Regulatory Sequence Analysis

Pattern matching

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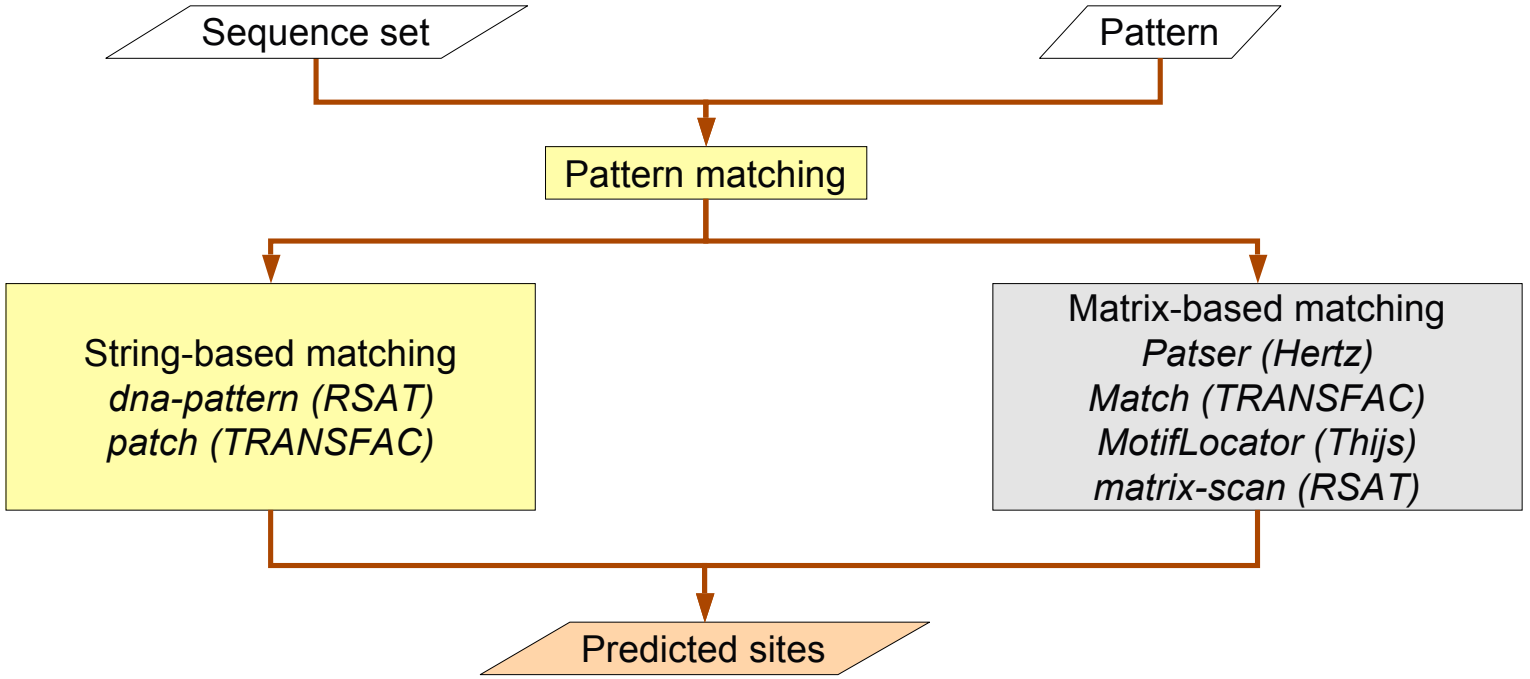
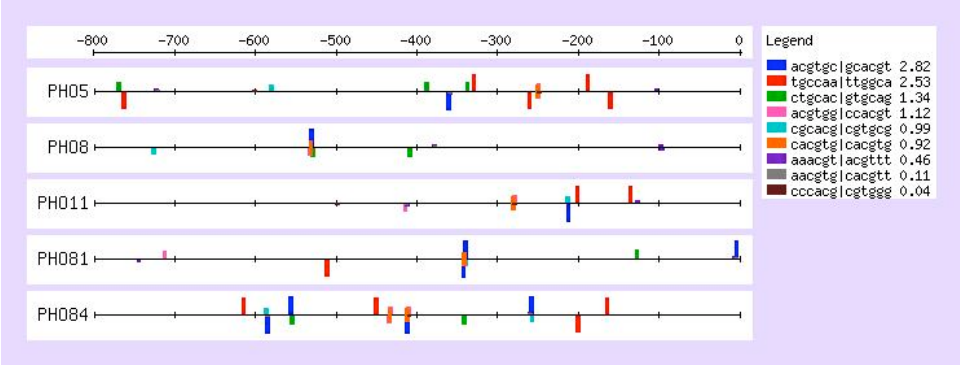
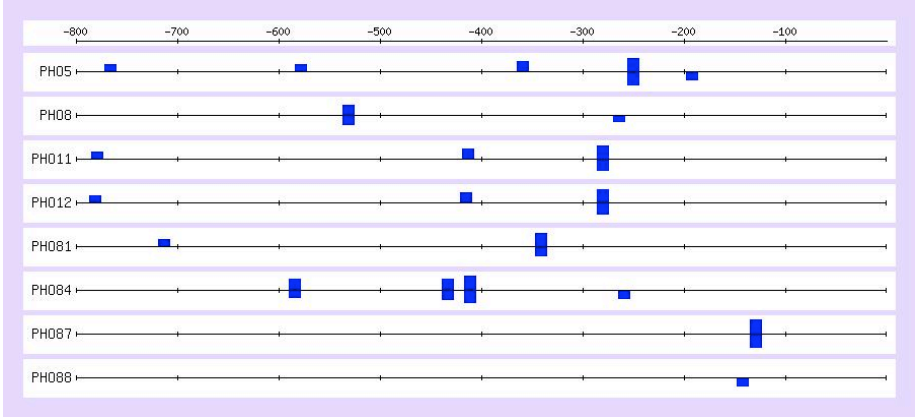
Pattern matching







