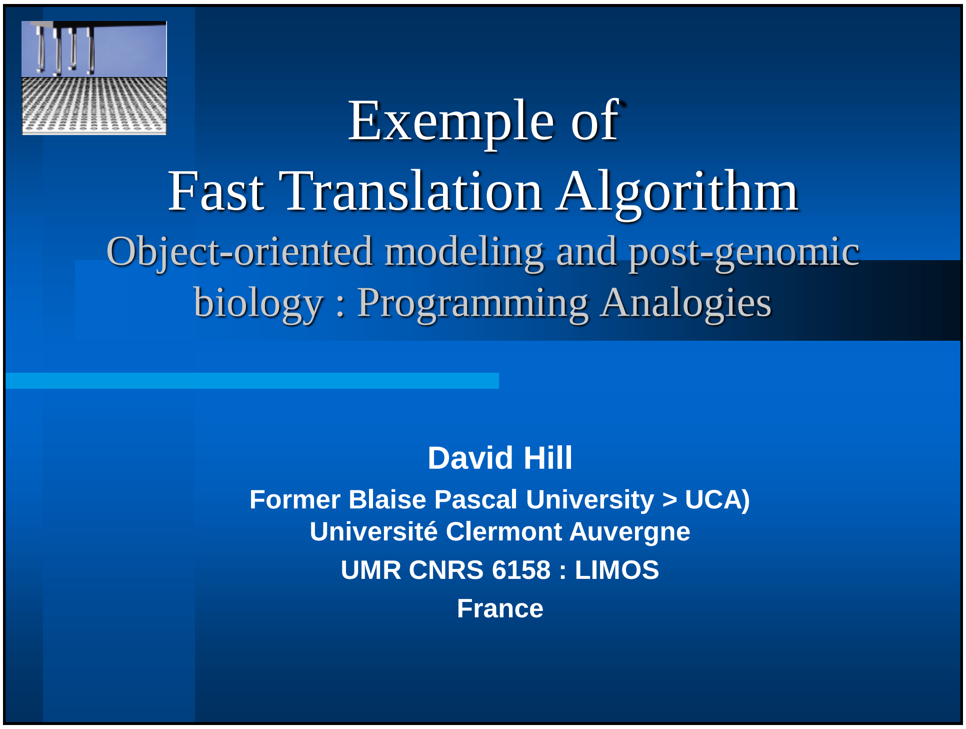
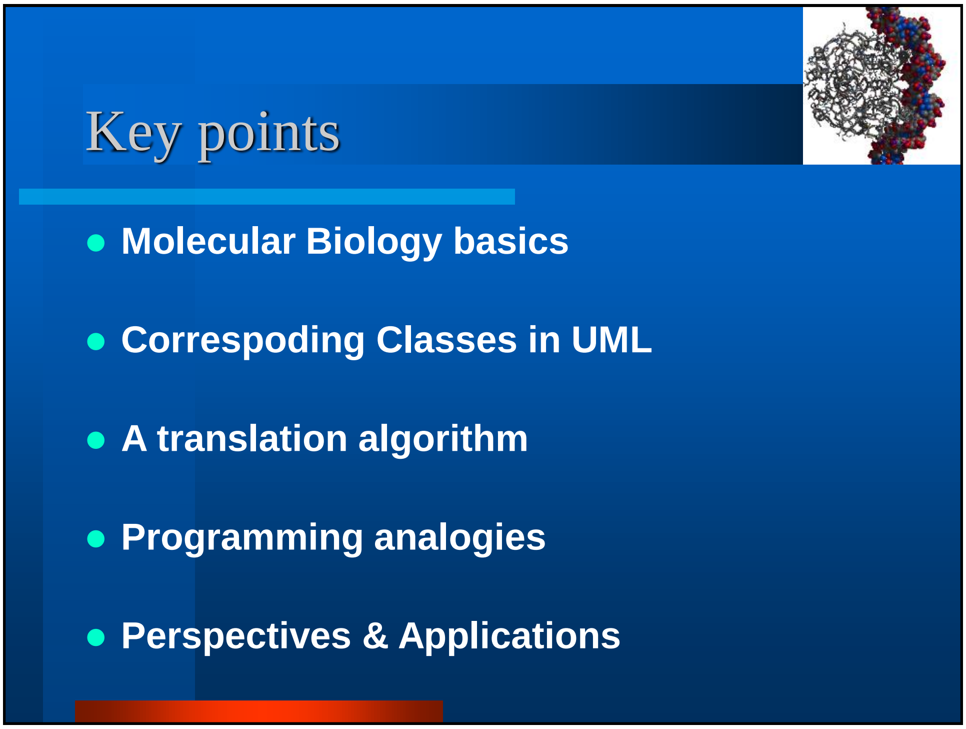


Exemple of Fast Translation Algorithm

Object-oriented modeling and post-genomic biology : Programming Analogies

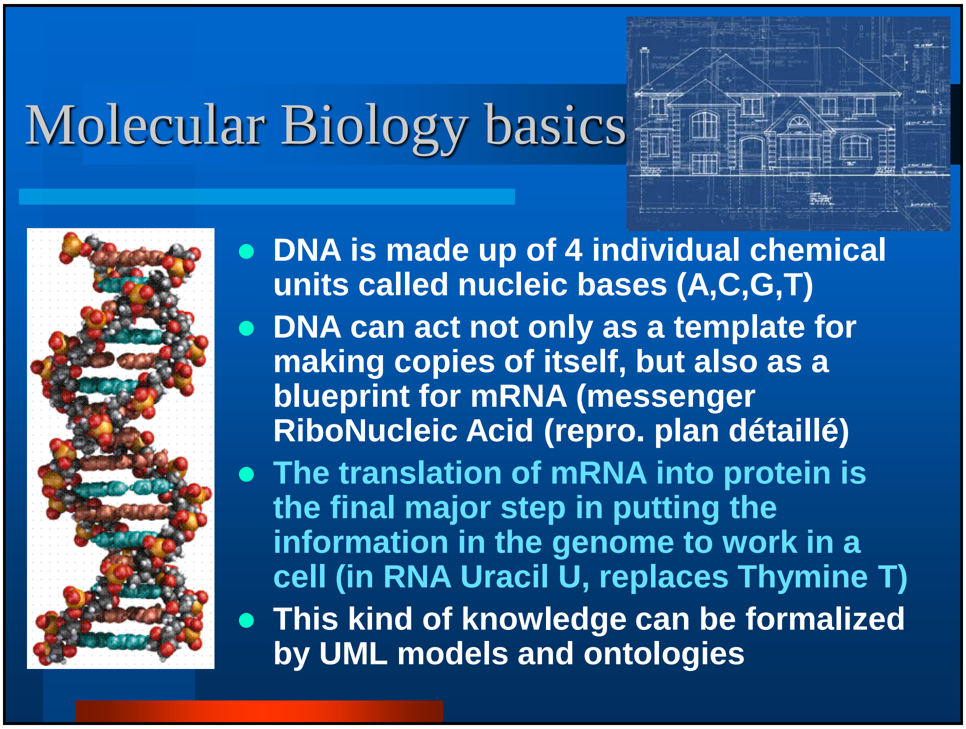
David Hill

Former Blaise Pascal University > UCA)
Université Clermont Auvergne
UMR CNRS 6158 : LIMOS
France



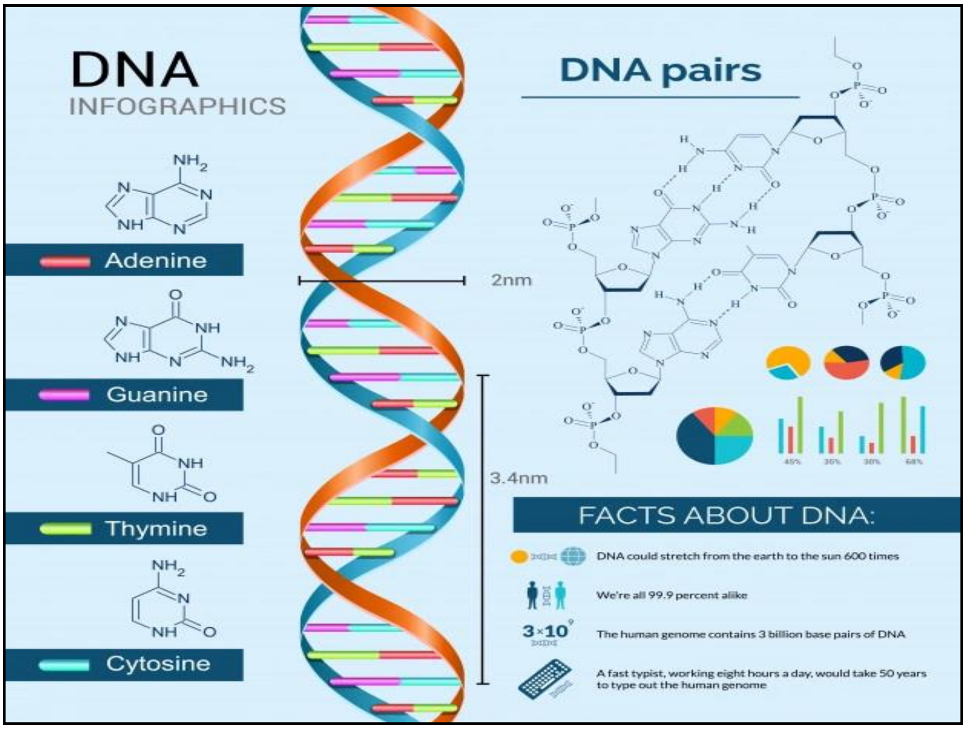
Key points

- Molecular Biology basics
- Correspoding Classes in UML
- A translation algorithm
- Programming analogies
- Perspectives & Applications



Molecular Biology basics

- DNA is made up of 4 individual chemical units called nucleic bases (A,C,G,T)
- DNA can act not only as a template for making copies of itself, but also as a blueprint for mRNA (messenger RiboNucleic Acid (repro. plan détaillé)
- The translation of mRNA into protein is the final major step in putting the information in the genome to work in a cell (in RNA Uracil U, replaces Thymine T)
- This kind of knowledge can be formalized by UML models and ontologies



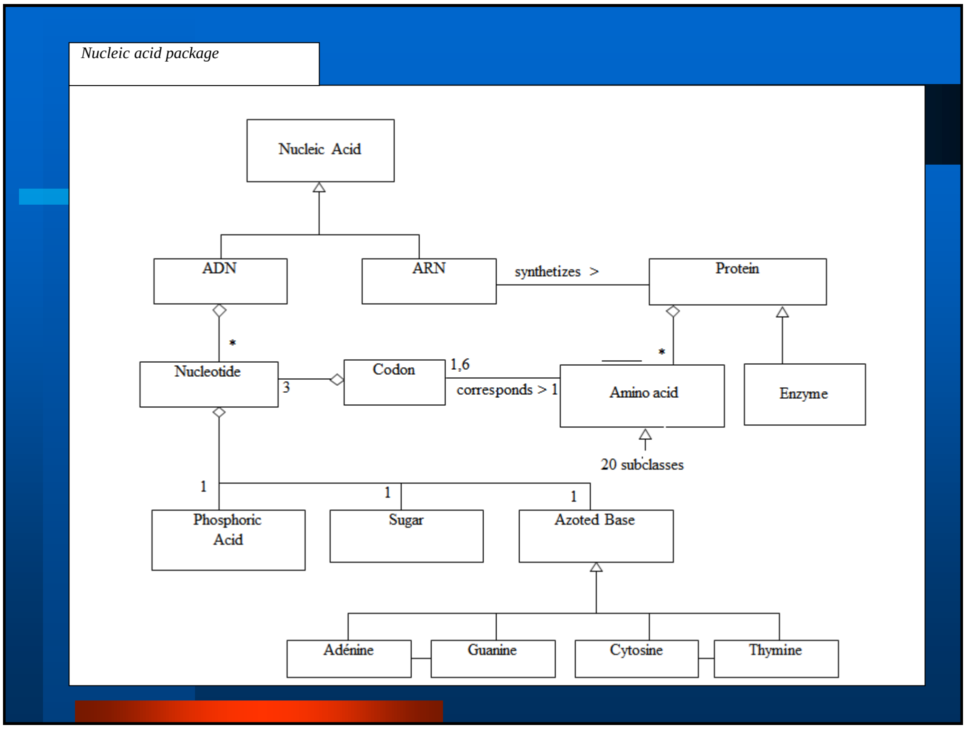
FACTS ABOUT DNA:

