Bioinformatics and other advanced technologies for Africa and all developing regions
• Some general remarks about use and misuse of bioinformatics

(2) Initiatives that may be relevant for spreading advanced technologies in Africa and other southern areas
Some general remarks about use and misuse of bioinformatics

- Preliminary warnings
- A recommendable strategy for the (many) labs that don’t have big technologies
- Tasks of bioinformatics
- Traps
- The relevance of recombination in pathogens
- Relevant megaprogrammes in human genetics
- The gap between genotype and phenotype
- (Another) call for an integrated approach
Preliminary warnings
Relevance of field data
Never forget environment and socioeconomical factors
Avoid to make it a big fishing expedition

Deductive research (design working hypotheses and collect data to falsify them)

Vs

Inductive research (collect data and see what’s going on)
Molecular Idiots
Schistosoma, in copula

(by P.W. Pappas and S.M. Wardrop)
Don’t forget the dear old things
POUR LUTTER DANS VOTRE VILLAGE CONTRE LA MALADIE DU SOMMEIL INSTALLEZ DES PIEGES A MOUCHES TSÉ-TSÉ

RECOMMANDÉ PAR L’OMS ET VOTRE GOUVERNEMENT

SA PIQUE PEUT TRANSMETTRE LA MALADIE DU SOMMEIL. CETTE MALADIE EST MORTELLE SI ELLE N’EST PAS SOIGNÉE.

TOUT LE VILLAGE DOIT PARTICIPER EN NETTOYANT AUTOUR DU PIÈGE ET EN COMPTANT LES MOUCHES CAPTUREES CHAQUE MOIS DANS LE SAC PLASTIQUE.

PLACER LE PIÈGE PARTOUT OÙ SONT LES MOUCHES TSÉ-TSÉ
Do not forget

Bioinformatics is not only for molecular data:

- Computer-assisted taxonomy

- Morphometrics
A recommendable strategy for the (many) labs that don’t have big technologies
The remora’s strategy
What may have « weak » teams to sell to big sharks?

Biodiversity
Data
Strain banks
Access to the field
Field and clinical expertise
Other complementary expertise: population genetics, etc
Little remoras, don’t sell yourself for nothing:

Data mining = Gold mining
Tasks of bioinformatics

Either: look for individual relevant genes (susceptibility to disease, drug resistance)

Or (better): draw a comprehensive survey of the whole genetic variability of the species under study
Phylogenetic Character Mapping or PCM (Avise, 2006)

Assignment of relevant characters on the phylogenetic picture of the species
Traps
Bootstrap religion
Gene trees and species trees are not the same
Figure 23.5 : Arbre phylogénétique de 64 allèles du locus DQB1 chez 10 espèces de primates. L’arbre a été obtenu par la méthode du neighbor-joining sur des distances évaluées par la méthode de Kimura sur les 270 nucléotides de l’exon 2. Hs, homme ; Pp et Pt, chimpanzés ; Gg, gorille ; Or, orang-outan ; Hl, gibbon ; Ma, Mf, Mm et Ph, macaques et hamadryas. (D’après Ayala & Escalante, 1996.)
Typologist approach

A major concern for sequencers
Typologism

The approach that considers that each species is well represented by an ideal "«type»" – the specimen used for the first description – and that all variability around this type is to be ignored
What are the limits of the entity under study?

What is a species?

What is a strain?
Recombination rate in pathogens: sexual vs clonal?

