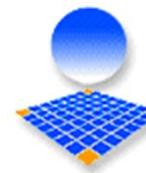




# Recherche d'ARNs de fusion dans les données de RNA-seq de patients atteints de leucémies myéloïdes. Applications et perspectives pour le diagnostic, pronostic et suivi des patients



GSO OCTOBRE 2014

17 octobre 2014

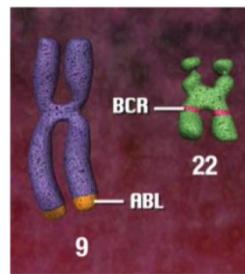
« Transcriptomics, bioinformatics & myeloid leukemias »

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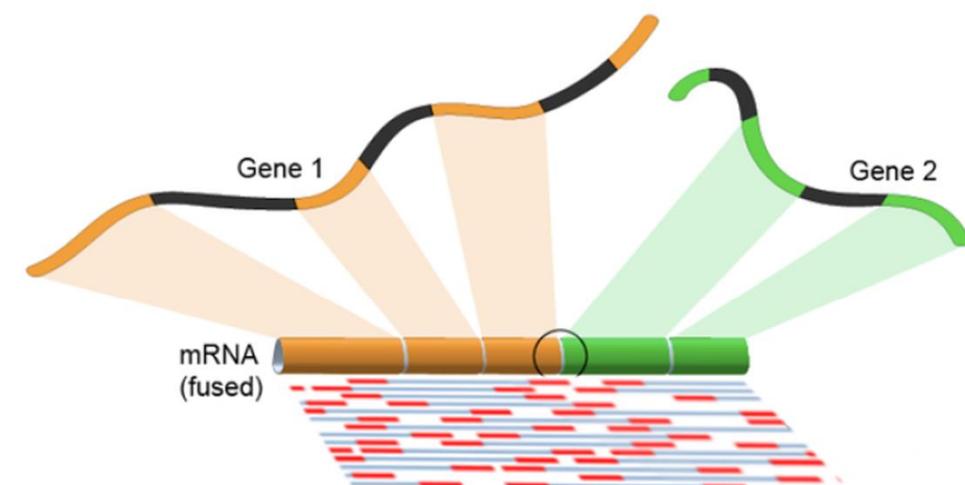
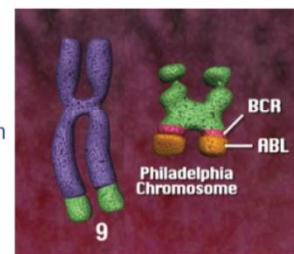
## *Detection of fusion RNA from RNA-seq in myeloid leukemia*

**Fusion RNA :** abnormal messenger produced in cancer cells resulting from chromosome translocation or « fused » RNAs

Leukemia with gene fusion



translocation



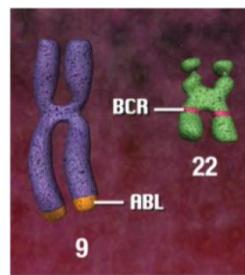
*A tool for diagnosis, prognosis, disease follow-up*