DNA could stretch from the earth to the sun 600 times

We're all 99.9 percent alike

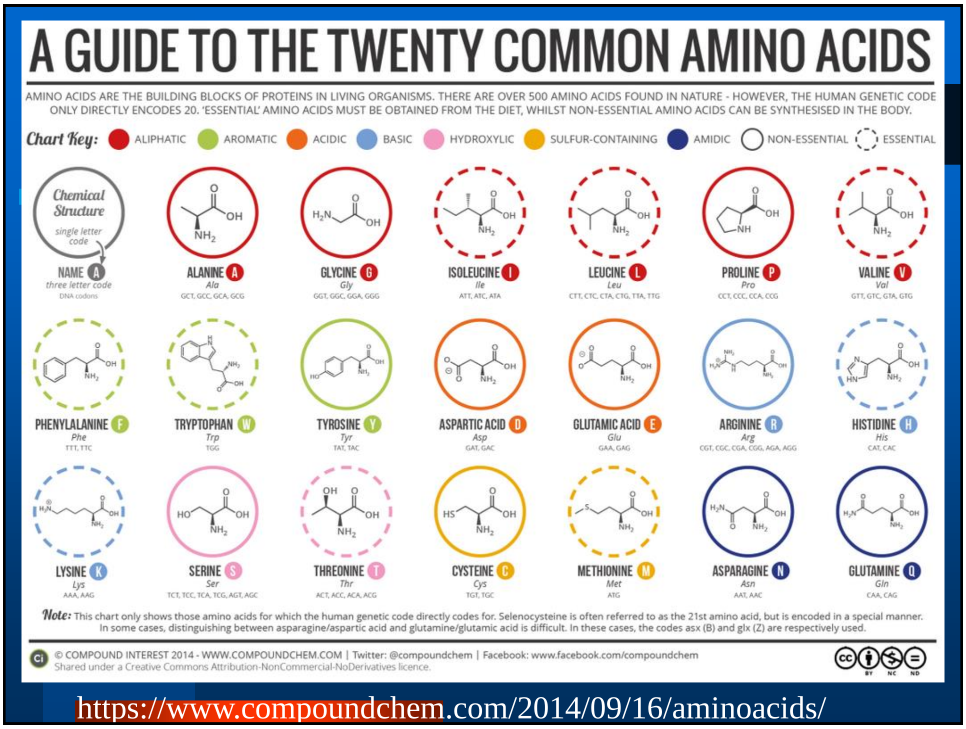
3×10^9 The human genome contains 3 billion base pairs of DNA

A fast typist, working eight hours a day, would take 50 years to type out the human genome



mRNA Translation process

- A group of 3 bases is called a codon
- To each codon corresponds an amino acid
- There are 20 different amino acids
- We have coding redundancies since different codons give the same amino acid.
  64 codons => 20 amino acids
- The amino acid sequence specifies a protein (with start & stop sequences) or the enzymes.



A GUIDE TO THE TWENTY COMMON AMINO ACIDS

AMINO ACIDS ARE THE BUILDING BLOCKS OF PROTEINS IN LIVING ORGANISMS. THERE ARE OVER 500 AMINO ACIDS FOUND IN NATURE - HOWEVER, THE HUMAN GENETIC CODE ONLY DIRECTLY ENCODES 20. 'ESSENTIAL' AMINO ACIDS MUST BE OBTAINED FROM THE DIET, WHILST NON-ESSENTIAL AMINO ACIDS CAN BE SYNTHESISED IN THE BODY.

Chart Key: ● ALIPHATIC ● AROMATIC ● ACIDIC ● BASIC ● HYDROXYLIC ● SULFUR-CONTAINING ● AMIDIC ○ NON-ESSENTIAL ◌ ESSENTIAL

Chemical Structure – *single letter code*

NAME A – *three letter code* – DNA codons

- ALANINE A – *Ala* – GCT, GCC, GCA, GCG
- GLYCINE G – *Gly* – GGT, GGC, GGA, GGG
- ISOLEUCINE I – *Ile* – ATT, ATC, ATA
- LEUCINE L – *Leu* – CTT, CTC, CTA, CTG, TTA, TTG
- PROLINE P – *Pro* – CCT, CCC, CCA, CCG
- VALINE V – *Val* – GTT, GTC, GTA, GTG
- PHENYLALANINE F – *Phe* – TTT, TTC
- TRYPTOPHAN W – *Trp* – TGG
- TYROSINE Y – *Tyr* – TAT, TAC
- ASPARTIC ACID D – *Asp* – GAT, GAC
- GLUTAMIC ACID E – *Glu* – GAA, GAG
- ARGININE R – *Arg* – CGT, CGC, CGA, CGG, AGA, AGG
- HISTIDINE H – *His* – CAT, CAC
- LYSINE K – *Lys* – AAA, AAG
- SERINE S – *Ser* – TCT, TCC, TCA, TCG, AGT, AGC
- THREONINE T – *Thr* – ACT, ACC, ACA, ACG
- CYSTEINE C – *Cys* – TGT, TGC
- METHIONINE M – *Met* – ATG
- ASPARAGINE N – *Asn* – AAT, AAC
- GLUTAMINE Q – *Gln* – CAA, CAG

Note: This chart only shows those amino acids for which the human genetic code directly codes for. Selenocysteine is often referred to as the 21st amino acid, but is encoded in a special manner. In some cases, distinguishing between asparagine/aspartic acid and glutamine/glutamic acid is difficult. In these cases, the codes asx (B) and glx (Z) are respectively used.

https://www.compoundchem.com/2014/09/16/aminoacids/

From Amino Acids to proteins

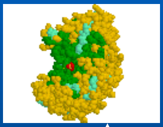
- All the proteins that make up living organisms are huge molecules, but they're composed of tinier building blocks, known as amino acids.
- There are over 500 amino acids found in nature, yet, of these, the human genetic code only directly codes for 20.
- Every protein in your body is made up of some linked combination of these amino acids
- The previous graphic shows the structure of each, as well as giving a little information on the notation used to represent them.

Essentials or not ? (Covid again ?)

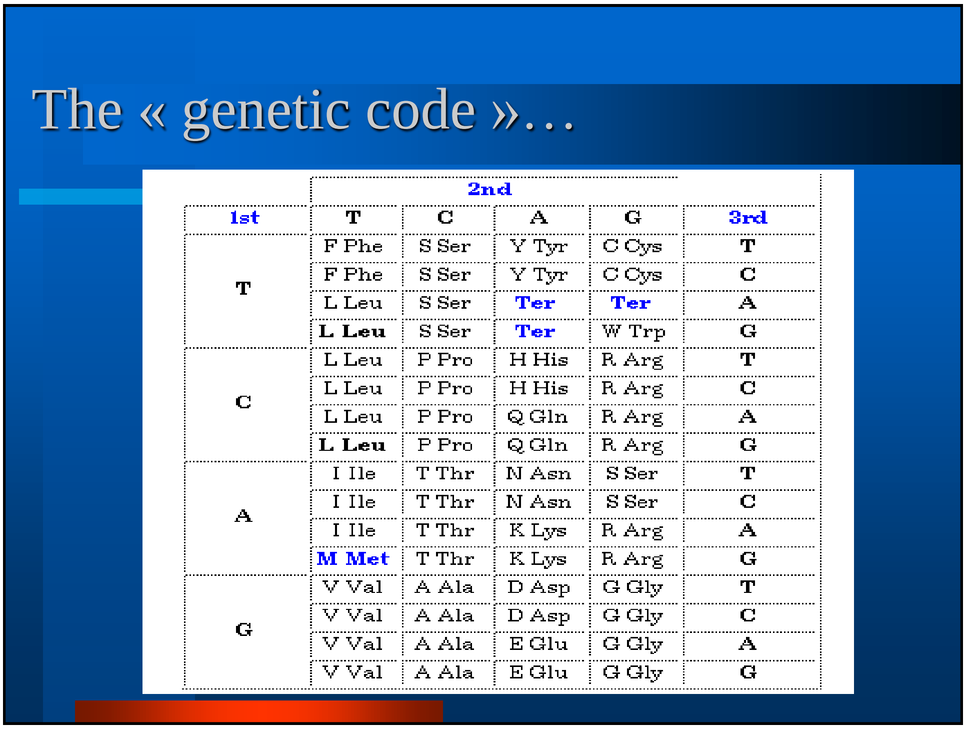
- Broadly, these twenty amino acids can be sorted into two groups: essential and non-essential.
- Non-essential amino acids are those which the human body is capable of synthesising, whereas essential amino acids must be obtained from the diet.
- Some can also be termed ‘conditionally essential’, meaning that they may be needed from the diet during illness or as a result of health problems. This sub-category includes arginine, glycine, cysteine, tyrosine, proline, and glutamine.
- The essentials amino acids are histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan and valine.

Start & stop codons…

- Usual START codon : ATG (AUG)
- 3 STOP codons : TAG, TGA, TAA

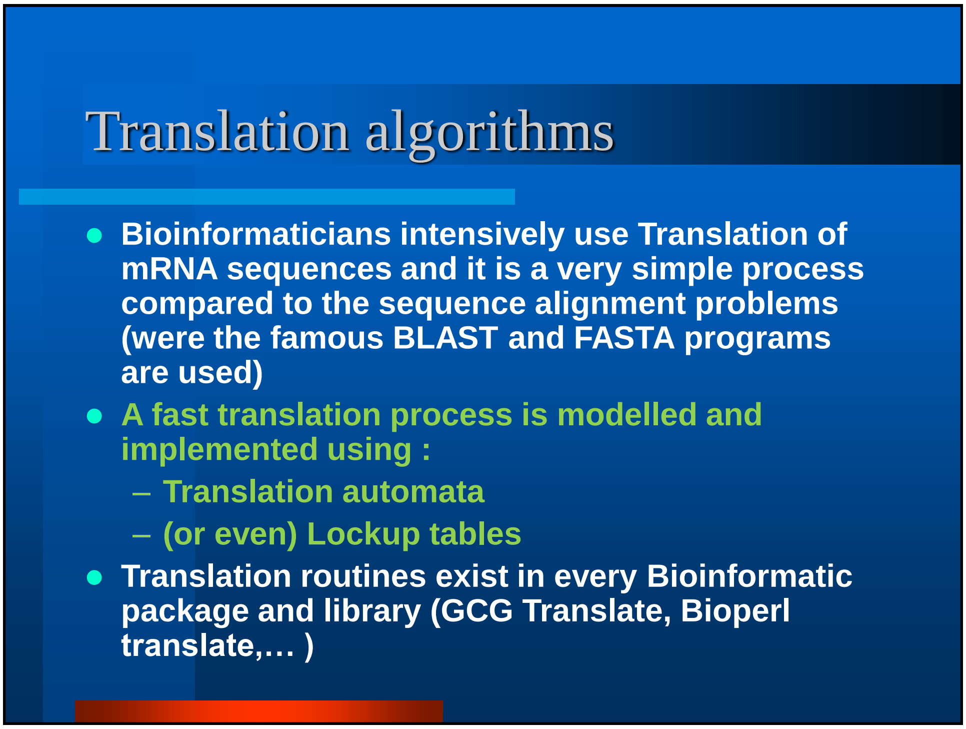


- Sequences between 2 stop codons are called open reading frames (ORFs), they are potentially coding for a protein
- With codons of 3 bases there are potentially 6 reading frames (3 on each complementary strands