Highly relevant for data mining and phylogenetic character mapping
Recombining species

*Plasmodium falciparum*: highly recombining, although able of some clonal propagation

No linkage disequilibrium between characters: they are transmitted independently: no strain typing
Predominantly clonal species

*Trypanosoma cruzi*


Linkage disequilibrium
(nonrandom association)

Between genetic characters

Between genetic and phenotypic characters
Reticulate evolution in pathogens

In most if not all pathogens, there is a combination of clonal propagation and genetic exchange

To be taken into account in phylogenetic studies and Phylogenetic Character Mapping
Relevance of population genetics
Challenge: population genomics

The ultimate cure against typologism
Relevant megaprogrammes in human genetics

Human diversity genome project (HDGP)

HapMap project
The HapMap Gold Rush: Researchers Mine a Rich Deposit

Scientists are parsing a raft of new data on genetic variation for clues to disease and evolution

CAMBRIDGE, MASSACHUSETTS—For a conference on the next generation in genomics, the setting was just right: a pristine auditorium in a gleaming new building near the Massachusetts Institute of Technology (MIT). More than 200 people gathered here at the Broad Institute earlier this month to discuss the HapMap, a database cataloging human genetic variation. Begun in 2002, the map has been assembled primarily to boost the analysis of inheritance using pieces of DNA that are often transmitted as intact blocks.

Nearly complete, the HapMap is now being tested for a number of uses: to find genetic variants behind common diseases, to examine the genome’s architecture, and to study natural selection. The human HapMap has even inspired the launch of a parallel effort for *Plasmodium falciparum*, the deadly malaria parasite.

Five countries kicked in about $138 million to fund the human project, properly known as the International HapMap Project. One early challenge was to allow for the fact that haplotypes differ somewhat across populations. To include a sweep of variants, the HapMap gathered DNA from 270 individuals of African, Japanese, Chinese, and European ancestry.
Is DNA sequence so relevant?
Patchwork people

For years it was assumed that tiny differences in our genetic make-up gave us our individual traits. Now it seems that those characteristics are caused by rearrangements of large chunks of our DNA — variations that could be the key to understanding disease. Erika Check investigates.
The abyss between genotype and phenotype
Integrated approach
Impact, on the transmission and severity of infectious diseases, of the genetic variability of

The host

The pathogen

The vector
A unique biological phenomenon (coevolution)
Durty propaganda:

How to circulate bioinformatics and other advanced technologies?
International congresses
Molecular Epidemiology and
Evolutionary Genetics of
Infectious Diseases
(MEEGID)
I: CDC Atlanta 1996
II: Montpellier 1997
III: Rio de Janeiro 1998
IV: Dakar 1999
V: Hyderabad 2000
VI: Pasteur Institute Paris 2002
VII: Valencia 2004
VIII: Bangkok 2006
IX: Nairobi 2008
Meeting Announcement

9th International Congress on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases (MEEGID IX)
(coorganized by CDC, USA, and IRD, Bangkok)

NAIROBI, KENYA, 30th October-1st November 2008
Infection, Genetics and Evolution
(Elsevier)
http://www.elsevier.com/locate/meegid
Started 2001
30th issue presently being compiled
6 issues per year
2005 impact factor evaluated by Elsevier: 3.554
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Source: 2005 Journal Citation Reports, ScienceEdition ©ThomsonScientific, 2006 and data from Web of Science®, as well as other databases.

<sup>a</sup> To all papers ever published.
Genetics and Evolution in the broad sense: includes population genetics and biology, evolution, phylogeny, genomics, proteomics, **bioinformatics**

All infectious models: bacteria, viruses, parasites, fungi. Human, animal, plant diseases
South-South Collaboration

Latin America-Africa-Thailand Initiative for Scientific Partnership (LAATISP)

Under the auspices of
TICA (Thailand International Cooperation Agency)
IRD
French Ministry of Foreign Affairs
French Agency for Development
The « World CDC Belt »
Origin: The « Euro-CDC » Proposal


- US CDC
- European CDC considerably magnified, involving former USSR and Turkey.
- Asean CDC, involving all countries of this region of the World
- A Latin American CDC
- An African CDC +++
All centres should feature:

- Triple mission: advanced research, surveillance and control, training
- Powerful technologies
- Multidisciplinary approaches: advanced technologies, traditional know-hows, field research, human science
- Large, multinational teams
Utopia: what has not happened yet (the author).
Mankind beauty is diversity