AN·ALGORITHM·TO·CREATE·PHENOTYPE-FITNESS·MAPS

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Motivation

- **Overall goal:** uncovering the relationships between phenotypic characteristics and fitness, in both evolutionary biology and evolutionary computation.
- **Common approach:** perform selection based on fitness and study the phenotypes that evolve.
- **Problem:** computational evolution tends to be highly convergent, which makes difficult to understand of how fitness would change along key phenotypic dimensions 'had evolution searched there'
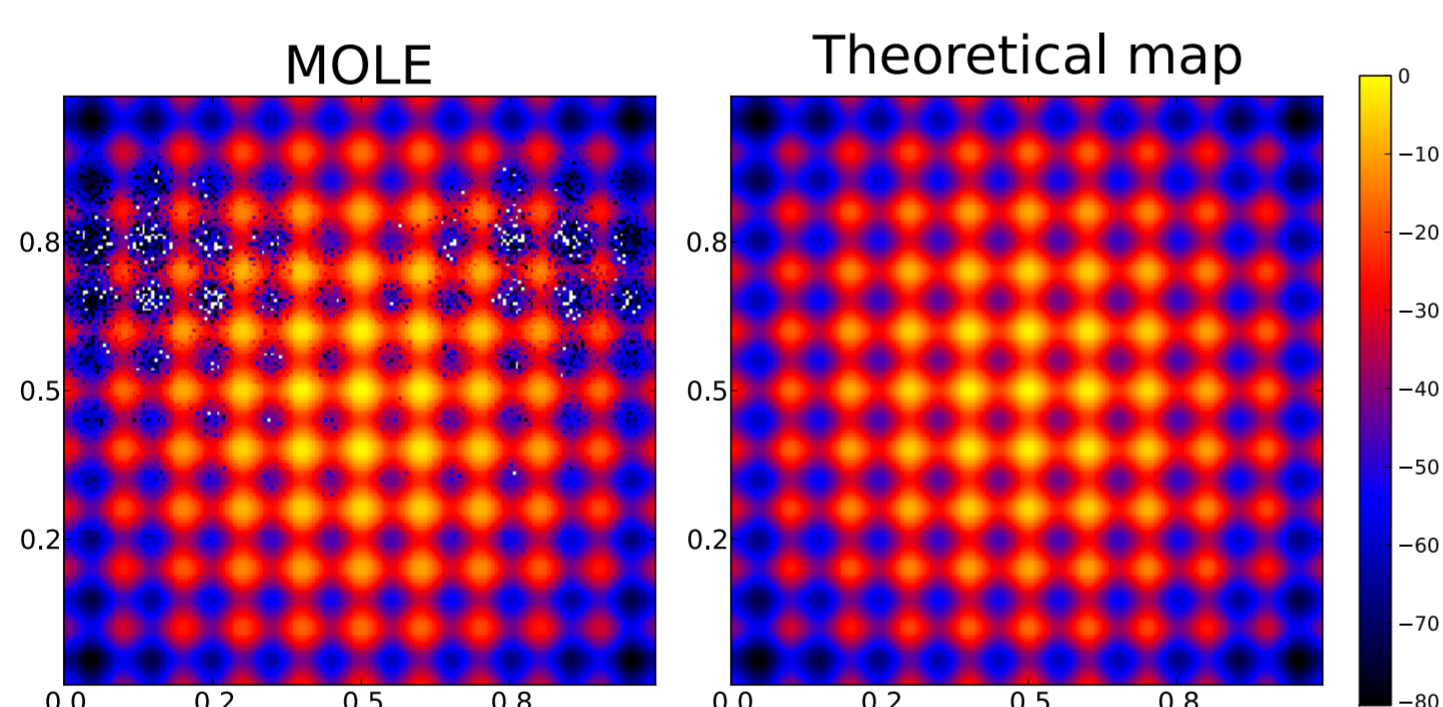
Contribution: the MOLE algorithm

We introduce the MOLE (Multi-Objective Landscape Exploration) algorithm to generate phenotype-fitness maps.

- **Main idea:** explicitly select for fit organisms in all areas of a phenotype landscape, where the axes of that landscape are defined by phenotypic dimensions of interest.
- **MOLE algorithm:**
  - choose two relevant dimensions;
  - create a grid G to store the result (e.g. a 200×200 grid); initialize each value to $-\infty$;
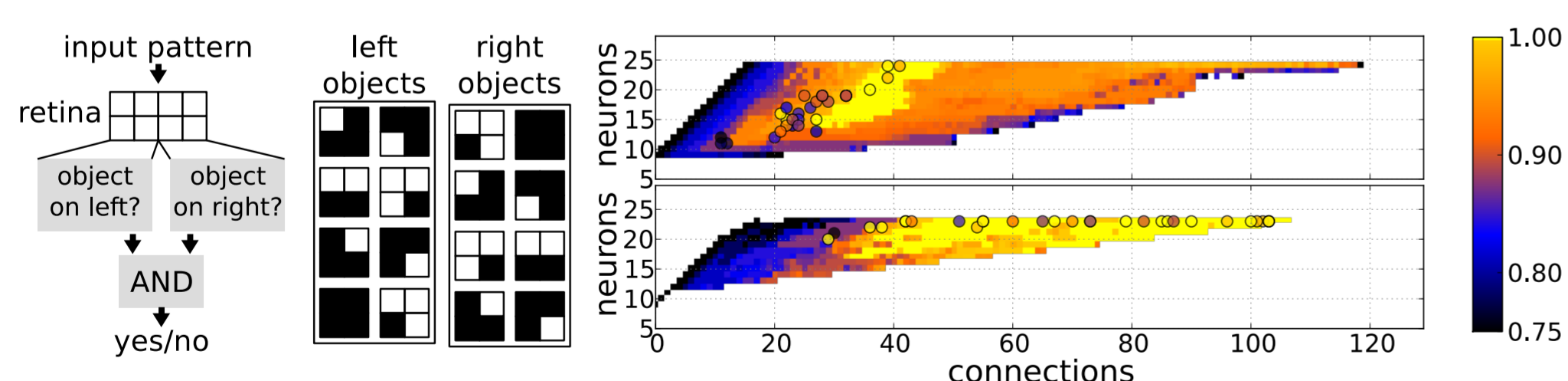 - use a multi-objective evolutionary algorithm (e.g. NSGA-II) to optimize:

$$\text{optimize} \begin{cases} \text{Fitness}(x) \\ \sum_{i \in N_x} \frac{1}{k_i} ||p_x - p_i|| \end{cases}$$