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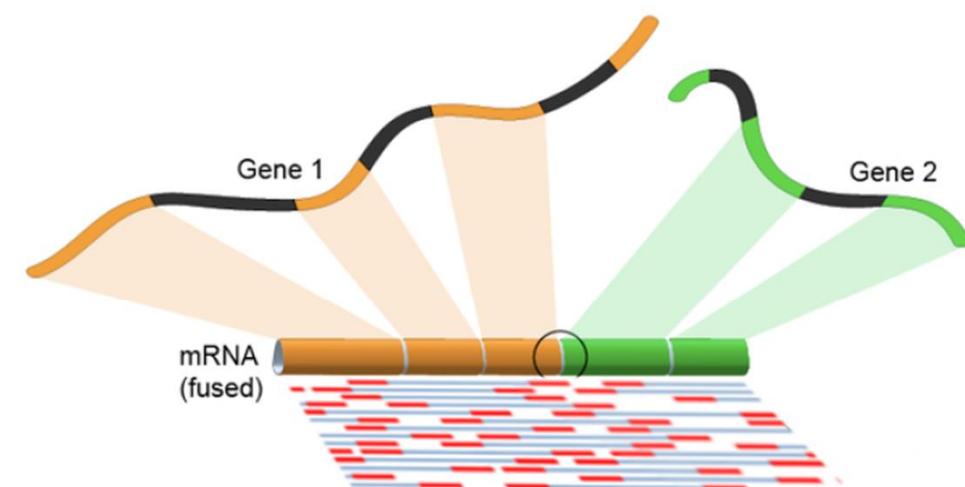
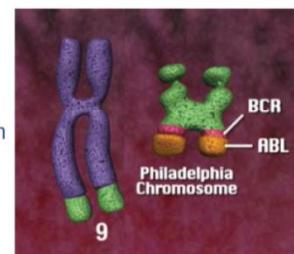
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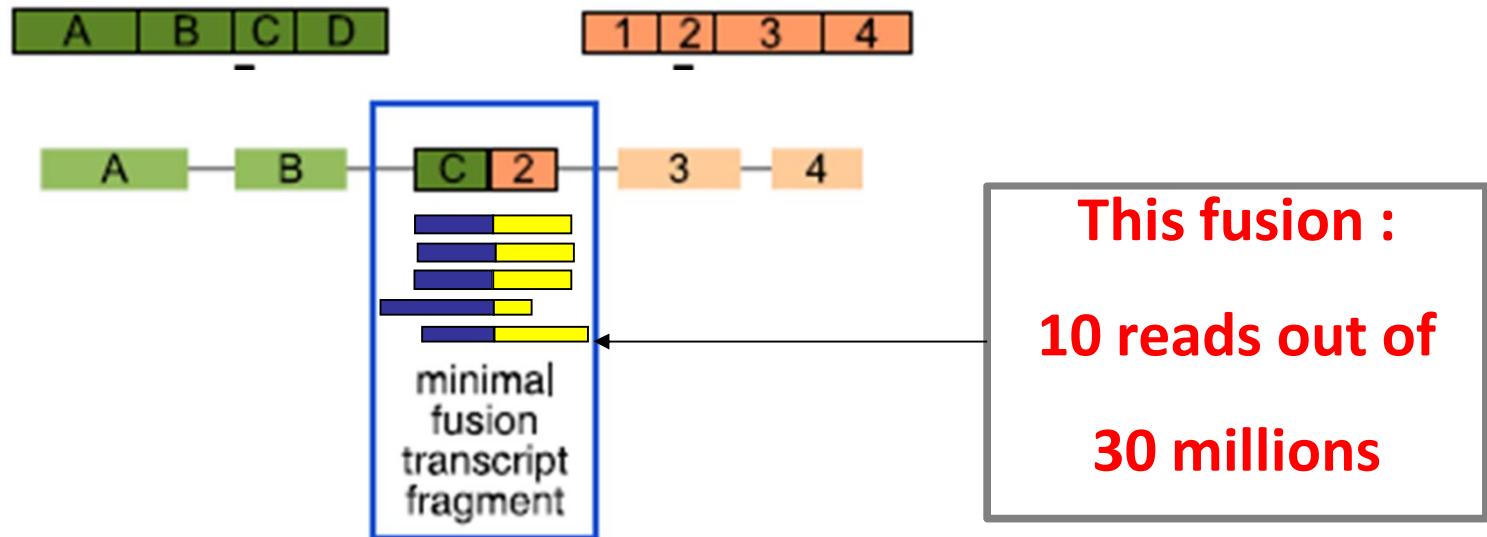
translocation



*« A methodological challenge »*

## The problem

- 1/ To find rare specific sequences in a huge read collection of RNA-seq  
Read (10 reads / $30 \cdot 10^6$ )