Pattern matching in a small set of sequences

- Goal: knowing the pattern, find the matching positions in the sequence set of interest
- Assign a score to each position
  - Indicate quality of the match
    - Substitutions for string-based pattern matching
    - Weight scores for matrix-based pattern matching
  - Indicate a priori importance of each pattern
    - e.g. significance from pattern discovery

Expected matches for a consensus in whole genomes

- How many matches would we expect from a genome-scale pattern matching
  - Assuming a perfectly conserved hexanucleotide, with strand-insensitve activity
  - Expected matching rate: 1 occ / 2 kb

Organism	Size Mb	Genes	Kb/gene Kb	Non-coding size Mb	non-coding /gene Kb	exp_occ / reg_seq
Mycoplasma genitalium	0.6	481	1.25	0.1	0.12	0.06
Haemophilus influenzae	1.8	1 717	1.05	0.3	0.15	0.07
Escherichia coli	4.6	4 289	1.07	0.6	0.14	0.07
Saccharomyces cerevisiae	12	6 286	1.91	3.4	0.53	0.26
Arabidiopsis thaliana	120	27 000	4.44	84.0	3.11	1.50
Caenorhabditis elegans	97	19 000	5.11	70.8	3.73	1.79
Drosophila melanogaster	165	16 000	10.31	140.3	8.77	4.21
Homo sapiens	3 200	31 000	103.23	3 104.0	100.13	48.14

Genome-scale pattern matching

- Goal : given a pattern, find matches in the whole genome
  - → identify genes potentially regulated by a given transcription factor
- In general, a search based on a single signal returns many false positive
- Improvements
  - search for a repeated signal (e.g. GATA boxes)
  - search for combinations of signals
  - constraints on positions
  - combination of coding sequence information