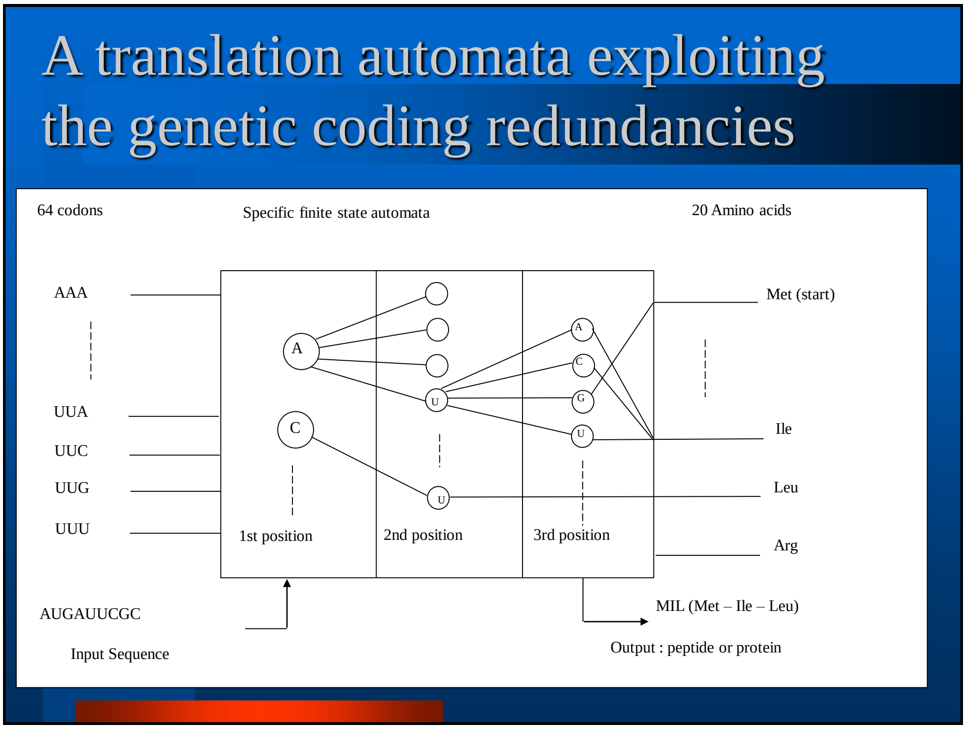
The « genetic code »…

	2nd				
1st	**T**	**C**	**A**	**G**	**3rd**
T	F Phe	S Ser	Y Tyr	C Cys	**T**
	F Phe	S Ser	Y Tyr	C Cys	**C**
	L Leu	S Ser	**Ter**	**Ter**	**A**
	L Leu	S Ser	**Ter**	W Trp	**G**
C	L Leu	P Pro	H His	R Arg	**T**
	L Leu	P Pro	H His	R Arg	**C**
	L Leu	P Pro	Q Gln	R Arg	**A**
	L Leu	P Pro	Q Gln	R Arg	**G**
A	I Ile	T Thr	N Asn	S Ser	**T**
	I Ile	T Thr	N Asn	S Ser	**C**
	I Ile	T Thr	K Lys	R Arg	**A**
	M Met	T Thr	K Lys	R Arg	**G**
G	V Val	A Ala	D Asp	G Gly	**T**
	V Val	A Ala	D Asp	G Gly	**C**
	V Val	A Ala	E Glu	G Gly	**A**
	V Val	A Ala	E Glu	G Gly	**G**



Translation algorithms

- **Bioinformaticians intensively use Translation of mRNA sequences and it is a very simple process compared to the sequence alignment problems (were the famous BLAST and FASTA programs are used)**
- **A fast translation process is modelled and implemented using :**
  - **Translation automata**
  - **(or even) Lockup tables**
- **Translation routines exist in every Bioinformatic package and library (GCG Translate, Bioperl translate,…)**



A translation automata exploiting the genetic coding redundancies

64 codons

Specific finite state automata

20 Amino acids

AAA

UUA

UUC

UUG

UUU

Met (start)

Ile

Leu

Arg

1st position

2nd position

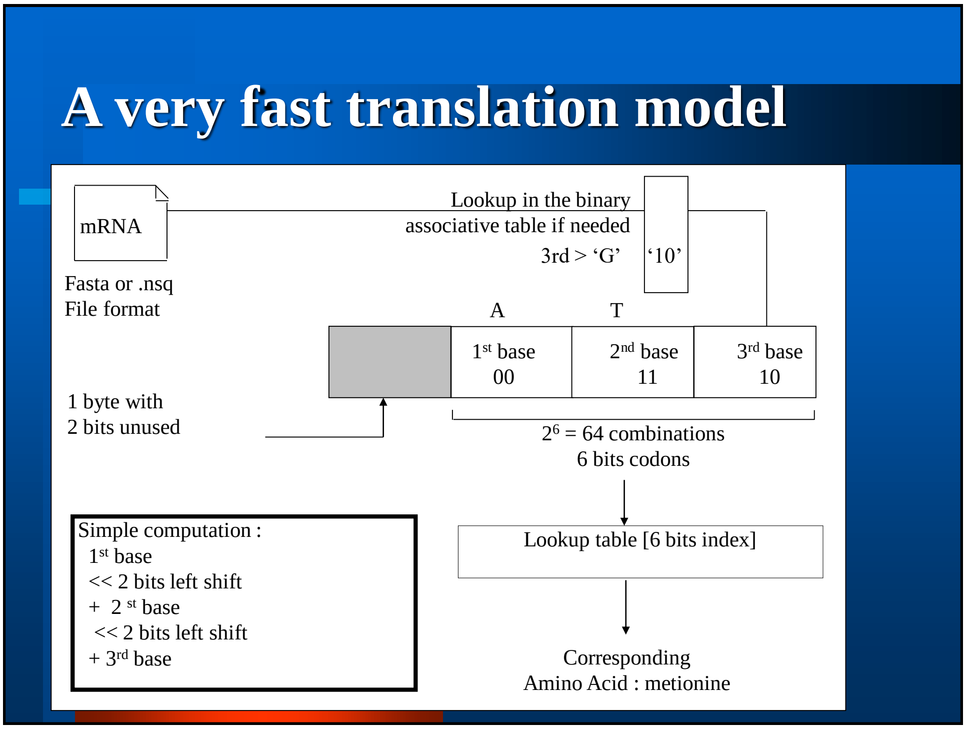
3rd position

AUGAUUCGC

Input Sequence

MIL (Met – Ile – Leu)

Output : peptide or protein



A very fast translation model

mRNA

Fasta or .nsq
File format

Lookup in the binary
associative table if needed
3rd > ‘G’

‘10’

A

T

1st base
00

2nd base
11

3rd base
10

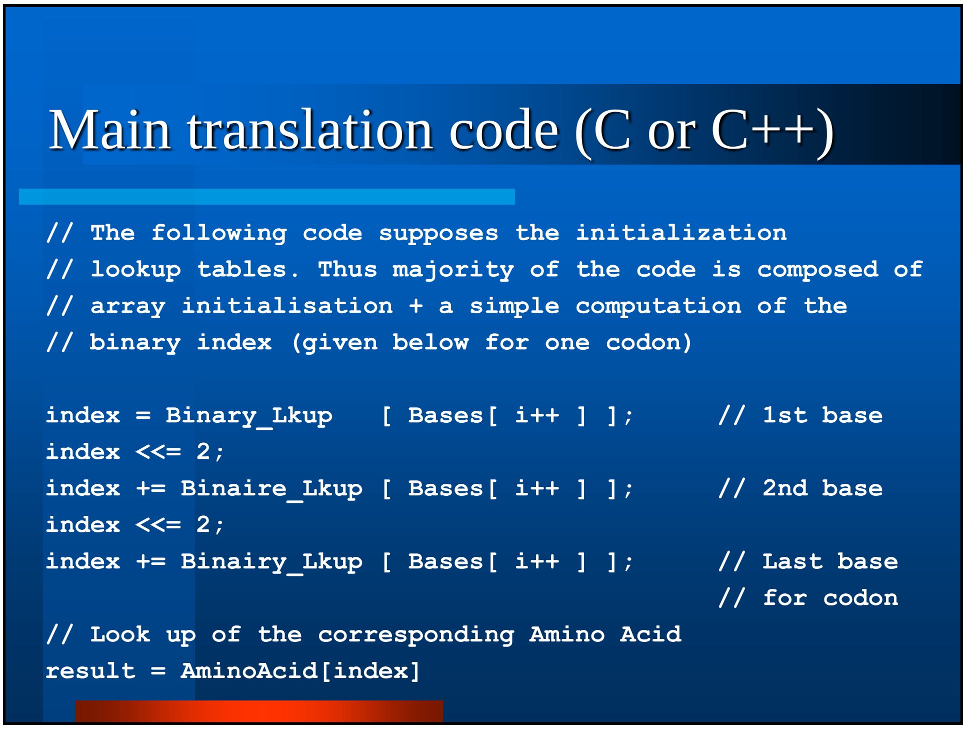
1 byte with
2 bits unused

$2^6 = 64$ combinations
6 bits codons

Lookup table [6 bits index]

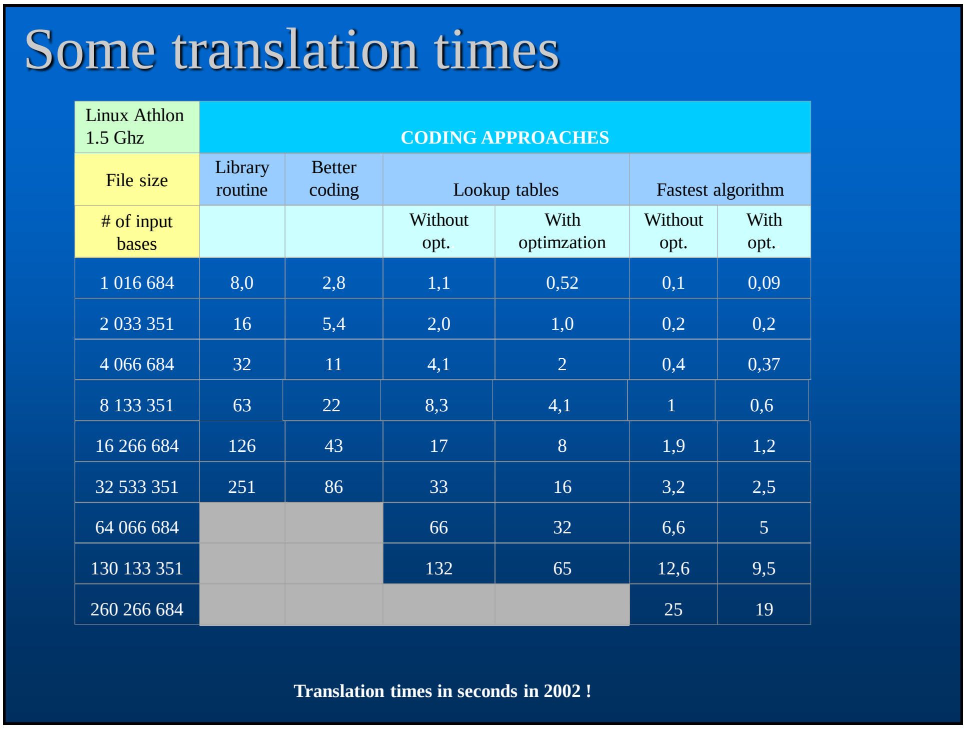
Corresponding
Amino Acid : metionine

Simple computation :
1st base
<< 2 bits left shift
+ 2 st base
<< 2 bits left shift
+ 3rd base



Main translation code (C or C++)