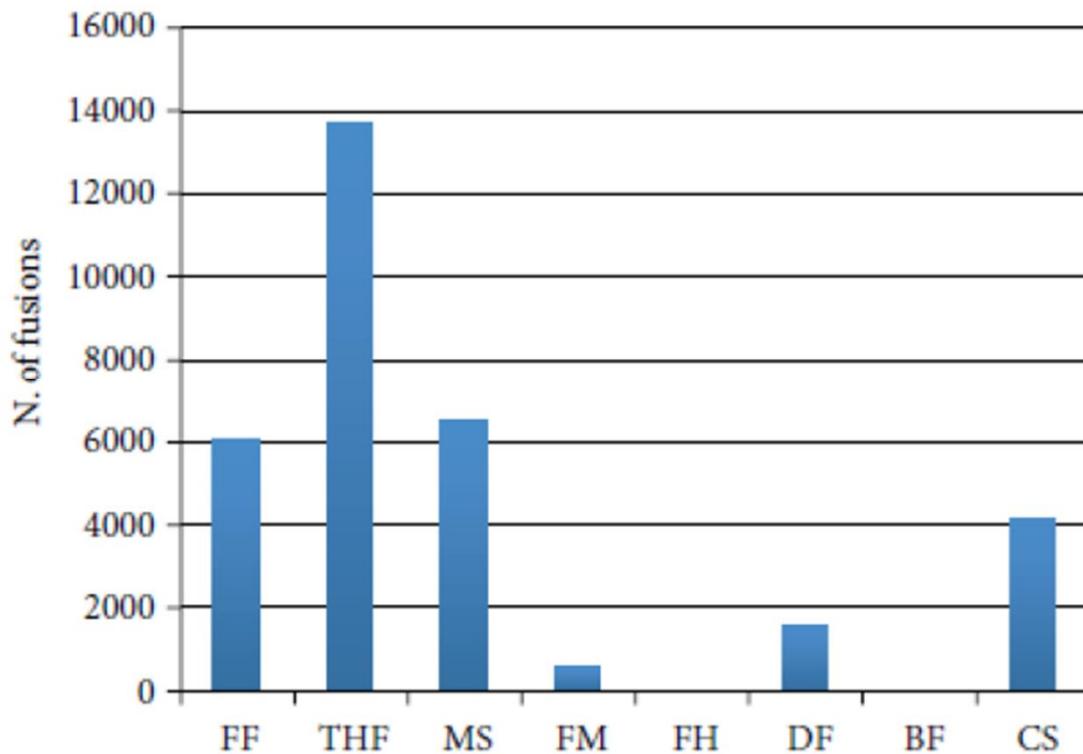


- 2/ To distinguish all biological events
- 3/ To distinguish biological events from technical artefacts

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## The problem

Differences between bioinformatics tools

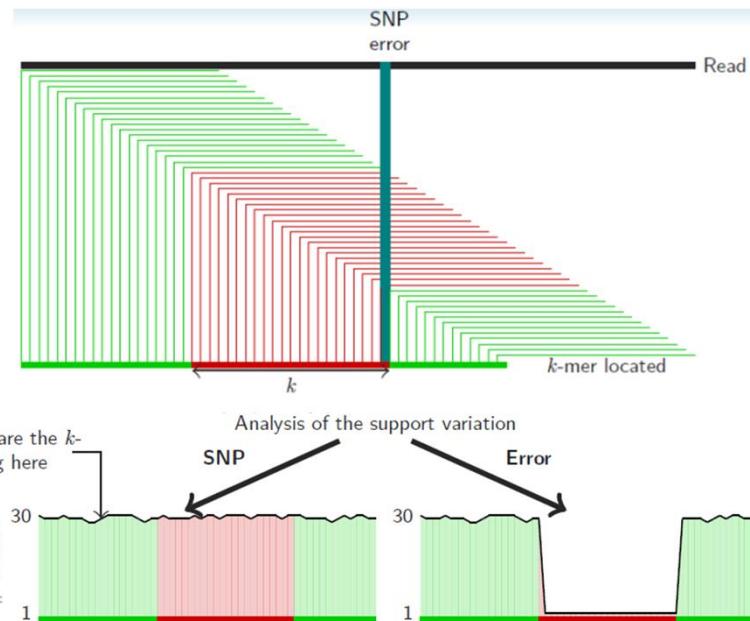


*State-of-the-art fusion-finder algorithms sensitivity and specificity.*  
*BioMed research international, 2013*



