# Searching for non-coding RNAs and predicting their structure Young Investigators Day 2011

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### non-coding RNA search



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## an improved Infernal grammar

- three meaningful semantics: *alignment*, trace, and structural
- prove alignment grammar unambiguous
- trace (and structural) semantics more likely to capture remote family members
- higher sensitivity!

alignment 1 ACAGGGGCAG	alignment 2 ACAGGGGCAG	trace ACA[GGGG]CAG

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## discrimininatory power of RNA family models



- at most one model should produce a hit for any given genome position
- compare *family models* with each other
- find weakly separated models
- higher specificity

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# Example: A Clan of High-Scoring Families



### blue: clan members

- red: highest scoring non-member
- red scores: above trusted cutoff

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### extended RNA secondary structures



- canonical Watson-Crick base pairs are the most common pairs
- virtually every RNA structure contains non-canonical nucleotide pairs (Eric Westhof)
- non-canonical 2–1 pairings occur as well

### parsing 2-diagrams



... and each pair can be non-canonical!

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### current problems & outlook

we are working on:

- full grammar with prior/posterior models based on 2-diagrams
- large-scale training (RNAstrand, PDB)
- large-scale convex optimization ( $\approx \mathbb{R}^{100000}$ )
- derived algorithms

and later this year:

- improved index structures for genome-scale (ncRNA) scans
- *switchable* grammars for scanning algorithms (trace grammar)

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