VARNA: Recent features and alignement related stuffs. . .

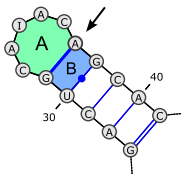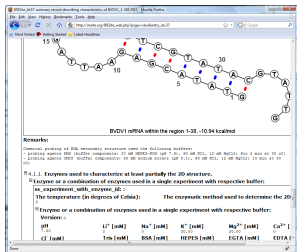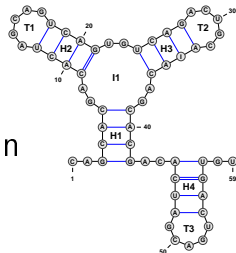Yann Ponty[⋆]   Alain Denise[†]   Raphaël Champeimont[†]   Hayet Bezzeghoud[†]

[†] Université Paris Sud/CNRS/INRIA AMIB – France

[⋆] École Polytechnique/CNRS/INRIA AMIB – France

November 14, 2010

Initial goal(s): To draw RNA secondary structure

1. Webservers companion
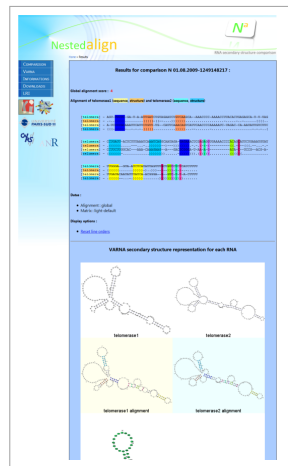2. Interactive visualization
3. Publication-ready drawings production

IRESSite DB
`http://iresite.org/`

Varna, Bulgaria

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Main features

- Client-side
- Cross-platform (Java)
- No external dependencies
- Fully customizable
- Self-adapting to available space
- Accepts most formats (RNAML, CT...)
- Four(+) layout algorithms
- Vector/bitmap output formats
- Standalone editor
- Supports drag and drop
- Command-line version
- Basic support for Pseudonoeuds.
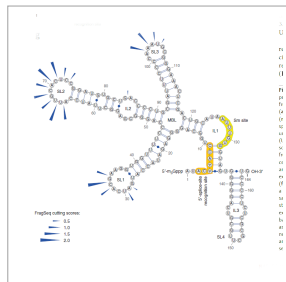- 3^{ary} interactions ...

Webserver NestedAlign
`http://nestedalign.lri.fr`

- Session save/restore
  $\rightarrow$ Snapshots within GUI

- Better selection mechanisms

- PseudoBase pseudoknots support
  Example: (((...[[[...)))...]]]

- Print structure feature

- Color maps

- Bases/Basepairs/regions annotations...

- Interactive JS library

▶ Démo site VARNA

Underwood *et al*, Nat. Meth. 2010

Halvorsen *et al*, Plos Gen. 2010

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Honestly, RNA alignments are mainly about sequences (so far. . .)

Paradigm: One structure $\Rightarrow$ Many sequences!
Problem: Structural variability leads to horizontal expansion.

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But 2^{ary} structure visualization can complement alignments.

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Toy example: Two alternative structures:

- Similarities should be self-evident
  - Same annotation/color codes
  - Common parts should be superimposed (easy algorithmically!)
- Differences should *pop up* (Animations can help)
- Alt.: Superstructure (tree alignment *à la* RNAForester)
- Pattern-based drawing based on coarse-grain layouts (in progress. . .)

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VARNA@ROC

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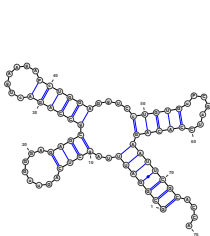Toy example: Two alternative structures:
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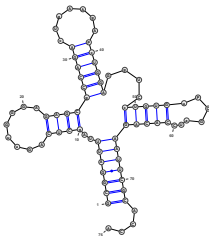
Soon in VARNA...

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  For new motifs and families of RNA, automated layouts are ok.
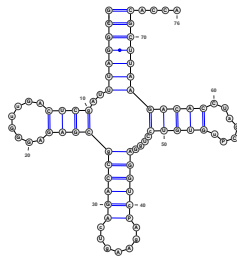 But for *older* classes, people are used to see things in a certain way.

Radiate algorithm   NAView algorithm   Standard view

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  But for *older* classes, people are used to see things in a certain way.
  - Draw layout at a coarse-grain level (template)
  - Use tree alignment algorithm to map specific RNA sec. str. to template elements (Resilience to structural variations).
  - Reconstruct layout based on mapping (technically tricky!)

  Bonus: Template discriminated automatically from alignment score.
  Dream: A distributed database of templates???
- Automated visualization of multi-strand 3^{ary} motifs

Many thanks to

Collaborators for hard work

Kévin Darty   Raphaël Champeimont

Alain Denise   Hayet Bezzeghoud

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VARNA is available at `http://varna.lri.fr`

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