IBIS PWM Submissions

# Regulatory Sequence Analysis Tools (RSAT)

## Team name

RSAT

## Primary Disciplines

A2G-PWM, G2A-PWM

## Models

k-mers; oligonucleotides; dyads; over-representation; position bias; PSSM; PCM; matrix clustering; optimisation; genetic algorithm

# Summary

We describe the procedure used to produce the Position-Weight Matrices (PSM) submitted by the RSAT team to the IBIS challenge 2024. Our approach combines the detection of exceptional k-mers in the training sequences, using these k-mers to build position-count matrices (PCM) based on the collection of binding sites in the training sequences, clustering of the resulting PCMs, and a new genetic algorithm-based optimisation approach to optimize the capability of these matrices to discriminate between a positive and a negative sequence set (measured by area under the ROC curve). .

# Implementation & Software

**{Please provide a brief list of software tools and frameworks used for your solution, e.g. 'CNN implementation: PyTorch'. You are very welcome to include a URL (e.g. GitHub repo) pointing to the complete code or illustratory pieces of code. Note: reproducible protocols will be requested from winners of the primary disciplines.}**

## RSAT software suite

* <https://github.com/rsa-tools/rsat-code>
* <https://github.com/rsa-tools/installing-RSAT>
* <https://hub.docker.com/r/eeadcsiccompbio/rsat/tags>

## optimize-matrix-GA

* <https://github.com/pvhelden/optimize-matrix-GA>

## RSAT scripts and protocol for the IBIS challenge 2024

* <https://github.com/jvanheld/IBIS_2024>

# Methods

## Motif discovery

We used the tool *peak-motifs* [1] from the software suite *Regulatory Sequence Analysis Tools (RSAT)* [2] to discover motifs in the train sequences using a Docker container [3]. Motif discovery relies on the detection of exceptional over-represented k-mers (*oligo-analysis*) or dyads (*dyad-analysis*) as well as positionally biased k-mers (*position-analysis*). We systematically analyzed 6-mers and 7-mers for *oligo-analysis* and *position-analysis*. Significant k-mers serve as seed to build a position-count matrix by collecting putative binding sites in the train sequences. For GCS, GHTS, HTS and SMS experiments, a Markov background model of order k-2 was estimated from the train sequences themselves, For PBM data, *peak-motifs* was used in differential mode to detect oligos and dyads over-represented in the top 500 spots (having the strongest signal) versus the 3500 bottom spots (considered as background sequences).

## Motif clustering

Primary motifs returned by *peak-motifs* were fed to the RSAT tool *matrix-clustering* [4] in order to regroup similar motifs (e.g. discovered by the different algorithms or with different k-mer lengths).

## Motif optimisation

Both primary discovered and clustered motifs were used as seeds for a new software named *optimize-matrices-GA* [5] that runs a genetic algorithm to optimize motifs with respect to a given objective function. In our case, the objective function was the area under the ROC curve (AuROC) measured with a positive and a negative sequence set. For the negative sequence set, we alternatively considered two approaches:

1. Train versus random
   * positive set: the training sequence for the considered dataset
   * negative set: random genome fragments of the same sizes as the training sequences (picked up with the RSAT tool *random-genome-fragments*)
2. TF versus others
   * The positive sequence set was a collection of all the training sequences for the considered factor in the considered experiment type (replicates and multi-cycle sequence sets were thus merged).
   * The negative set was the concatenation of all the sequence sets of all the other factors in the same experiment type.

We used the following parameters for *optimize-matrices-GA* at each generation:

* 20 generations after (the initial matrices is referred to as generation 0)
* 10 children per parent matrix
* for each child, we mutated 1 position by changing the frequency of a randomly chosen residue by a factor sampled randomly (uniform distribution between 5 and 25 percent)
* we keep the 5 top-ranking individuals for the next generation
* note that the 5 parent matrices from the previous generation are included in the current generation (they are competing with their own children)

## Matrix selection

For the IBIS submission, we gathered all the motifs produced in these different steps (primary peak-motifs discovered, clustered matrices, optimized matrices), measured their performances in binary classification, sorted them altogether by decreasing AuROC, and selected the top-ranking matrices for each TF:experiment couple. This first selection criterion systematically returned motifs of the 20th or 19th generation.

However, these matrices were optimized based on the training set, and some of them may fail to generalize to new data. We thus also included some of the pre-optimization matrices (generation 0).

Note that before the submission deadline, we had no time to implement the classical methods to mitigate over-fitting (e.g. k-fold cross-validation on the training set). This functionality will be implemented in a future version of *optimize-matrix-GA*.

## WET Disciplines

**{Optionally, you describe the way you were producing predictions for WET disciplines, i.e., when training and predicting on the same type of experimental data}**

# Results & Discussion

## Significance of the discovered motifs

… (peak-motifs)

## Performances of the motifs for binary classification

* comment the ROC curves
* provide a link to the html report on github

## Motif optimization

* comment the AuROC profile plots

## Leaderboard tests

**{This is an optional section where you may share your observations regarding the model performance during your internal validation, or any insights from the Leaderboard stage.}**

# References

1. Morgane Thomas-Chollier, Carl Herrmann, Matthieu Defrance, Olivier Sand, Denis Thieffry, Jacques van Helden, RSAT peak-motifs: motif analysis in full-size ChIP-seq datasets, *Nucleic Acids Research*, Volume 40, Issue 4, 1 February 2012, Page e31,<https://doi.org/10.1093/nar/gkr1104>
2. Walter Santana-Garcia, Jaime A Castro-Mondragon, Mónica Padilla-Gálvez, Nga Thi Thuy Nguyen, Ana Elizondo-Salas, Najla Ksouri, François Gerbes, Denis Thieffry, Pierre Vincens, Bruno Contreras-Moreira, Jacques van Helden, Morgane Thomas-Chollier, Alejandra Medina-Rivera, RSAT 2022: regulatory sequence analysis tools, Nucleic Acids Research, Volume 50, Issue W1, 5 July 2022, Pages W670–W676, <https://doi.org/10.1093/nar/gkac312>
3. Najla Ksouri, Jaime A Castro-Mondragón, Francesc Montardit-Tarda, Jacques van Helden, Bruno Contreras-Moreira, Yolanda Gogorcena, Tuning promoter boundaries improves regulatory motif discovery in nonmodel plants: the peach example, *Plant Physiology*, Volume 185, Issue 3, March 2021, Pages 1242–1258,<https://doi.org/10.1093/plphys/kiaa091>
4. Jaime Abraham Castro-Mondragon, Sébastien Jaeger, Denis Thieffry, Morgane Thomas-Chollier, Jacques van Helden, RSAT matrix-clustering: dynamic exploration and redundancy reduction of transcription factor binding motif collections, *Nucleic Acids Research*, Volume 45, Issue 13, 27 July 2017, Page e119,<https://doi.org/10.1093/nar/gkx314>
5. Philémon van Helden, Bruno Contreras-Moreira, Jacques van Helden (*in prep*). Machine learning strategies to optimize motifs discovered in transcription factor binding sequences.