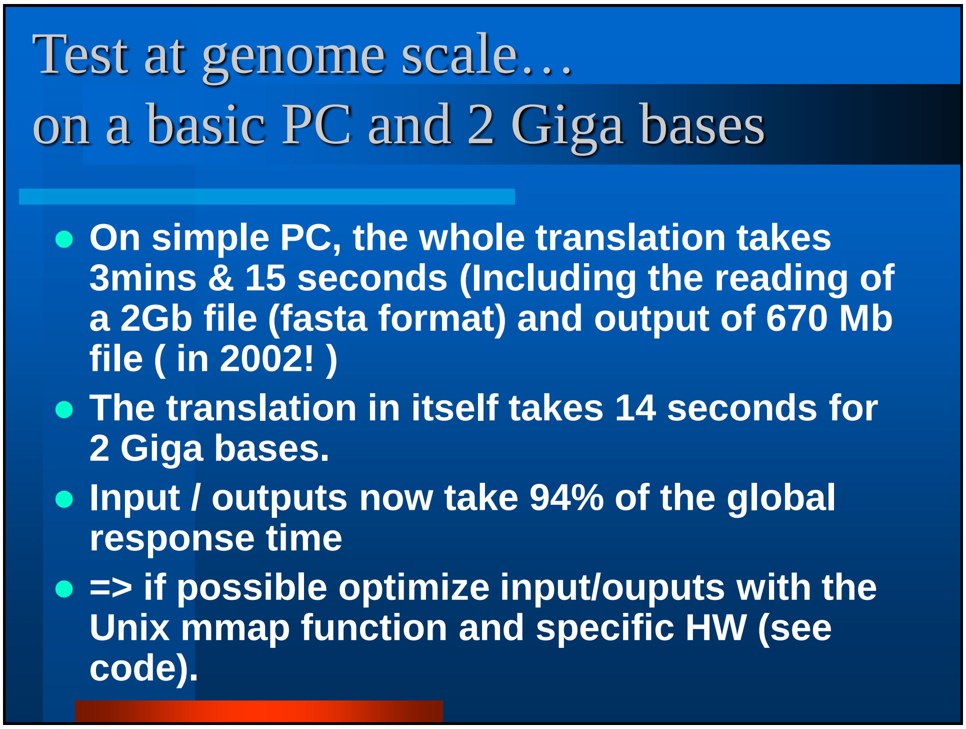
```
// The following code supposes the initialization
// lookup tables. Thus majority of the code is composed of
// array initialisation + a simple computation of the
// binary index (given below for one codon)

index = Binary_Lkup   [ Bases[ i++ ] ];      // 1st base
index <<= 2;
index += Binaire_Lkup [ Bases[ i++ ] ];      // 2nd base
index <<= 2;
index += Binairy_Lkup [ Bases[ i++ ] ];      // Last base
                                             // for codon
// Look up of the corresponding Amino Acid
result = AminoAcid[index]
```



Some translation times

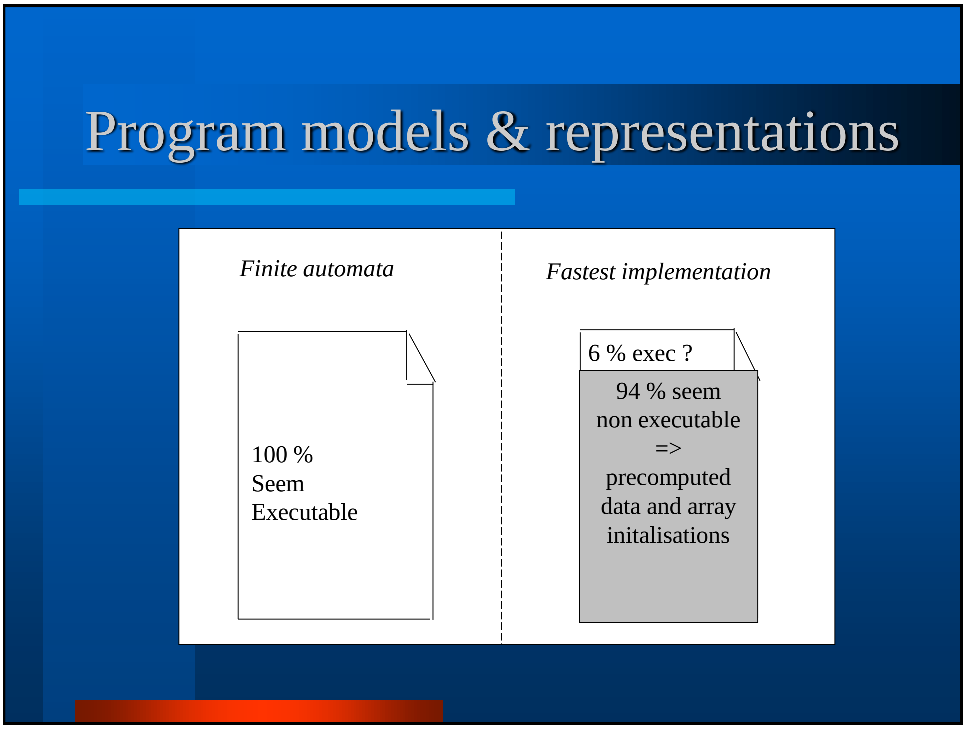
Linux Athlon 1.5 Ghz	CODING APPROACHES					
File size	Library routine	Better coding	Lookup tables		Fastest algorithm	
# of input bases			Without opt.	With optimzation	Without opt.	With opt.
1 016 684	8,0	2,8	1,1	0,52	0,1	0,09
2 033 351	16	5,4	2,0	1,0	0,2	0,2
4 066 684	32	11	4,1	2	0,4	0,37
8 133 351	63	22	8,3	4,1	1	0,6
16 266 684	126	43	17	8	1,9	1,2
32 533 351	251	86	33	16	3,2	2,5
64 066 684			66	32	6,6	5
130 133 351			132	65	12,6	9,5
260 266 684					25	19

Translation times in seconds in 2002 !



Test at genome scale…
on a basic PC and 2 Giga bases

- On simple PC, the whole translation takes 3mins & 15 seconds (Including the reading of a 2Gb file (fasta format) and output of 670 Mb file (in 2002!)
- The translation in itself takes 14 seconds for 2 Giga bases.
- Input / outputs now take 94% of the global response time
- => if possible optimize input/ouputs with the Unix mmap function and specific HW (see code).



Program models & representations

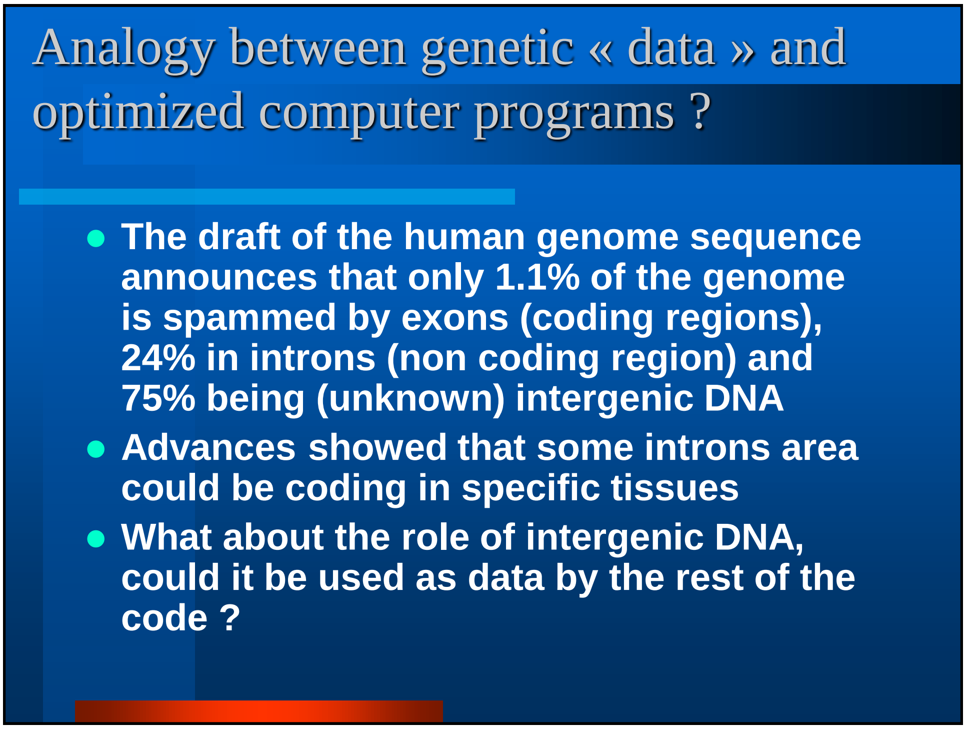
Finite automata

100 %
Seem
Executable

Fastest implementation

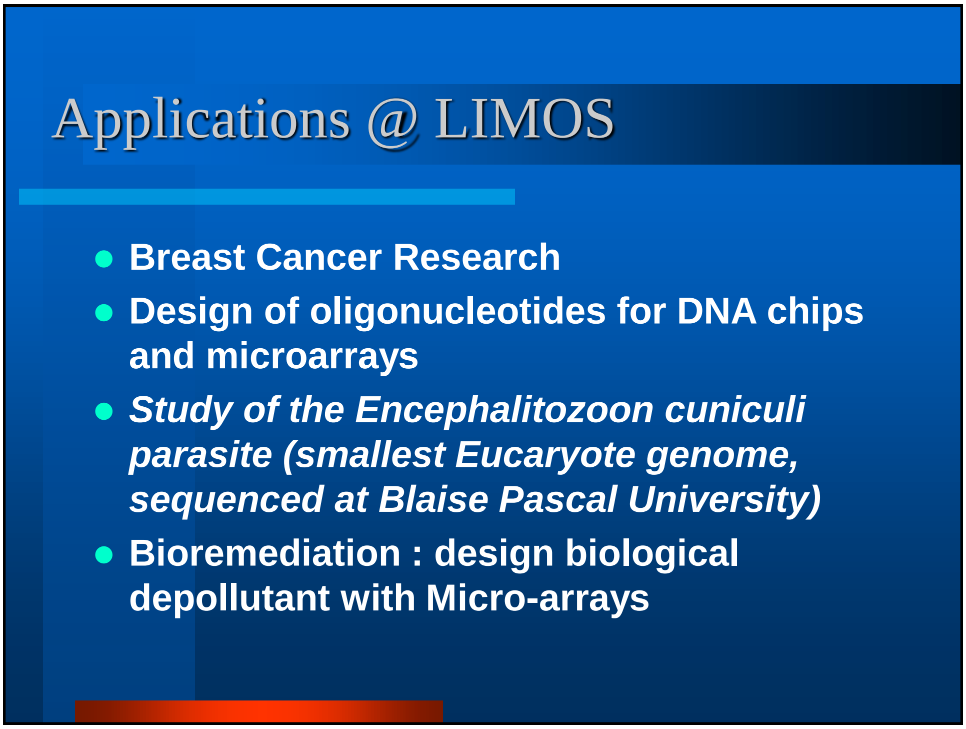
6 % exec ?

94 % seem
non executable
=>
precomputed
data and array
initalisations



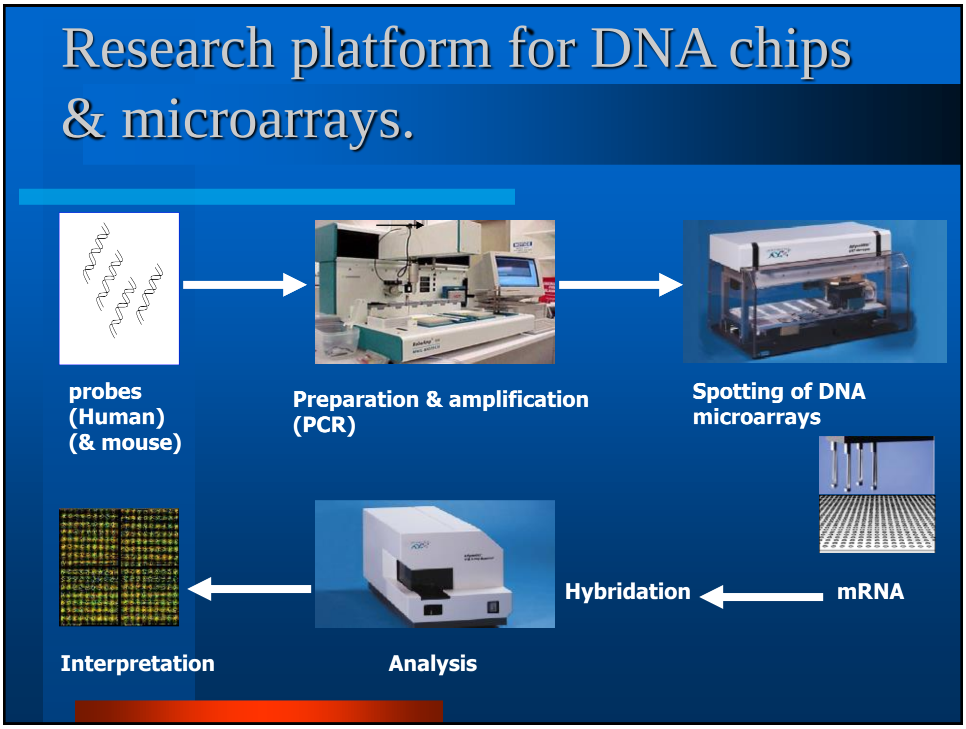
Analogy between genetic « data » and optimized computer programs ?