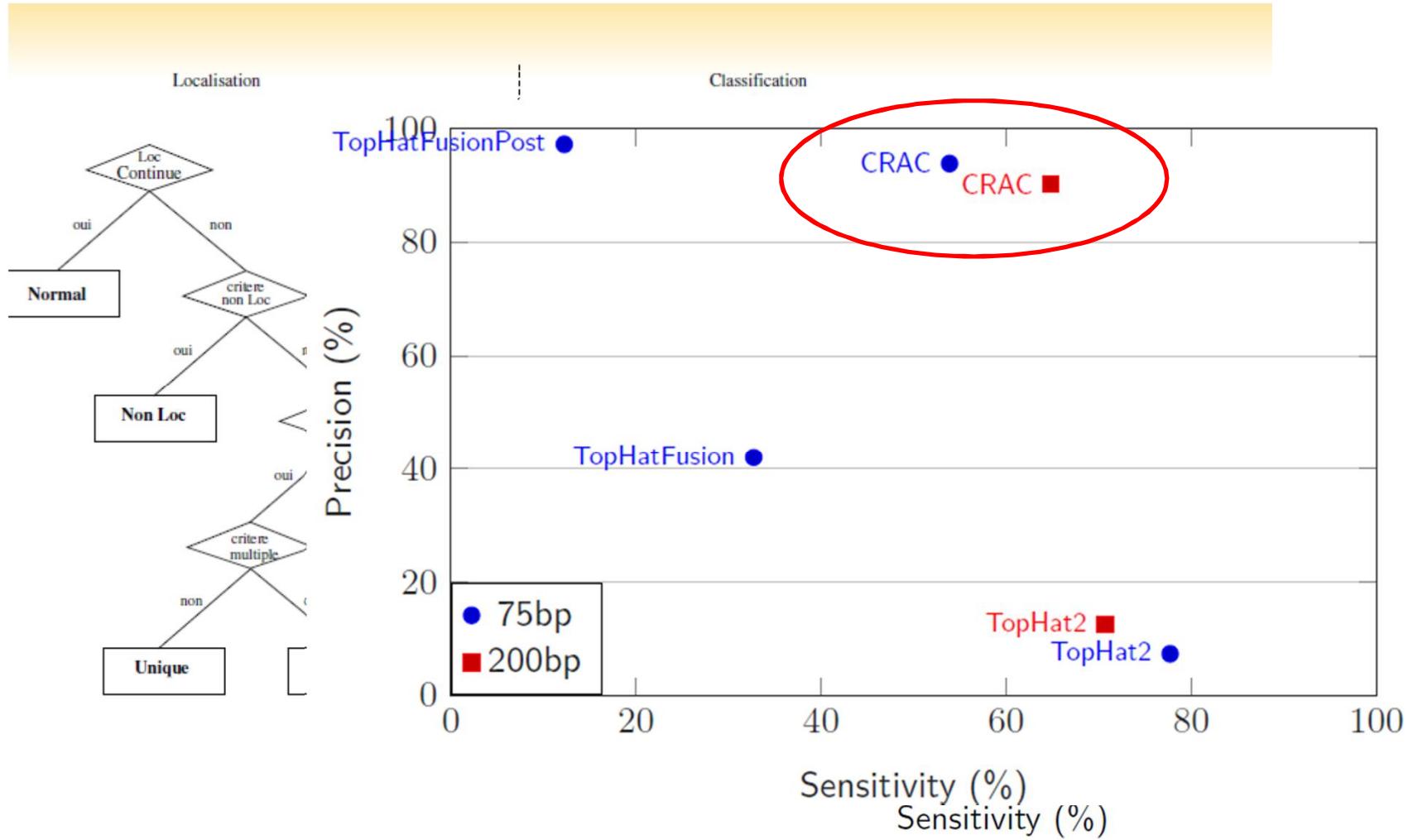
<http://crac.gforge.inria.fr>

The screenshot shows the CRAC software interface. At the top, there is a navigation bar with links: News, What is it?, Download, Getting started (which is highlighted in blue), Results, Manual, and FAQ. Below the navigation bar, there are two main sections: "Getting started" and "Installing CRAC". The "Getting started" section contains text about installing CRAC and provides links for "From the deb package" and "Latest version" (which can be downloaded here). The "Installing CRAC" section also has a "From the deb package" link. At the bottom of the page, there is a section titled "Software" which includes the title "CRAC: an integrated approach to the analysis of RNA-seq reads", authors "Nicolas Philippe, Mikaël Salson, Thérèse Combes and Eric Rivals", and publication details: "Genome Biology 2013, 14:R30 doi:10.1186/gb-2013-14-3-r30 Published: 28 March 2013". A note at the bottom says "For all author emails, please log on."



