Prediction of Translation Initiation Sites in Prokaryotic Genomes with TICO

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Project TICO

TICO: A tool for improving predictions of prokaryotic translation initiation sites

Maike Tech, Nico Pfeifer, Burkhard Morgenstern und Peter Meinicke,
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Problems in prokaroptic gene prediction

- Annotation of translation starts is difficult
- Lage number of False Positives
- Insufficient results for *heterogeneous* genomes

Algorithm of TICO

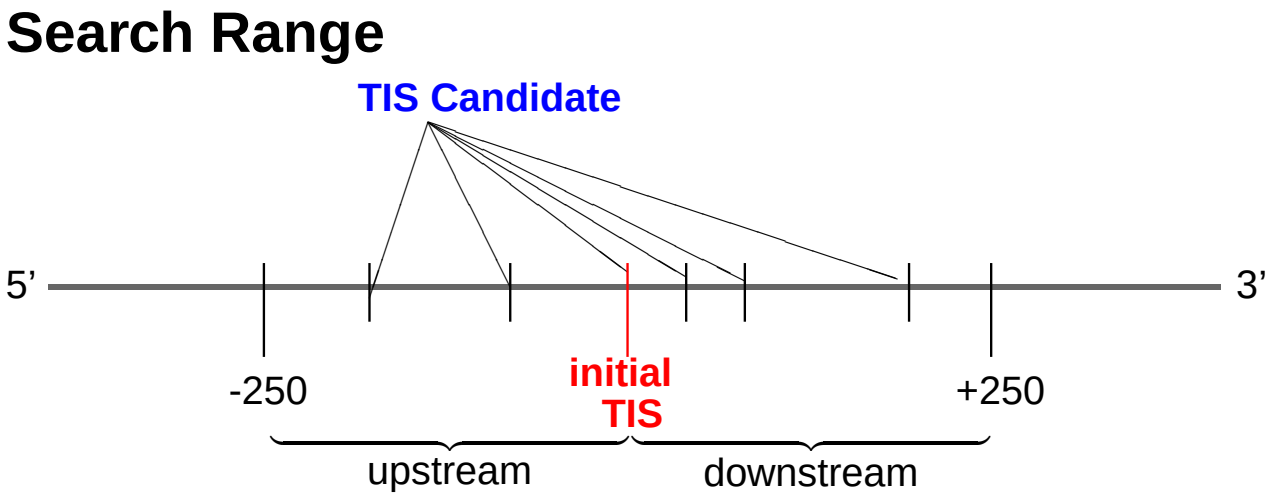
Initialization: Search for TIS candidates with the initial annotation.

Iterative Optimization:

1. Estimation of the smoothed trinucleotide probabilities for all candidates
2. Calculation of a Position Weight Matrix (PWM)
3. Calculation of a score for each candidate
4. Reallocation of the labels

Break condition: No alteration of the labels during classification.

TIS candidates



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Calculation of the PWM

The smoothing is realized as simple matrix product with a smoothing matix **S**.

$$\begin{aligned} \widetilde{\mathbf{P}} &= \mathbf{P} \cdot \mathbf{S} \\ \mathbf{W} &= \log \widetilde{\mathbf{P}}_{strong} - \log \widetilde{\mathbf{P}}_{weak} \end{aligned}$$

The Position Weight Matrix $\mathbf{W} \in \mathbb{R}^{4^K \times L}$ is calculated from the difference of the elementwise logarithms of the probabilities of *strong* candidates and *weak* candidates.

Calculation of the smoothing matrix

The smoothing matrix $\mathbf{S} \in \mathbb{R}^{L \times L}$ is calculated as

$$s_{ij} = \frac{e^{\left(-\frac{1}{2\sigma^2}(i-j)^2\right)}}{\sum_k e^{\left(-\frac{1}{2\sigma^2}(k-j)^2\right)}},$$