- The draft of the human genome sequence announces that only 1.1% of the genome is spammed by exons (coding regions), 24% in introns (non coding region) and 75% being (unknown) intergenic DNA
- Advances showed that some introns area could be coding in specific tissues
- What about the role of intergenic DNA, could it be used as data by the rest of the code ?



Applications @ LIMOS

- Breast Cancer Research
- Design of oligonucleotides for DNA chips and microarrays
- *Study of the Encephalitozoon cuniculi parasite (smallest Eucaryote genome, sequenced at Blaise Pascal University)*
- Bioremediation : design biological depollutant with Micro-arrays



Research platform for DNA chips & microarrays.

probes
(Human)
(& mouse)

Preparation & amplification
(PCR)

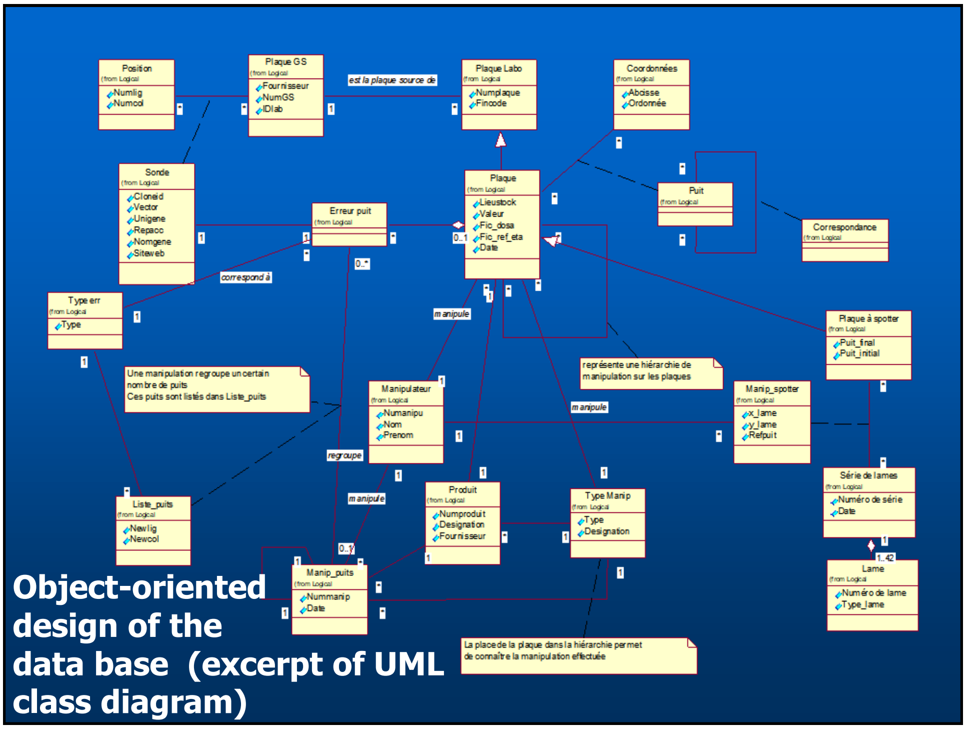
Spotting of DNA
microarrays

mRNA

Hybridization

Analysis

Interpretation



Position
(from Logical
Numlig
Numcol

Plaque GS
(from Logical
Fournisseur
NumGS
IDlab

Plaque Labo
(from Logical
Numplaque
Fincode

Coordonnées
(from Logical
Abcisse
Ordonnée

Sonde
(from Logical
Cloneid
Vector
Unigene
Repacc
Nomgene
Siteweb

Erreur puit
(from Logical

Plaque
(from Logical
Lieustock
Valeur
Fic_dosa
Fic_ref_eta
Date

Puit
(from Logical

Correspondance
(from Logical

Type err
(from Logical
Type

Plaque à spotter
(from Logical
Puit_final
Puit_initial

Une manipulation regroupe un certain nombre de puits
Ces puits sont listés dans Liste_puits

représente une hiérarchie de manipulation sur les plaques

Manipulateur
(from Logical
Numanipu
Nom
Prenom

Manip_spotter
(from Logical
x_lame
y_lame
Refpuit

Liste_puits
(from Logical
Newlig
Newcol

Produit
(from Logical
Numproduit
Designation
Fournisseur

Type Manip
(from Logical
Type
Designation

Série de lames
(from Logical
Numéro de série
Date

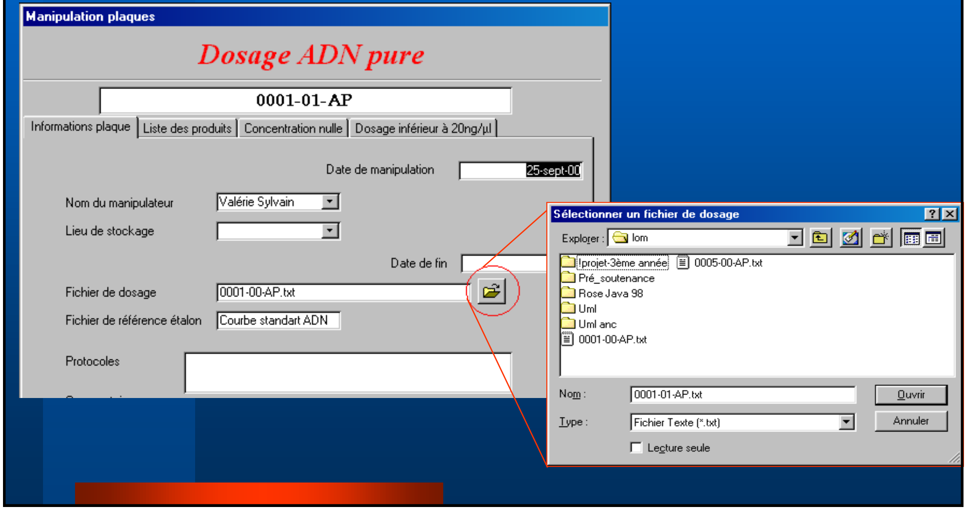
Manip_puits
(from Logical
Nummanip
Date

Lame
(from Logical
Numéro de lame
Type_lame

La place de la plaque dans la hiérarchie permet de connaître la manipulation effectuée

Object-oriented design of the data base (excerpt of UML class diagram)

Example of input screens



Manipulation plaques

Dosage ADN pure

0001-01-AP

Date de manipulation: 25-sept-00

Nom du manipulateur: Valérie Sylvain

Lieu de stockage:

Date de fin:

Fichier de dosage: 0001-00-AP.txt

Fichier de référence étalon: Courbe standart ADN

Protocoles:

Sélectionner un fichier de dosage

Explorer : lom

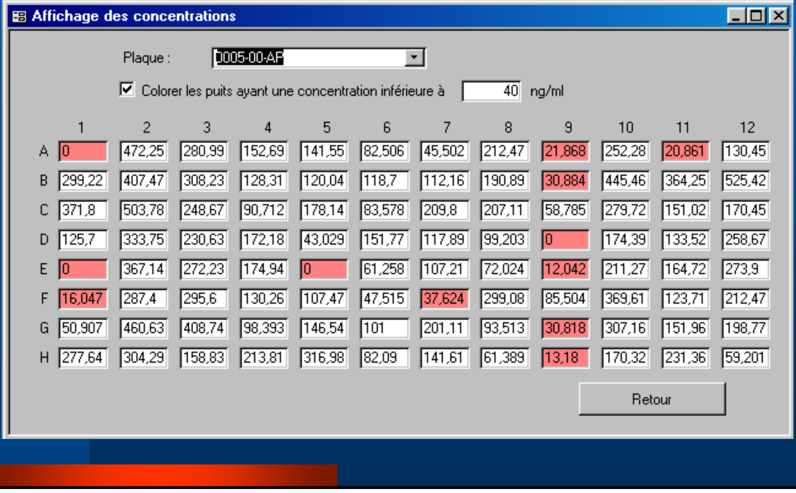
- !projet-3ème année
- Pré_soutenance
- Rose Java 98
- Uml
- Uml anc
- 0001-00-AP.txt
- 0005-00-AP.txt

Nom : 0001-01-AP.txt

Type : Fichier Texte (*.txt)

□ Lecture seule

Verification of values in 96 holes plates



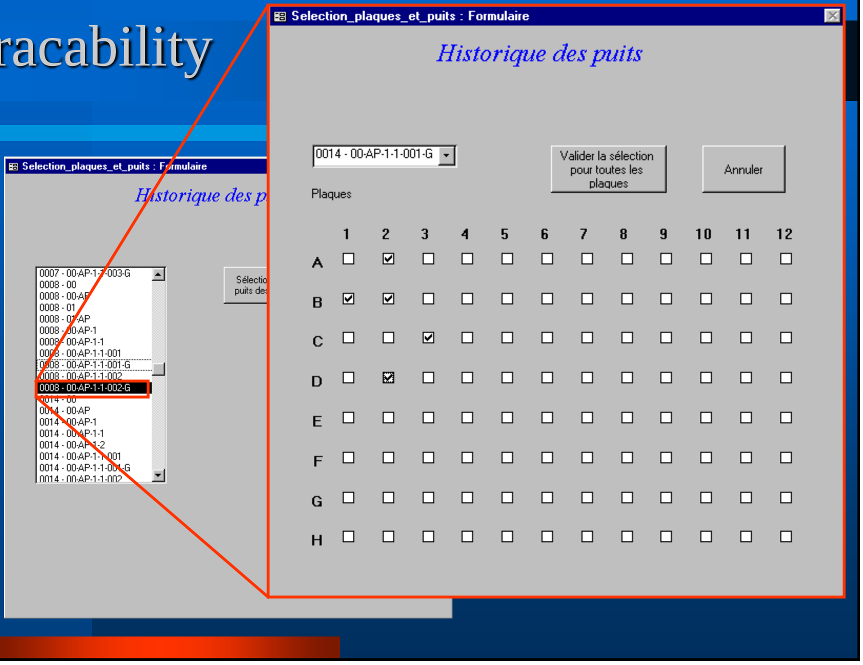
Affichage des concentrations

Plaque : 0005-00-AP

☑ Colorer les puits ayant une concentration inférieure à 40 ng/ml

	1	2	3	4	5	6	7	8	9	10	11	12
A	0	472,25	280,99	152,69	141,55	82,506	45,502	212,47	21,868	252,28	20,861	130,45
B	299,22	407,47	308,23	128,31	120,04	118,7	112,16	190,89	30,884	445,46	364,25	525,42
C	371,8	503,78	248,67	90,712	178,14	83,578	209,8	207,11	58,785	279,72	151,02	170,45
D	125,7	333,75	230,63	172,18	43,029	151,77	117,89	99,203	0	174,39	133,52	258,67
E	0	367,14	272,23	174,94	0	61,258	107,21	72,024	12,042	211,27	164,72	273,9
F	16,047	287,4	295,6	130,26	107,47	47,515	37,624	299,08	85,504	369,61	123,71	212,47
G	50,907	460,63	408,74	98,393	146,54	101	201,11	93,513	30,818	307,16	151,96	198,77
H	277,64	304,29	158,83	213,81	316,98	82,09	141,61	61,389	13,18	170,32	231,36	59,201

Holes Tracability



Selection_plaques_et_puits : Formulaire

Historique des p

0007 - 00-AP-1-1-003-G
0008 - 00
0008 - 00-AP
0008 - 01
0008 - 01-AP
0008 - 00-AP-1
0008 - 00-AP-1-1
0008 - 00-AP-1-1-001
0008 - 00-AP-1-1-001-G
0008 - 00-AP-1-1-002
0008 - 00-AP-1-1-002-G
0014 - 00
0014 - 00-AP
0014 - 00-AP-1
0014 - 00-AP-1-1
0014 - 00-AP-1-2
0014 - 00-AP-1-1-001
0014 - 00-AP-1-1-001-G
0014 - 00-AP-1-1-002