*CRAC an open source software, provides a standard File format (SAM mapping file)*

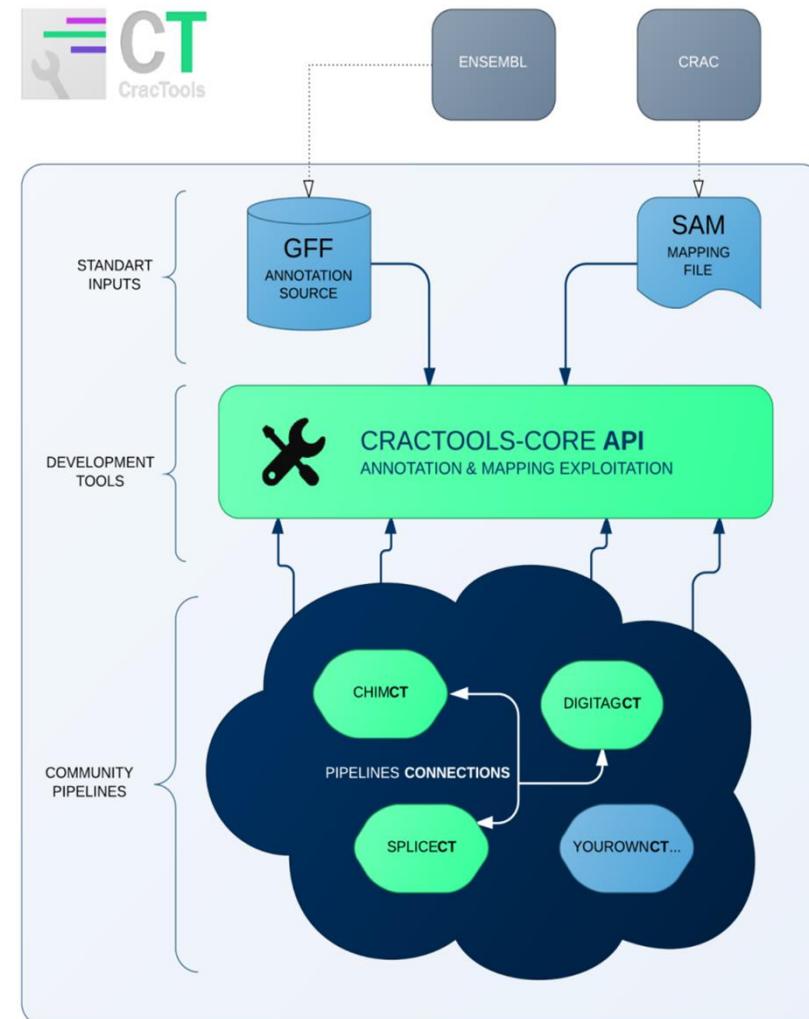
# A global view of all the biological causes in RNA-seq