mit $i, j, k \in \{1, \ldots L\}$

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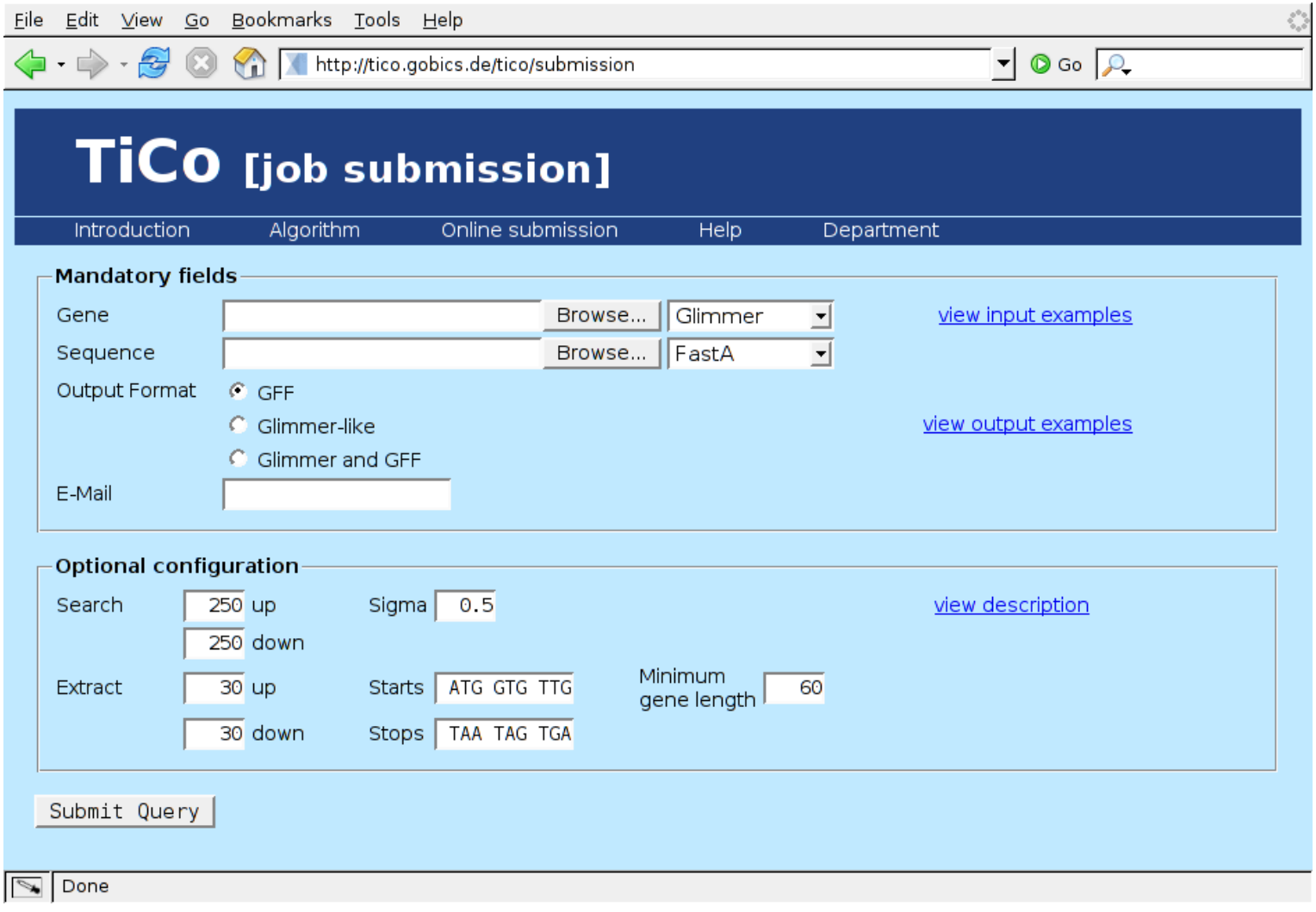
Web-Interface: http://tico.gobics.de/



Comparison of TICO's performance with other post processors

Data		GLIMMER	Post processors			
			GS-f.	MED	RBSf.	TICO
EcoGene	854	63.2	90.3	92.0	81.9	**94.3**
Bsub	1248	61.3	87.9	89.2	78.5	**89.4**
PseudoCAP	3281	57.8	83.6	3.6	67.7	**84.7**

Notation: % correct predicted TIS

Outlook TICO

- Evaluation of TIS predicition with TICO on *heterogeneous* genomes
- Reduce False Positives in predictions through the score calucated by TICO
- Add our own ORF-finder based on a clustering algorithm

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