Selection_plaques_et_puits : Formulaire

Historique des puits

0014 - 00-AP-1-1-001-G

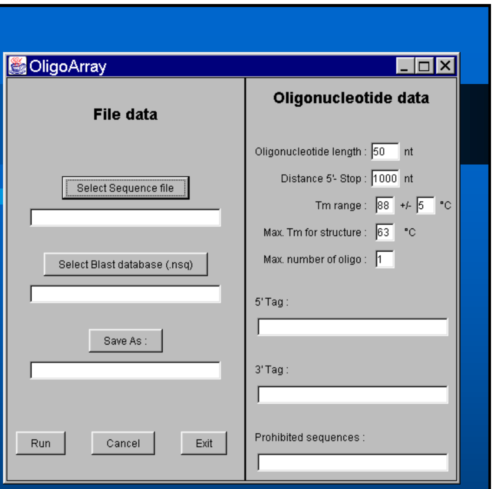
Plaques

	1	2	3	4	5	6	7	8	9	10	11	12
A	□	☑	□	□	□	□	□	□	□	□	□	□
B	☑	☑	□	□	□	□	□	□	□	□	□	□
C	□	□	☑	□	□	□	□	□	□	□	□	□
D	□	☑	□	□	□	□	□	□	□	□	□	□
E	□	□	□	□	□	□	□	□	□	□	□	□
F	□	□	□	□	□	□	□	□	□	□	□	□
G	□	□	□	□	□	□	□	□	□	□	□	□
H	□	□	□	□	□	□	□	□	□	□	□	□

Oligonucleotide design

Criteria :

- Melting Temperature
- Secondary Structure
- Distance from 3’ end

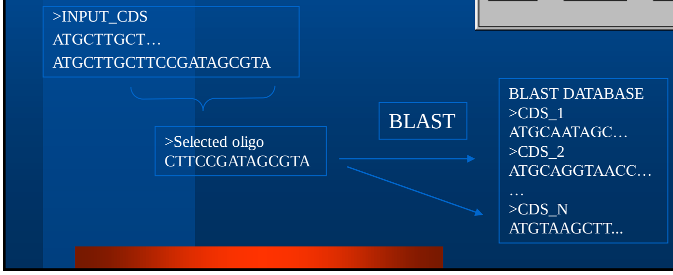


OligoArray

File data

Oligonucleotide data

Oligonucleotide length : 50 nt
Distance 5'- Stop : 1000 nt
Tm range : 88 +/- 5 °C
Max. Tm for structure : 63 °C
Max. number of oligo : 1
5' Tag :
3' Tag :
Prohibited sequences :

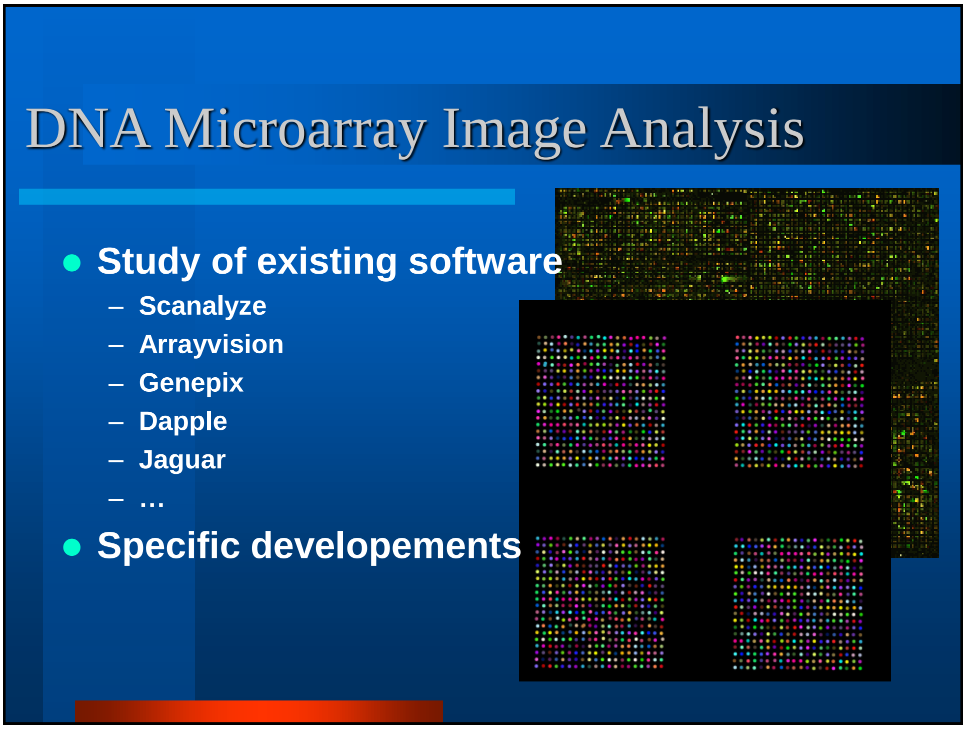


>INPUT_CDS
ATGCTTGCT…
ATGCTTGCTTCCGATAGCGTA

>Selected oligo
CTTCCGATAGCGTA

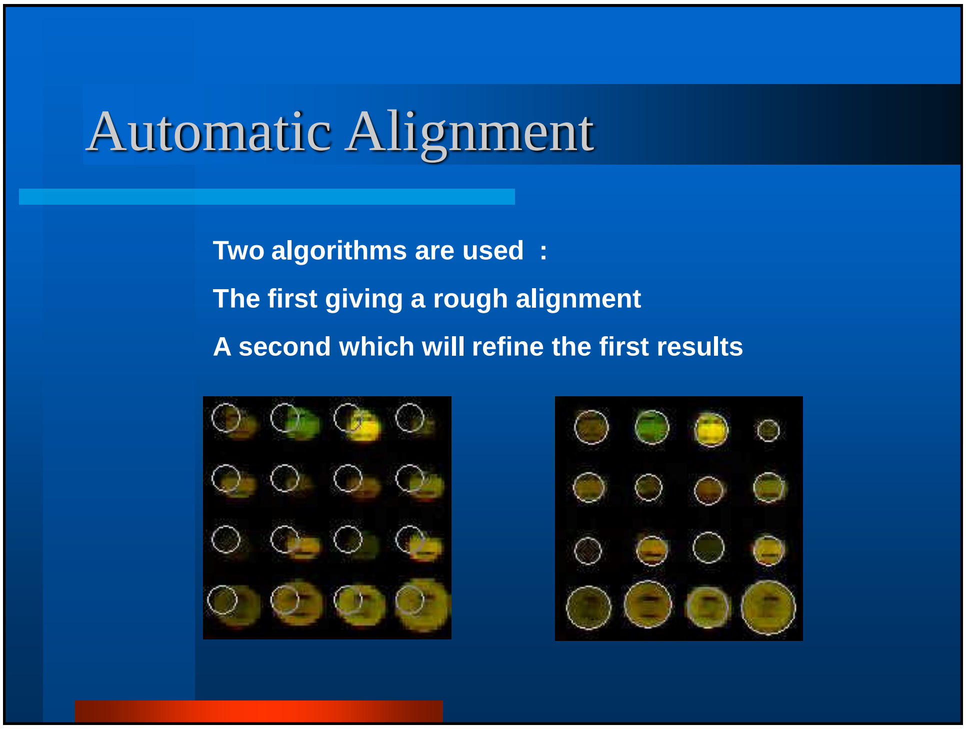
BLAST

BLAST DATABASE
>CDS_1
ATGCAATAGC…
>CDS_2
ATGCAGGTAACC…
…
>CDS_N
ATGTAAGCTT...



DNA Microarray Image Analysis

- Study of existing software
  - Scanalyze
  - Arrayvision
  - Genepix
  - Dapple
  - Jaguar
  - …
- Specific developements



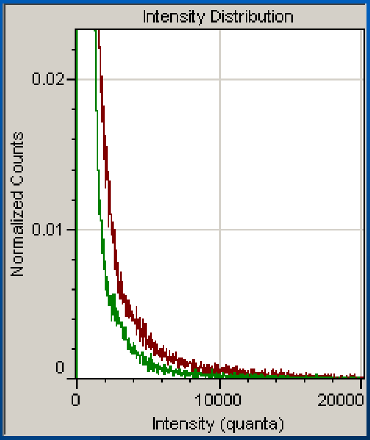
Automatic Alignment

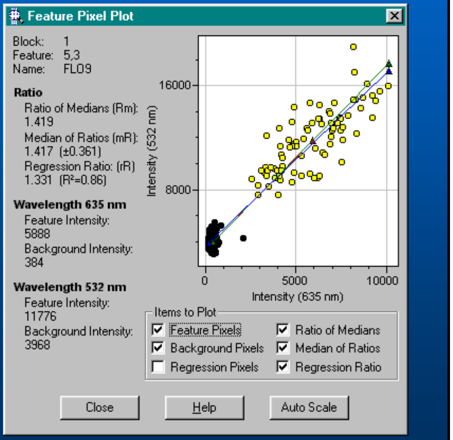
Two algorithms are used :

The first giving a rough alignment

A second which will refine the first results

Study of pixels distribution




Feature Pixel Plot

Block: 1
Feature: 5,3
Name: FL09

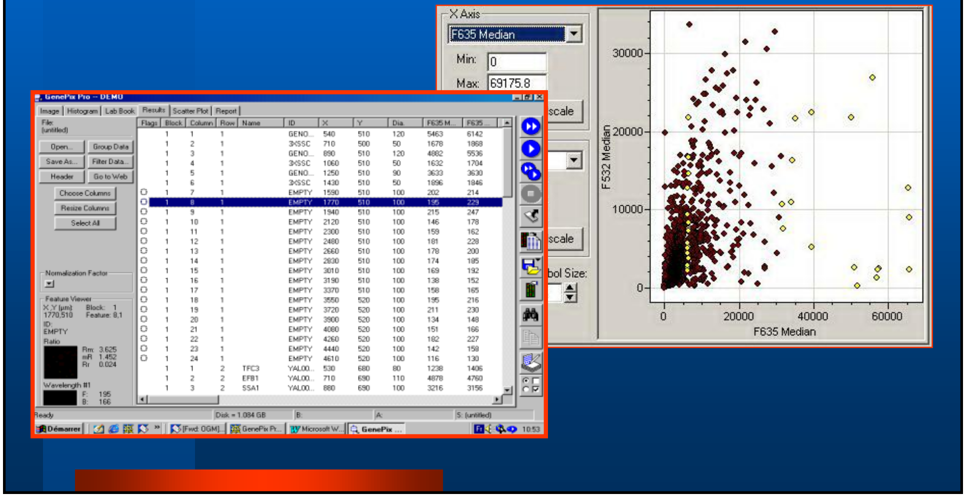
Ratio
Ratio of Medians (Rm): 1.419
Median of Ratios (mR): 1.417 (±0.361)
Regression Ratio: (rR) 1.331 (R^2=0.86)

Wavelength 635 nm
Feature Intensity: 5888
Background Intensity: 384

Wavelength 532 nm
Feature Intensity: 11776
Background Intensity: 3968

Items to Plot
☑ Feature Pixels ☑ Ratio of Medians
☑ Background Pixels ☑ Median of Ratios
□ Regression Pixels ☑ Regression Ratio

