

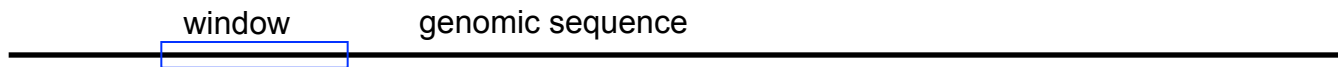
# 1. Genomic texts

- The cell, atom of the living world
- At the heart of the cell: the DNA macromolecule
- DNA codes for genetic information
- What is an algorithm?
- Counting nucleotides
- GC and AT contents of DNA sequence
- DNA walk
- Compressing the DNA walk
- Predicting the origin of DNA replication?
- **Overlapping sliding window**

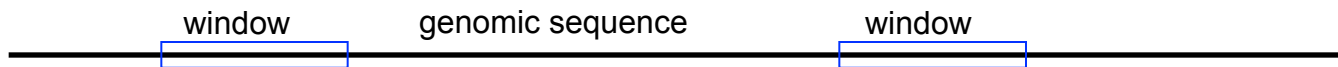
# Overlapping sliding windows

# Nucleotide frequencies along a sequence

- Compute nucleotide frequencies in a sliding window



$$\frac{\text{nbG} - \text{nbC}}{\text{nbG} + \text{nbC}} = -0.3$$



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$$\frac{\text{nbG} - \text{nbC}}{\text{nbG} + \text{nbC}} = +0.4$$

# Variation of nucleotide frequencies along the genome

- Compute nucleotide frequencies in a sliding window
- Make the windows overlap

window



window





window



window



# Variation of nucleotide frequencies along the genome

- Compute nucleotide ratio (G vs. C) in a sliding window
- Make the windows overlap
- Store the value of the ratio for each window
- Display the values as a curve,  
colinear with the sequence

SeqLength, L, J, InitW, nbC,nbG, OveLap: **integer**

sequence: **character string** [1:\*)

RatioGC: **array** [1:\*) of **real**

InitW, J  $\leftarrow$  1

**repeat**

nbC,nbG  $\leftarrow$  0

**for** i **from** InitW **to** min (InitW + L - 1, SeqLength) **do**

**case sequence** [i] **of**

        "C": nbC  $\leftarrow$  nbC + 1

        "G": nbG  $\leftarrow$  nbG + 1

        "A", "T" :

**endcase**

**endfor**

RatioGC [J]  $\leftarrow$  (nbG - nbC) / (nbG + nbC)

J  $\leftarrow$  J + 1

InitW  $\leftarrow$  InitW + (L - OverLap)

**until** InitW > SeqLength

