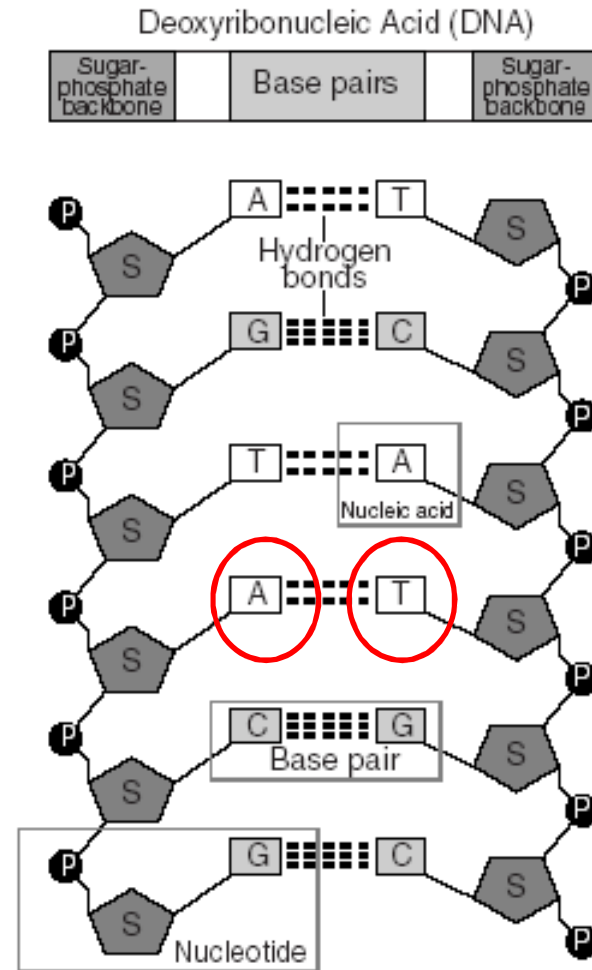
all hopping parameters in meV

(2b) complementary bases within a base-pair,

**intra-base-pair hopping parameters**

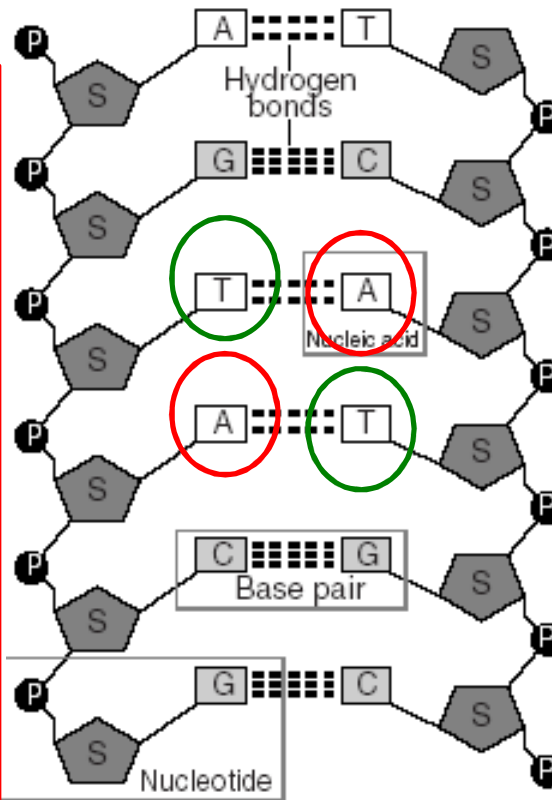
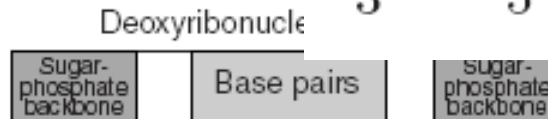
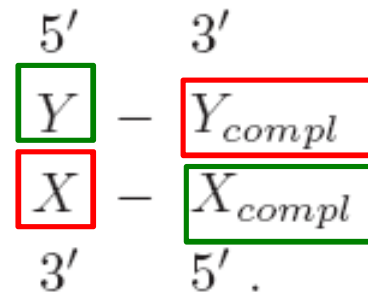
Base-pair	$t_H^b$	$t_H^b$	$t_L^b$	$t_L^b$
		[86]		[86]
A-T	-12	26	-9	34
G-C	-12	5	16	63

all hopping parameters in meV



(2c) diagonally located bases in opposite strands of successive base-pairs

$$t_{H/L} = \sum_{i=1}^{N_1} \sum_{j=1}^{N_2} c_{i(1)}^{H/L} \star c_{j(2)}^{H/L} V_{ij}$$



Base sequence	$t_H^b$	$t_H^b$	$ t_H^b $	$t_L^b$	$t_L^b$
		[88]	[86]		[86]
AA	48	49		29	
AT, TA	-3	-7	9	3	-13
AG, GA	-3	-11		-6	
AC, CA	-5	17		-3	
TT	0.5	6		0.2	
TG, GT	5	-14		2	
TC, CT	0.5	4		-0.2	
GG	-44	-32		-5	
GC, CG	4	22	48	-4	-15
CC	1	10		0.3	

all hopping parameters in meV

Base sequence	$t_H^b$	$t_H^b$	$ t_H^b $	$t_H^b$	$t_L^b$	$t_L^b$
		[88]	[87]	[86]		[86]
AA	2	31	31-35		6	
AT, TA	9	7	16-20	-11	2	-10
AG, GA	4	-13	19-24		3	
AC, CA	5	-1			-2	
TT	4	1	3-4		2	
TG, GT	5	-9			3	
TC, CT	2	0.3			-2	
GG	3	12	19		-2	
GC, CG	4	2		-8	-3	-12
CC	1	1	1		2	

all hopping parameters in meV

## Conclusions

All tight-binding parameters for charge transfer along B-DNA

- $\pi$  electronic structure of A, T, C, G by LCAO with a novel parametrization
- HOMO and LUMO of B-DNA A-T, G-C by LCMO
- took into account the slight deformation of bases within the base-pairs of B-DNA (compared to the isolated bases)  
A-T: HOMO in A, LUMO in T,  
G-C: HOMO in G, LUMO in G.
- HOMO energy of bases: deviation  $< 0.3$  eV from experiment  
(G, C: coincide T: 0-0.2 eV A: 0.2-0.3 eV)
- 1st  $\pi$ - $\pi^*$  transition of bases: deviations from experiment:  
C:0-0.2 eV T:0.4-0.5 eV, G:0.5-0.7 eV A:0.7-1.0 eV
- compared with other theoretical results from first principles calculations

## & Conclusions

- hopping parameters (electrons, holes) between
  - (1) successive base-pairs
  - (2) neighboring bases
    - (2a) successive bases in the same strand,
    - (2b) complementary bases within a base-pair,
    - (2c) diagonally located bases in opposite strands of successive base-pairs
- ~ hopping parameters for holes (HOMOs) > for electrons (LUMOs)  
=> probably hole transport more favorable

-**temporal** and **spatial** evolution of electron or hole along DNA  
can now be examined in experimentally relevant time and length scales

hole/electron **transmission coefficients** and **conductivities**  
can be calculated for any DNA segment



The end

Thank you

# References

scales. Important measurable quantities like hole/electron transmission coefficients and conductivities can be calculated for any DNA segment (of whatever base sequence) under consideration, since there are well-established techniques to compute such a quantities from tight-binding models. Furthermore, relative reaction rates for charge transfer between donors and acceptors within DNA segments can be calculated and compared with relevant experiments.

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