Assignment of results enabling the caracterization of genes expression


X Axis: F635 Median
Min: 0
Max: 69175.8

GenePix Pro -- DEMO

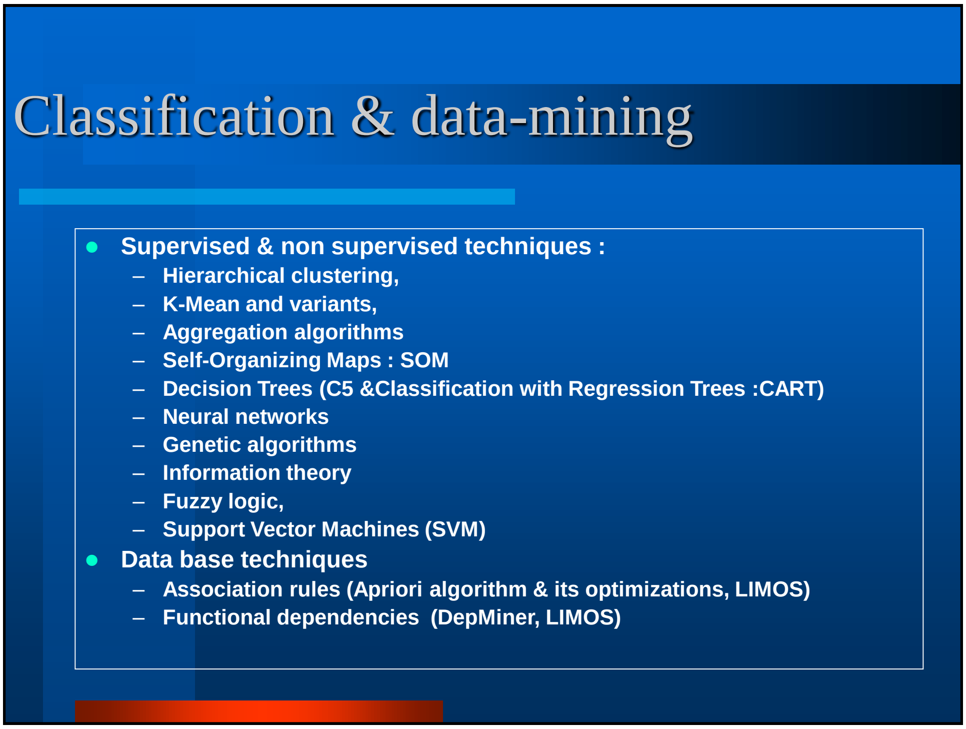
File: (untitled)

Normalization Factor

Feature Viewer
X,Y [µm]: 1770,510 Block: 1 Feature: 8,1
ID: EMPTY
Ratio
Rm: 3.625
mR: 1.452
Rr: 0.024
Wavelength #1
F: 195
B: 166

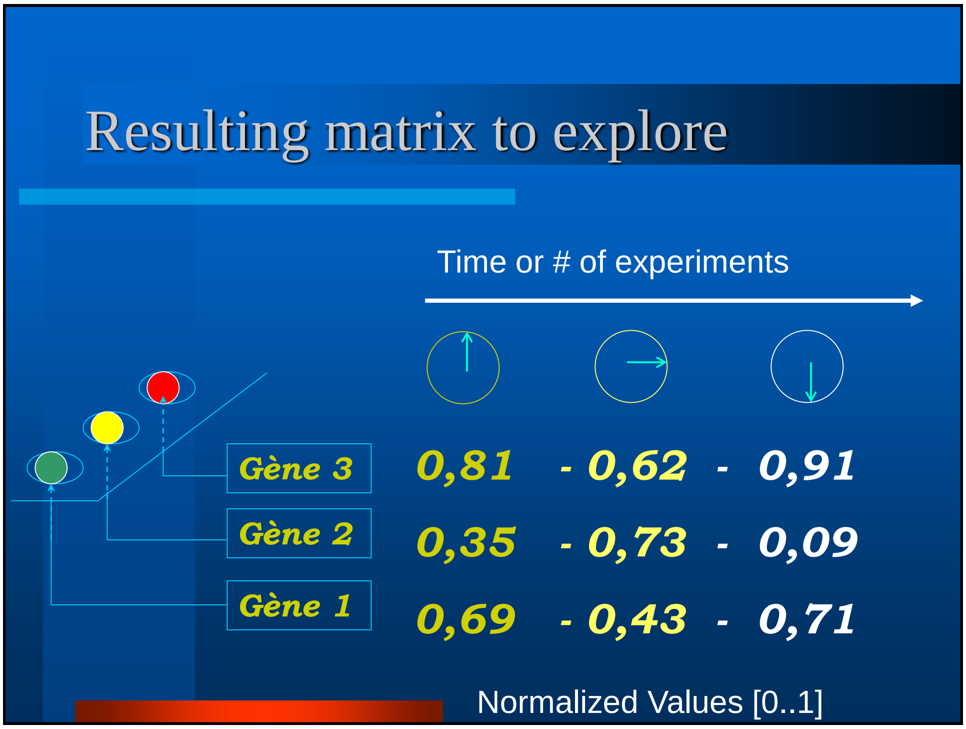
Flags	Block	Column	Row	Name	ID	X	Y	Dia.	F635 M...	F635 ...
	1	1	1		GENO...	540	510	120	5463	6142
	1	2	1		3XSSC	710	500	50	1678	1868
	1	3	1		GENO...	890	510	120	4882	5536
	1	4	1		3XSSC	1060	510	50	1632	1704
	1	5	1		GENO...	1250	510	90	3633	3630
	1	6	1		3XSSC	1430	510	50	1896	1846
○	1	7	1		EMPTY	1590	510	100	202	214
○	1	8	1		EMPTY	1770	510	100	195	229
○	1	9	1		EMPTY	1940	510	100	215	247
○	1	10	1		EMPTY	2120	510	100	146	178
○	1	11	1		EMPTY	2300	510	100	159	162
○	1	12	1		EMPTY	2480	510	100	181	228
○	1	13	1		EMPTY	2660	510	100	178	200
○	1	14	1		EMPTY	2830	510	100	174	185
○	1	15	1		EMPTY	3010	510	100	169	192
○	1	16	1		EMPTY	3190	510	100	138	152
○	1	17	1		EMPTY	3370	510	100	158	165
○	1	18	1		EMPTY	3550	520	100	195	216
○	1	19	1		EMPTY	3720	520	100	211	230
○	1	20	1		EMPTY	3900	520	100	134	148
○	1	21	1		EMPTY	4080	520	100	151	166
○	1	22	1		EMPTY	4260	520	100	182	227
○	1	23	1		EMPTY	4440	520	100	142	158
○	1	24	1		EMPTY	4610	520	100	116	130
	1	1	2	TFC3	YAL00...	530	680	80	1238	1406
	1	2	2	EFB1	YAL00...	710	690	110	4878	4760
	1	3	2	SSA1	YAL00...	880	690	100	3216	3156

Ready | Disk = 1.084 GB | B: | A: | 5: (untitled)



Classification & data-mining

- Supervised & non supervised techniques :
  - Hierarchical clustering,
  - K-Mean and variants,
  - Aggregation algorithms
  - Self-Organizing Maps : SOM
  - Decision Trees (C5 &Classification with Regression Trees :CART)
  - Neural networks
  - Genetic algorithms
  - Information theory
  - Fuzzy logic,
  - Support Vector Machines (SVM)
- Data base techniques
  - Association rules (Apriori algorithm & its optimizations, LIMOS)
  - Functional dependencies (DepMiner, LIMOS)



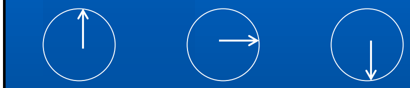
Resulting matrix to explore

Time or # of experiments

Gène 3	0,81	- 0,62	- 0,91
Gène 2	0,35	- 0,73	- 0,09
Gène 1	0,69	- 0,43	- 0,71

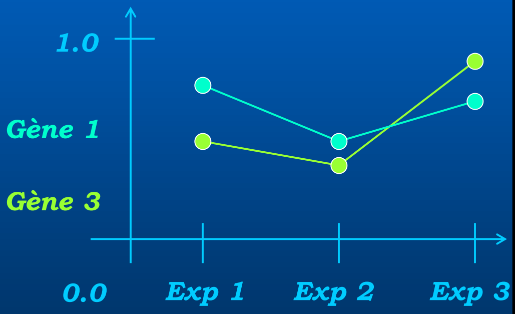
Normalized Values [0..1]

Research of similar or opposite behaviours



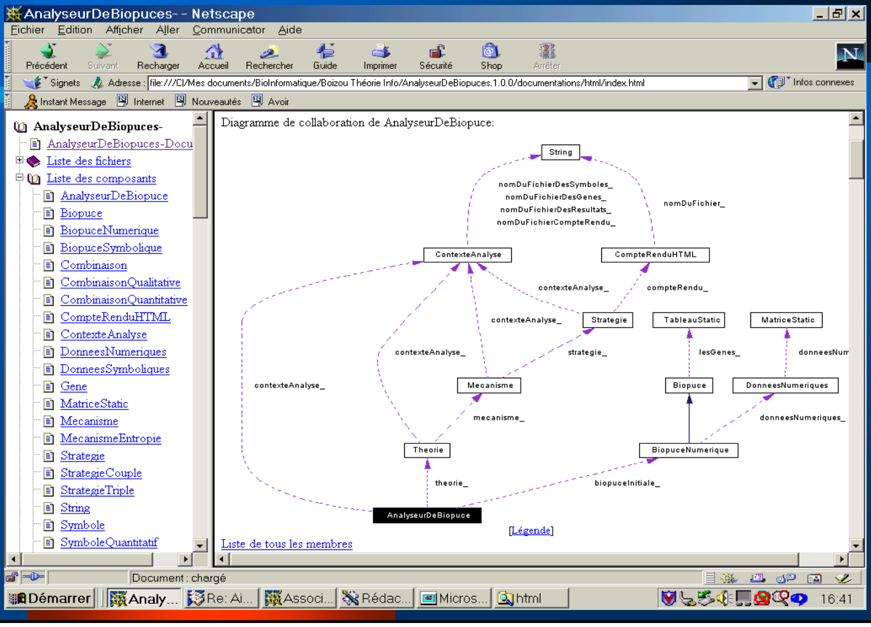
0,81 - 0,62 - 0,71

0,69 - 0,43 - 0,91



activators ? inhibitors ?
similarities in functionning ?

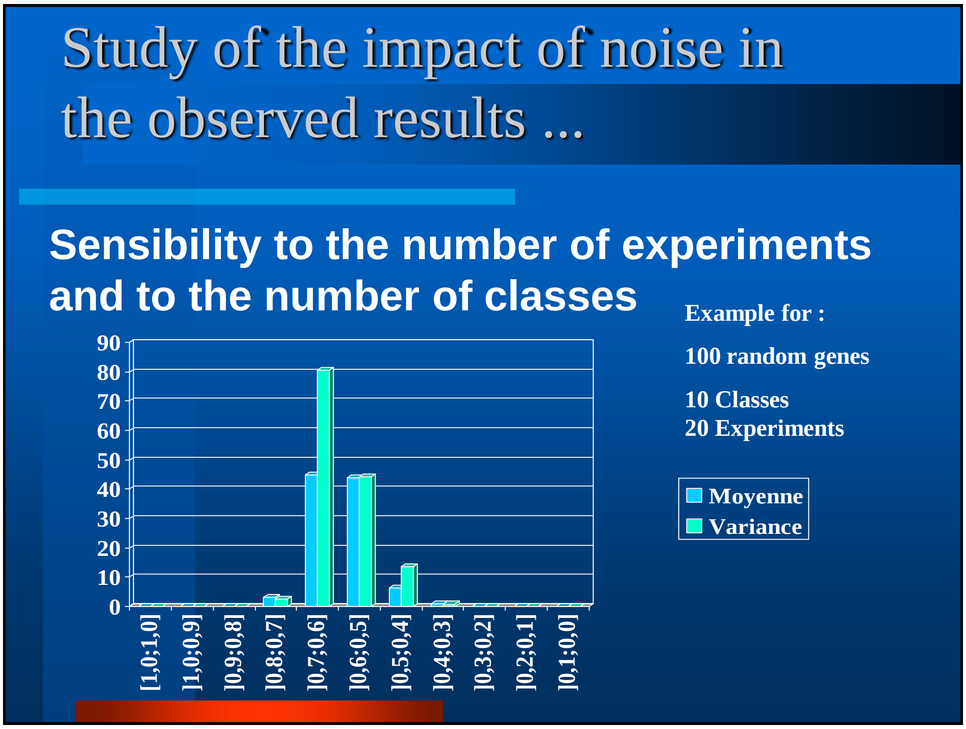
OO Modeling and development (UML Documentation of C++ program with Doxygen)


AnalyseurDeBiopuces- - Netscape
Fichier Edition Afficher Aller Communicator Aide
Précédent Suivant Recharger Accueil Rechercher Guide Imprimer Sécurité Shop Arrêter
Signets Adresse : file:///C|/Mes documents/BioInformatique/Boizou Théorie Info/AnalyseurDeBiopuces.1.0.0/documentations/html/index.html
Infos connexes
Instant Message Internet Nouveautés Avoir
Document : chargé
Démarrer Analy... Re: Ai... Associ... Rédac... Micros... html
16:41

