Weighted word collector

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RNA Structure

RNA = Sequence over $\{A, C, G, U\}$. RNA folds, establishing hydrogen bonds. Such base-pairs stabilize structure. Free-energy E_S assigned to each structure S.



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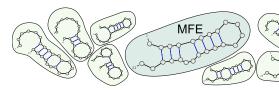
Simplified energy model [Nussinov-Jacobson, 78]
 Only non-crossing base-pairs allowed → Secondary Structures
 Free-Energy = -# Base-pairs

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• Boltzmann equilibrium [McCaskill, 90] Any structure S exists w.p. $p_S \propto e^{-\#E_S/RT}$.

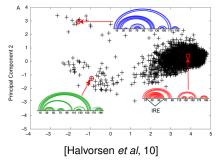


RNA *in silico* search: sequence \rightarrow functional secondary structure

MFE: Functional sec. str. = Most probable (aka min. free-energy) structure
 But approach lacks robustness to intrinsically uncertain energy models.

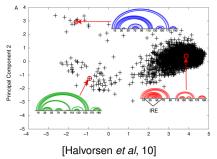
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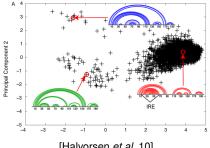


(Meta)-Algorithm:

- **1** Draw k sec. str. at random at Boltzmann equilibrium (\neq Boltzmann sampling)
- Cluster samples using your favorite machine learning method
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[Halvorsen et al, 10]

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- \bigcirc Draw k sec. str. at random at Boltzmann equilibrium (\neq Boltzmann sampling)
- Cluster samples using your favorite machine learning method
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 - ⇒ This simple idea greatly improved specificity of predictions.

A closer look at the (meta)-algorithm:

• Draw *k* sec. str. at random (with replacement!) in the Boltzmann distribution Redundancy is uninformative, one should aim for *k* distinct secondary structures.

Which additional cost is induced by the redundant generation?

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Coupon collector problem!











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$$E[C_m] = 1 + \tfrac{m}{m-1} + \tfrac{m}{m-2} + \ldots + \tfrac{m}{m-k} + \ldots = m \cdot \mathcal{H}_m \underset{m \to \infty}{\sim} m \ln m.$$

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$$E[C_m] = \int_0^\infty \left(1 - \prod_{i=1}^m \left(1 - e^{-p_i t}\right)\right) dt.$$

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(i) [David-Barton,62]
$$p_i = \frac{2i}{m(m+1)} \Rightarrow E[C_m] \underset{m \to \infty}{\sim} \left(\frac{2\pi}{\sqrt{3}} - 3\right) \cdot m \cdot (m+1).$$

(ii) [Hildebrand,93]
$$p_i = \frac{1}{iH_m} \Rightarrow E[C_m] \underset{m \to \infty}{\sim} m \cdot H_m \cdot \log m.$$

A more general result

• Distribution defined by a sequence of positive numbers $\{a_1,...,a_m\}$:

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If $f(i) := 1/a_i$ satisfies:

$$\textit{(i)} \ f(x) \nearrow \infty, \qquad \textit{(ii)} \ \frac{f'(x)}{f(x)} \searrow, \qquad \textit{and} \qquad \textit{(iii)} \ \frac{f''(x)/f'(x)}{(f'(x)/f(x))\log(f'(x)/f)(x)} \to 0,$$

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What about sequences whose weights appear with multiplicities? (e.g. unbounded #occurrences of some a_i as $m \to \infty$)

Word collector?

Random generation of words

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+
Coupon Collector

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Which probability distribution on words?

Definition (Weighted language)

- i \mathcal{L} is a language over $\Sigma = (a_1, ..., a_k)$, and \mathcal{L}_n its restriction to words of length n.
- ii Weight of a letter $a_i \to \pi_{a_i} \in \mathbb{R}^+$.
- iii Weight of a word $\omega \in \mathcal{L}_n \to \pi(\omega) = \prod_{a \in \omega} \pi_a$
- iv Weighted probability distribution, defined on \mathcal{L}_n by:

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Remark: Words having equal composition have equal probability:

$$\mathbb{P}[ababbabaaa] = \mathbb{P}[aababbbaaa] = \mathbb{P}[aaaaaabbbb] = \frac{\pi_a^6 \pi_b^4}{\mu_{10}}.$$

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Many coupons share equal weight, i.e. equal probability! \Rightarrow Large multiplicities \Rightarrow None of existing results applies...