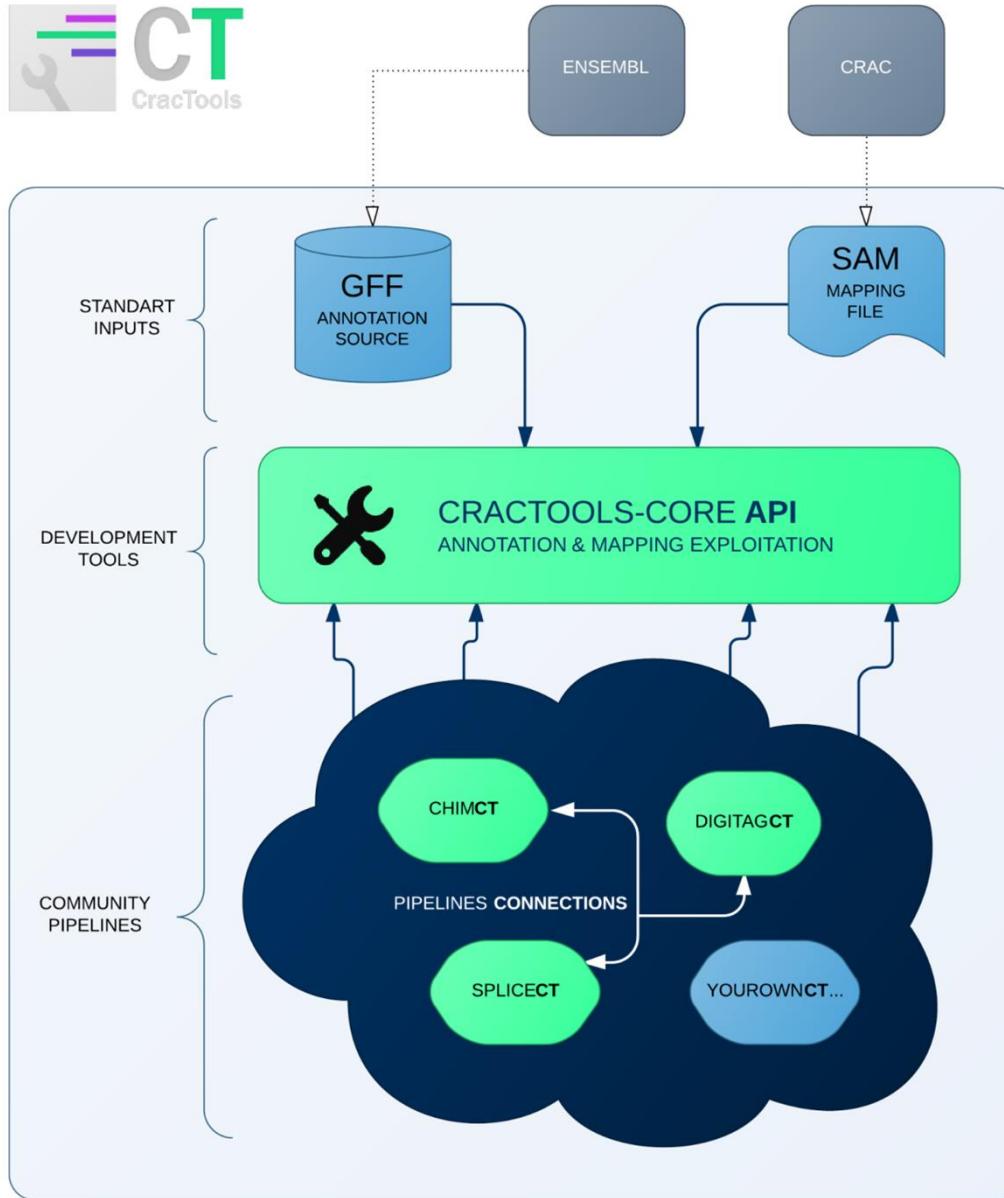


<http://crac.gforge.inria.fr>

The screenshot shows the "Getting started" section with a "Latest version" callout and the "Installing CRAC" section with "From the deb package". Below is a software citation for "CRAC: an integrated approach to the analysis of RNA-seq reads" by Nicolas Philippe, Mikaël Salson, Thérèse Combes and Eric Rivals, published in Genome Biology 2013, 14:R30, doi:10.1186/gb-2013-14-3-r30, published on 28 March 2013.



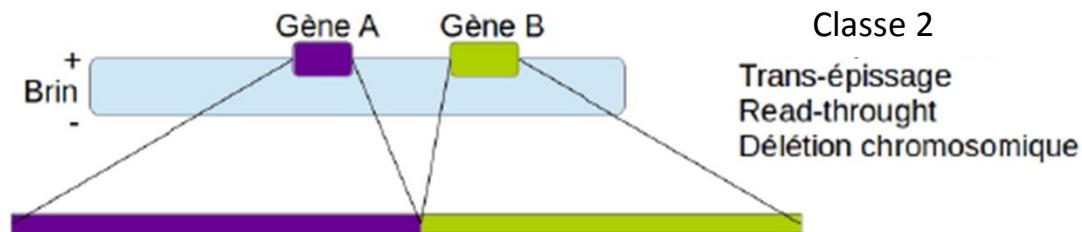
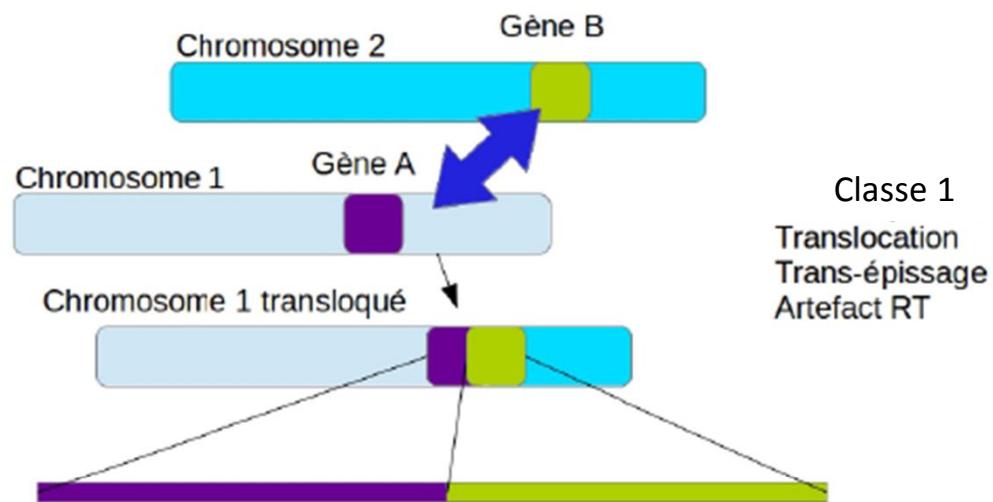
*CracTools : modules to build post-treatment workflow for integrative biology »*