AnalyseurDeBiopuces-
- AnalyseurDeBiopuces-Docu
- Liste des fichiers
- Liste des composants
  - AnalyseurDeBiopuce
  - Biopuce
  - BiopuceNumerique
  - BiopuceSymbolique
  - Combinaison
  - CombinaisonQualitative
  - CombinaisonQuantitative
  - CompteRenduHTML
  - ContexteAnalyse
  - DonneesNumeriques
  - DonneesSymboliques
  - Gene
  - MatriceStatic
  - Mecanisme
  - MecanismeEntropie
  - Strategie
  - StrategieCouple
  - StrategieTriple
  - String
  - Symbole
  - SymboleQuantitatif

Diagramme de collaboration de AnalyseurDeBiopuce:

Liste de tous les membres



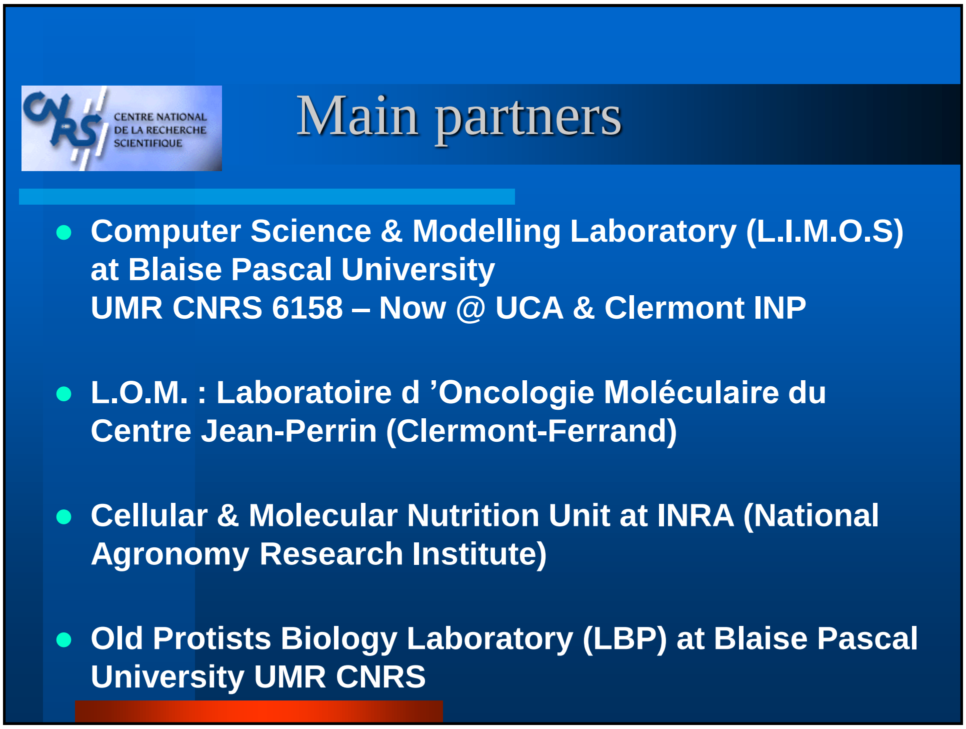
Study of the impact of noise in the observed results ...

Sensibility to the number of experiments and to the number of classes

Example for :

100 random genes

10 Classes
20 Experiments



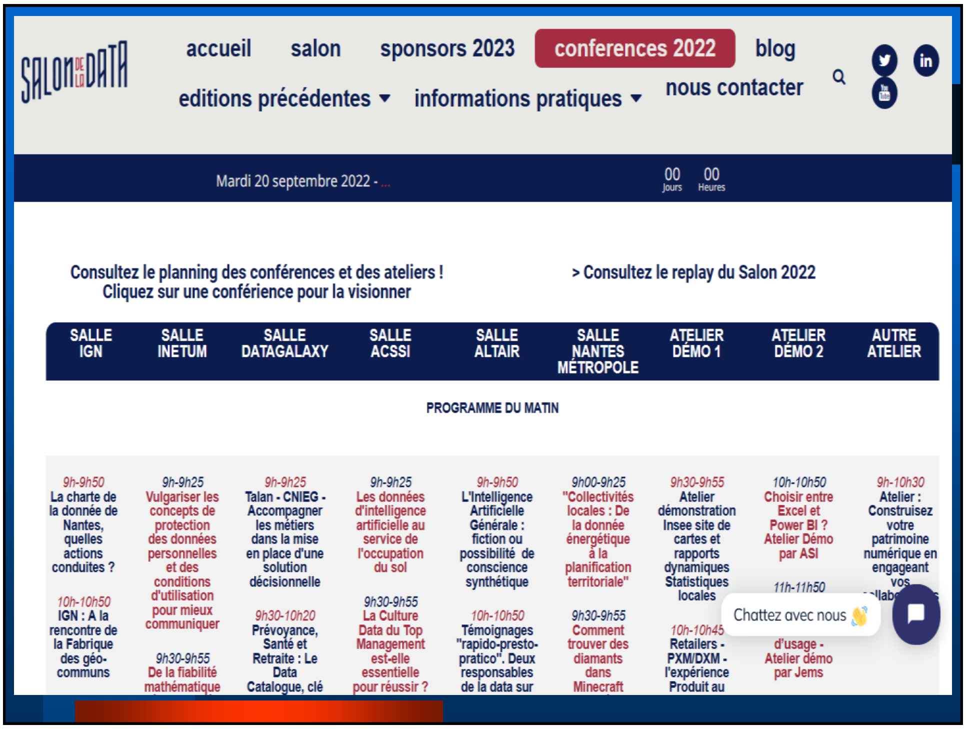
Main partners

CNRS
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE

- Computer Science & Modelling Laboratory (L.I.M.O.S) at Blaise Pascal University
UMR CNRS 6158 – Now @ UCA & Clermont INP
- L.O.M. : Laboratoire d ’Oncologie Moléculaire du Centre Jean-Perrin (Clermont-Ferrand)
- Cellular & Molecular Nutrition Unit at INRA (National Agronomy Research Institute)
- Old Protists Biology Laboratory (LBP) at Blaise Pascal University UMR CNRS

Perspectives

- Study of SNP surprises ! (Single Nucleotide Polymorphism) and developement of simulations
- Study of the bioremediation process thanks to reverse transcription
- Development of gene prediction models at genome scale, based on the fast algorithm presented (discovering ORFs)
- Evaluation of classification techniques



Mardi 20 septembre 2022 - ...

Consultez le planning des conférences et des ateliers !
Cliquez sur une conférence pour la visionner

> Consultez le replay du Salon 2022

SALLE IGN	SALLE INETUM	SALLE DATAGALAXY	SALLE ACSSI	SALLE ALTAIR	SALLE NANTES MÉTROPOLE	ATELIER DÉMO 1	ATELIER DÉMO 2	AUTRE ATELIER
PROGRAMME DU MATIN								
9h-9h50 La charte de la donnée de Nantes, quelles actions conduites ? 10h-10h50 IGN : A la rencontre de la Fabrique des géo-communs	9h-9h25 Vulgariser les concepts de protection des données personnelles et des conditions d'utilisation pour mieux communiquer 9h30-9h55 De la fiabilité mathématique	9h-9h25 Talan - CNIEG - Accompagner les métiers dans la mise en place d'une solution décisionnelle 9h30-10h20 Prévoyance, Santé et Retraite : Le Data Catalogue, clé	9h-9h25 Les données d'intelligence artificielle au service de l'occupation du sol 9h30-9h55 La Culture Data du Top Management est-elle essentielle pour réussir ?	9h-9h50 L'Intelligence Artificielle Générale : fiction ou possibilité de conscience synthétique 10h-10h50 Témoignages "rapido-presto-pratico". Deux responsables de la data sur	9h00-9h25 "Collectivités locales : De la donnée énergétique à la planification territoriale" 9h30-9h55 Comment trouver des diamants dans Minecraft	9h30-9h55 Atelier démonstration Insee site de cartes et rapports dynamiques Statistiques locales 10h-10h45 Retailers - PXM/DXM - l'expérience Produit au	10h-10h50 Choisir entre Excel et Power BI ? Atelier Démo par ASI 11h-11h50 d'usage - Atelier démo par Jems	9h-10h30 Atelier : Construisez votre patrimoine numérique en engageant vos

From Web developer… Salon de la DATA …to Bioinformatics

https://www.youtube.com/watch?v=ocvSY74narw&ab_channel=SalonData

Résultats pour **salon de la data code source du vaccin** ***Pfizer*** Essayez avec **salon de la data code source du vaccin Pfize**

A la découverte du code source du vaccin Pfizer/BioNTech

134 k vues • il y a 1 an

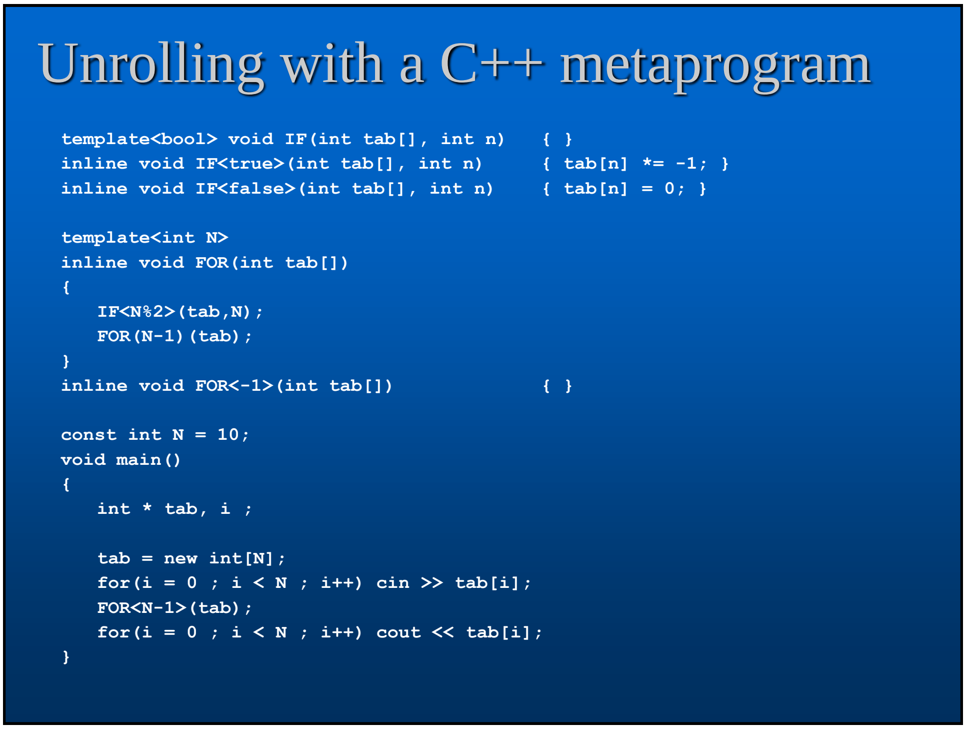
Salon Data

nouvelle technologie des **vaccins** ARNm est composé d'un **code source** d'un peu plus de 4000 caractères. nous ...

A la découverte du code source du vaccin Pfizer/BioNTech

Another possible optimization technique

- Among the programming optimization techniques the unrolling technique is sometimes used
- Meta-programming can exploit this directly within the C++ language
- It helps in the coding of programs that will be unrolled at compilation time.



Unrolling with a C++ metaprogram

```
template<bool> void IF(int tab[], int n)   { }
inline void IF<true>(int tab[], int n)     { tab[n] *= -1; }
inline void IF<false>(int tab[], int n)    { tab[n] = 0; }

template<int N>
inline void FOR(int tab[])
{
   IF<N%2>(tab,N);
   FOR(N-1)(tab);
}
inline void FOR<-1>(int tab[])             { }

const int N = 10;
void main()
{
   int * tab, i ;

   tab = new int[N];
   for(i = 0 ; i < N ; i++) cin >> tab[i];
   FOR<N-1>(tab);
   for(i = 0 ; i < N ; i++) cout << tab[i];
}
```

THANKS FOR YOUR ATTENTION

More to come
Invitation to C++ TMP ZZ3