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$$E[C_m] = \int_0^\infty \Phi(t) dt \qquad \text{with} \qquad \Phi(t) = 1 - \prod_{i=1}^m \left(1 - e^{-\rho_i t} \right).$$

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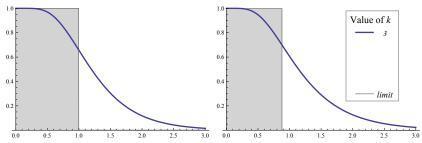
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Example: Plot of $\Psi(t)$ for uniform and weighted distributions on $\{a,b\}^k$, $(m=2^k)$.

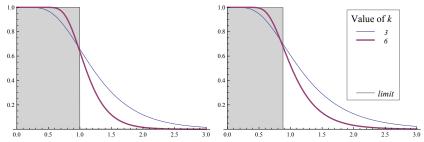


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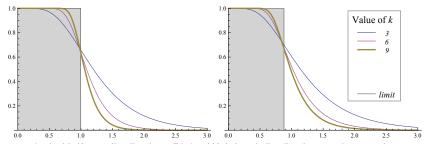


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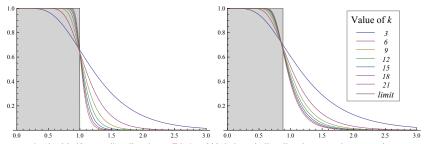


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Theorem (du Boisberranger-Gardy-P,2012)

If weight distribution satisfies hypotheses H1, H2 et H3, then

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Proposition (Waiting time – Full collection – Σ^*)

$$E[C_m] \sim \left\{ egin{array}{ll} \kappa_1 \cdot m^p \cdot \log\log m & \mbox{if } j=1, \\ \kappa_2 \cdot m^p \cdot \log m & \mbox{otherwise}. \end{array}
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where $p = \log_k(\pi_{a_1} + \cdots + \pi_{a_k}) > 1$.

Asymptotic waiting time differs from the uniform case.

Description: RNA sec. str. unambiguously generated by context-free grammar

$$S \to \left(\right. S_{\geq \theta} \left. \right) S \left. \right| \left. \bullet \right. S \left. \right| \varepsilon \qquad \text{ and } \qquad S_{\geq \theta} \to \left(\right. S_{\geq \theta} \left. \right) S \left. \right| \left. \bullet \right. S_{\geq \theta} \left. \right| \left. \bullet^{\theta} \right. .$$

where θ : minimal distance between matching parentheses ($\theta = 1$ or 3).

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Boltzmann probability distribution $\Rightarrow \pi_{\bullet} = 1$ and $\pi_{(} \times \pi_{)} = e^{1/RT} (\pi_{(} < \pi_{)}).$

... Verify Hypotheses H1, H2 and H3...

Properties:

- i Gen. fun. + Singularity analysis $\Rightarrow \mu_m \sim \kappa \cdot m \cdot (\log m)^{-3/2}$
- ii Smallest weight = Weight of unpaired structure $\bullet^n = 1$
- iii Dominating term for multiplicity growth: $g(m) \sim \log \log m$.

Description: RNA sec. str. unambiguously generated by context-free grammar

$$S o (S_{>\theta}) S \mid \bullet S \mid \varepsilon$$
 and $S_{>\theta} o (S_{>\theta}) S \mid \bullet S_{>\theta} \mid \bullet^{\theta}$.

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Proposition (Waiting time - Full collection - Boltzmann weighted Sec. Struct.)

$$E[C_m] \sim \kappa \cdot m^p \cdot (\log m)^{3p/2} \cdot \log \log m$$

where p > 1 depends on the dom. sing. of the cardinality and cumulated weight.

Again, asymptotic waiting time differs from the uniform case.

Corollary: On average, a sec. str. is generated $\Theta(m^{p-1}) = \mathcal{O}(\alpha^n)$ times, $\alpha > 1$.

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Thanks for listening Questions?

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