

# Graphes et Bioinfos

GdR ROD & GdR BIM



# Axe CAGDO - GdR ROD (Recherche Opérationnelle & Décision)

Complexité, Approximation et Graphes pour la Décision et l'Optimisation

**Animateur.rice.s :** E. Bampis (SU/LIP6), C. Bentz (CNAM/CEDRIC), B. Escoffier (SU/LIP6), V. Mitsou (UP/IRIF), A. Newman (CNRS/G-SCOP)

Actions et manifestations scientifiques

1. Animation GT AGAPE (Algorithmique à GARantie de PErformance) : complexité (classique ou paramétrée), algorithmes approchés (polynomiaux ou faiblement exponentiels, voire paramétrés), algorithmes exacts exponentiels, algorithmique en ligne
2. Sessions ROADEF annuelle (conférence française de RO & AD)
3. Interaction avec des GT d'autres GDR du CNRS : soutien financier et animation scientifique dans le cadre des JGA (« Journées Graphes & Algos. », organisées tous les ans par le GT Graphes du GDR IM) ...  
... et autres journées thématiques (ponctuelles ou non) → Nous y voici !

# GT MASIM - GdR BIM (BioInformatique Moléculaire)

Méthodes Algorithmiques pour les Structures et Interactions des Macromolécules

**Animateurs :** Frédéric Cazals (Inria Sophia), Yann Ponty (CNRS/LIX, Polytechnique)

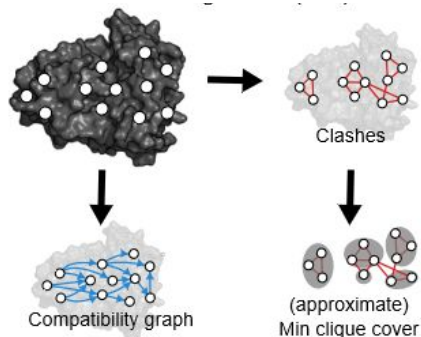
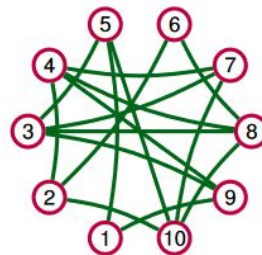
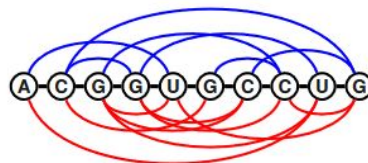
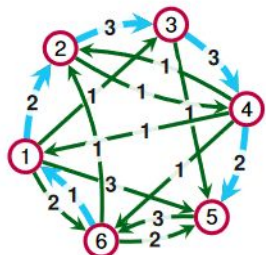
Actions et rencontres autour des méthodes bioinfo en Biologie Structurale :

- Ecole thématique annuelle AlgoSB
- Satellites annuels de JOBIM
- Évènements thématiques ciblés  
(2022 : ML, Sampling)
- Session aux rencontres bisannuelles du GdR BIM

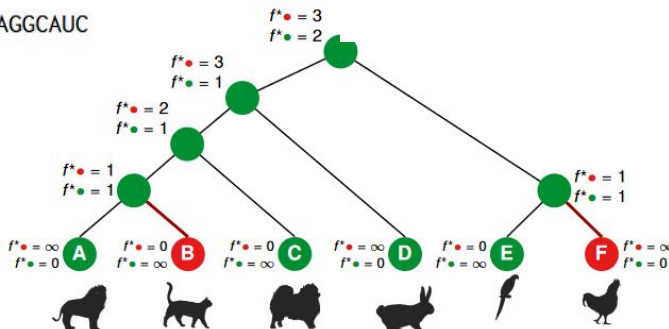
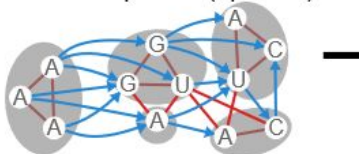


## NGS Reads

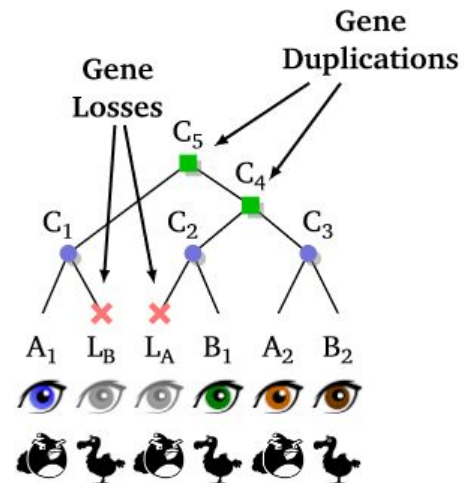
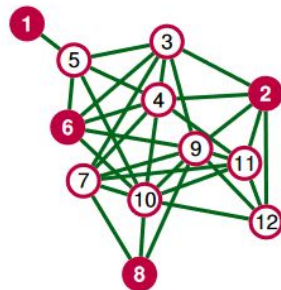
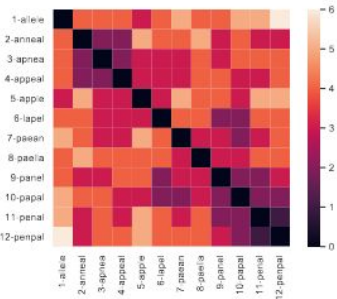
- 1: ACAU
- 2: AUAG
- 3: UAGGC
- 4: GGCA
- 5: CAUC
- 6: AUCA