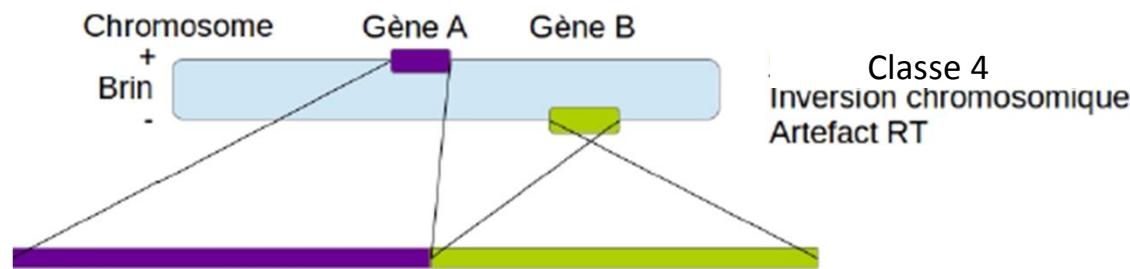
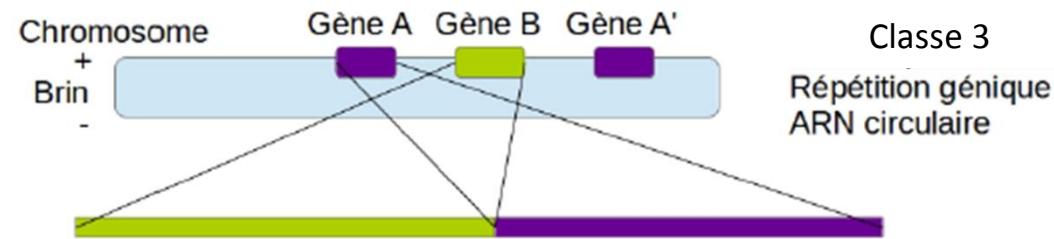
## ➤ chimCT

*Detecting fusion RNA (or chimeric RNA) based on CRAC software*

## 4 Fusion RNA classes



## 4 Fusion RNA classes



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## « *from high through-put data to biology* »

Parmi les projets soumis dans le cadre de l'APP 2012 « Grands Projets de Séquençage », le Comité Scientifique de France Génomique a retenu les projets suivants :			
Genomics in hematological	Génétique Humaine	Thérèse COMMES	CHU Montpellier - Université Montpellier 2



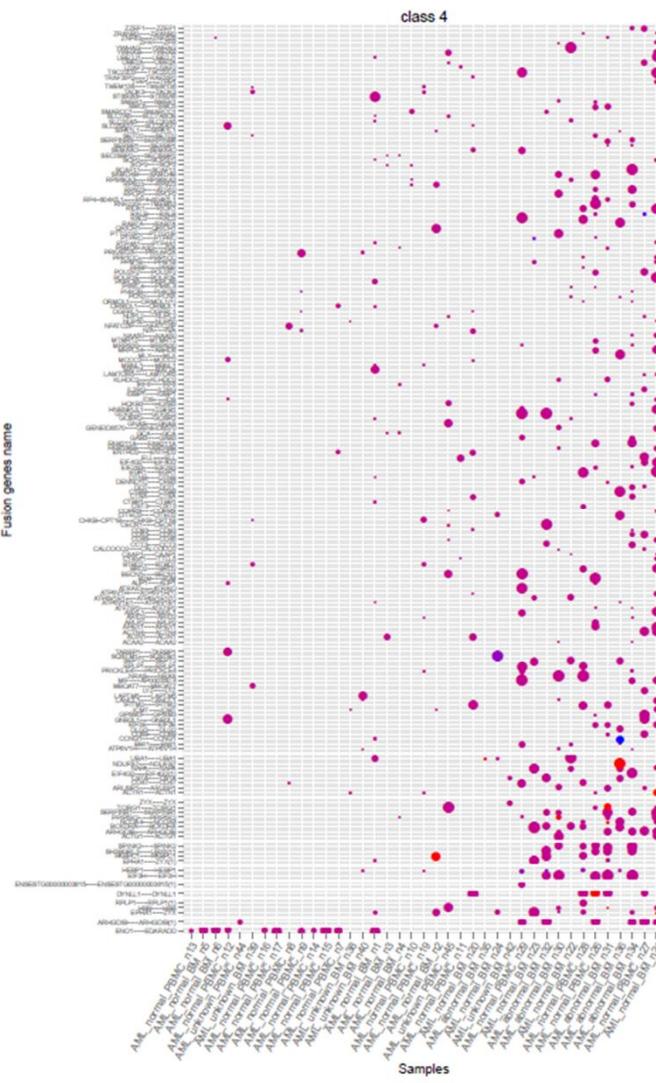
*Collaborative data acquisition (45 AML-RNA-seq)*  
*Dr Wang- University of Nebraska medical center*

## International network of cancer genome projects

The International Cancer Genome Consortium\*



The International Cancer Genome Consortium (ICGC) was launched to coordinate large-scale cancer genome studies in tumours from 50 different cancer types and/or subtypes that are of clinical and societal importance across the globe. Systematic studies of more than 25,000 cancer genomes at the genomic, epigenomic and transcriptomic levels will reveal the repertoire of oncogenic mutations, uncover traces of the mutagenic influences, define clinically relevant subtypes for prognosis and therapeutic management, and enable the development of new cancer therapies.

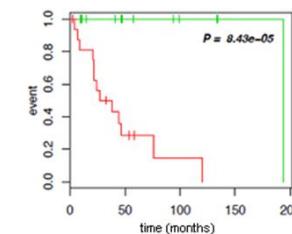
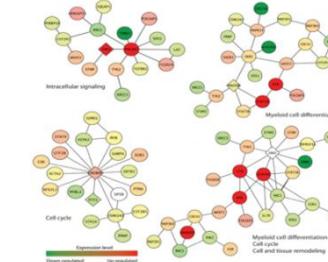


## 45 RNA-seq from AML patients

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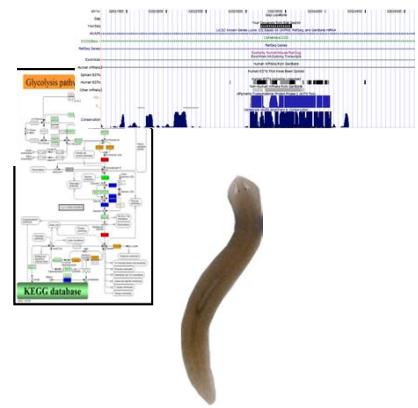
# Perspectives

- Global genomic studies
  - Rank/Score .....
  - Fonctionnal Gene ontology (gene networks),  
Comparison with normal tissues (classe 2)
- Clinical studies
  - Comparison with survival, response to treatment, comparison  
with gene expression profiles of known genes
- Transcriptome and peptidome profiling  
for Biomarkers design and large scale studies
- SATT. Project



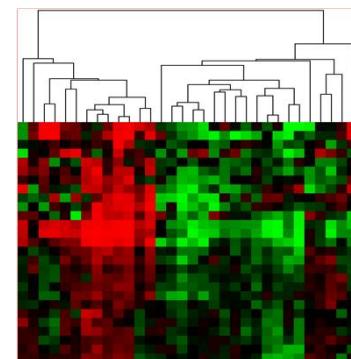
## Notre groupe

J Adoux  
A Boureux  
M Galloni  
N Philippe  
F Rufflé



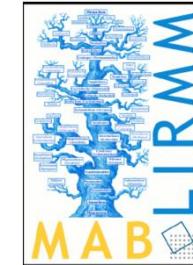
## CHU\_Nîmes/IGR

E Jourdan  
John Devos  
E Solary



## MAB

E Rivals  
A Mancheron  
L Brehelin



## LILF

M Salson



## Skuldtech

D Piquemal  
F Pierrat