+ ssRNA sequence (optional)

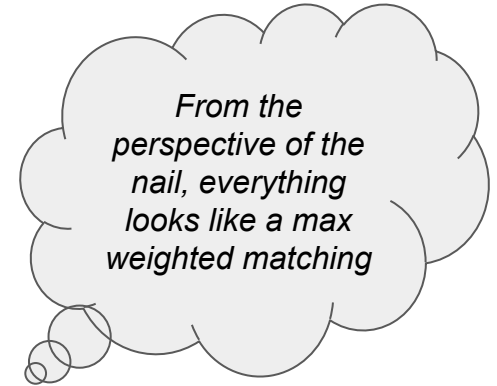


- 1-allele
- 2-anneal
- 3-apnea
- 4-appel
- 5-apple
- 6-lapel
- 7-paeen
- 8-paella
- 9-panel
- 10-papal
- 11-penal
- 12-penpa



# Discrete algorithms and Bioinfo: Love at first sight!

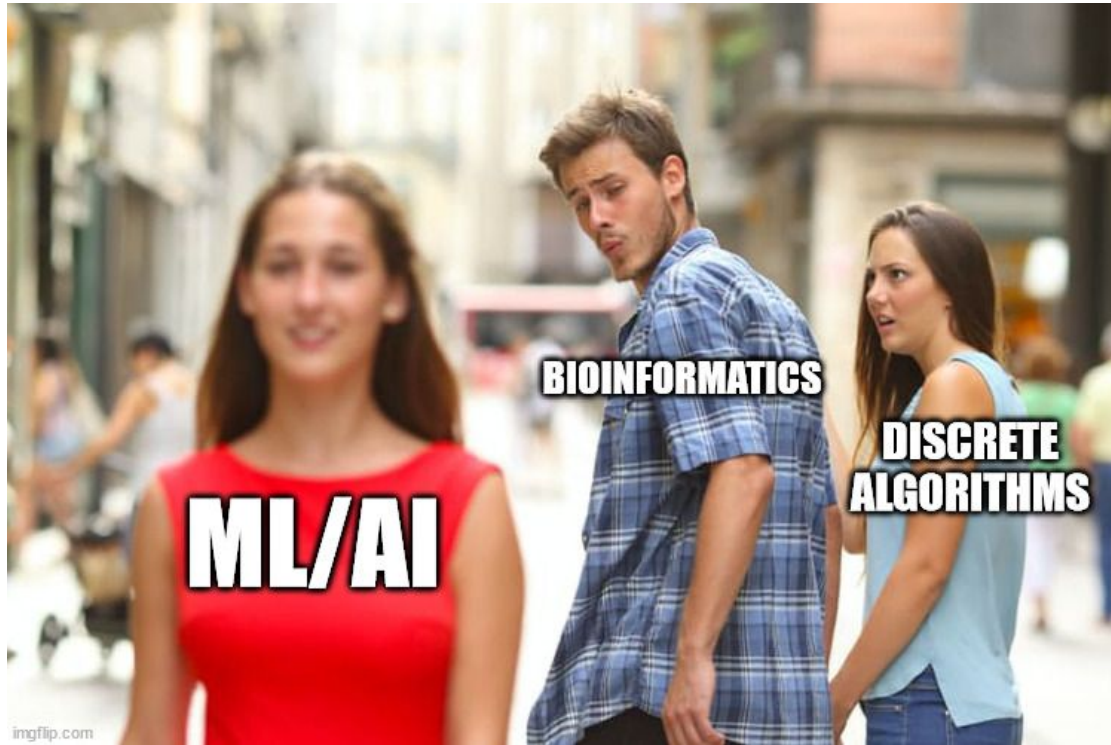
- Pairwise sequence alignment
- Molecular folding under discrete conformational spaces
- Sequence assembly
- Phylogenetic trees/networks
- Subgraph matching in regulatory/metabolic networks
- Pangenome graphs
- ...



Takeaways from three decades of Bioinformatics

- Practically-relevant graph modeling is a (dark) art
- Walk the fine line between **realistic** and **tractable**
- Informed by state-of-the-art algos and current biology

# A stress-tested relationship



# Goal of this meeting

- ▶ Spread the word on mature advanced algorithmic techniques
- ▶ Inspire new developments on Bioinfo specific problems (counting)
- ▶ Foster new conversations between RO/Algo folks and bioinfo nerds
- ▶ Provide examples and best practices in graph modeling for life sciences

Dynamic  
Programming



Probabilistic  
data structures



Mathematical  
programming



Small exponential  
algorithms



Parameterized  
complexity



# Program

9:30-10:15 - Accueil (café)

10:15-10:30 - Cédric Bentz – Yann Ponty - *Accueil et introduction des journées*

10:30-11:15 - **Laurent Bulteau**, LIGM (tutorial)

*Parameterized Complexity in Bioinformatics*

11h15-12:00 - **Karel Brinda**, INRIA/IRISA

*K-mers and their graphs in computational biology*

12:00-13:45 - Lunch break

13:45-14:30 - **Alain Denise**, LISN

*Search and analysis of recurrent patterns in 3D RNA structures and graph problems*

14:30-15:15 - **Geraldine Jean**, LS2N

*Genome rearrangements on both gene order and intergenic regions*

15:15-15:35 - Pause café

15:35-16:20 - **Arnaud Mary**, LBBE

*Enumeration algorithms in bioinformatics*

16:20-16:30 - Cédric Bentz – Yann Ponty - *Mot de la fin*