  - x: a candidate solution,
  - N_x: the set of the 8 closest neighbors of x in the map,
  - p_x: the 2D position of x in the map,
  - p_i: the 2D position of i in the map,
  - k_i: the number of times that the position of i has been hit during the search;
 - at each point, store the maximum fitness found so far.

Results

MOLE   Theoretical map

- **Task:** 10-dimensional Rastrigin function
- **Dimensions:** first two dimensions

input pattern   left objects   right objects

retina
object on left?   object on right?
AND
yes/no

connections
neurons

- **Task (left):** evolve neural networks for pattern recognition (8-pixels retina problem, Kashtan and Alon (2005))
- **Dimensions:** number of nodes vs. number of connections. Circles indicate the best solution from 30 runs of a standard EA (some overlap).
- **Top map:** Phenotype-fitness map obtained with an unconstrained direct encoding (Mouret and Doncieux, 2012). The MOLE algorithm found 98 distinct perfect solutions (bright yellow areas) whereas 30 runs of a standard EA found only 6 perfect solutions (bright yellow circles).
- **Bottom map:** Phenotype-fitness map obtained with a more constrained encoding (Kashtan and Alon, 2005). The MOLE algorithm found 221 perfect solutions whereas a standard EA found 15.

structural complexity   dynamic complexity   dynamic complexity
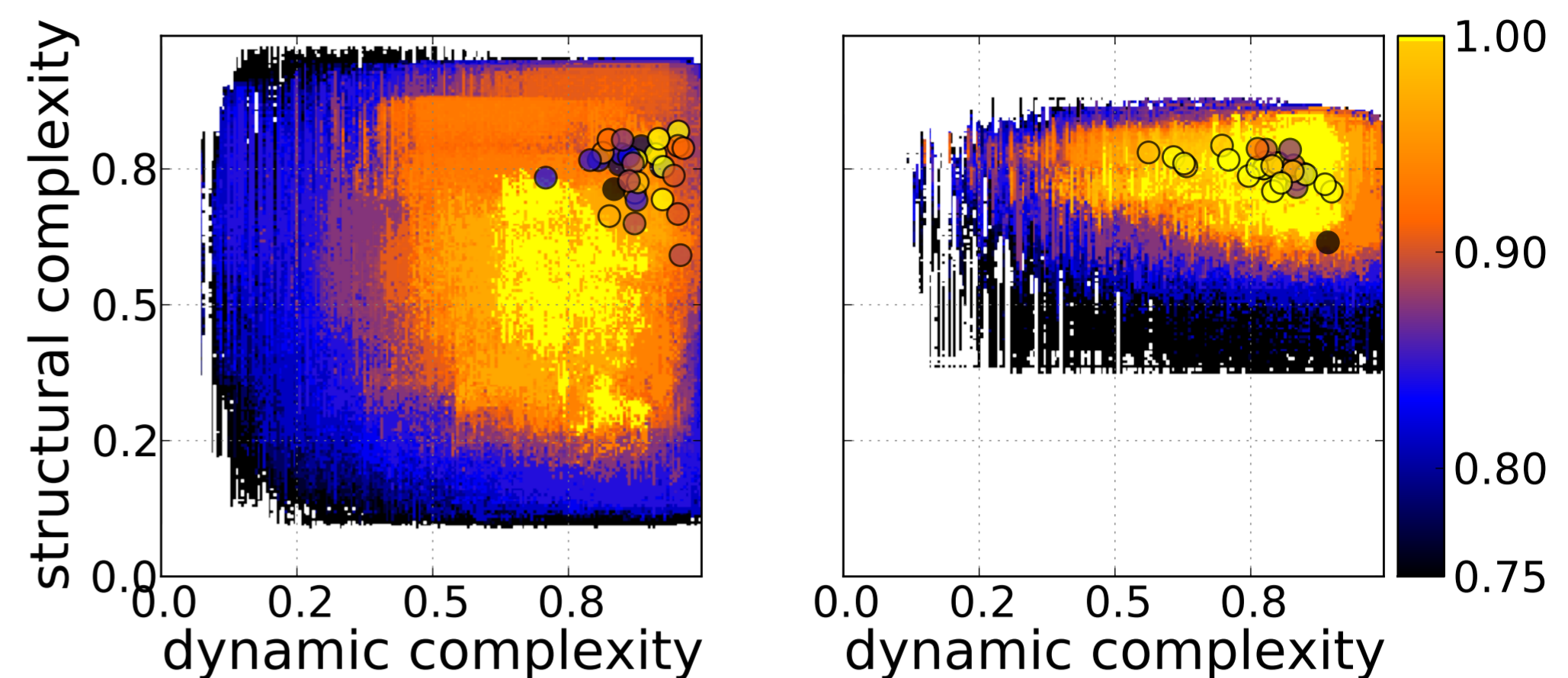
- **Task:** evolve neural networks for pattern recognition (8-pixels retina problem, Kashtan and Alon (2005))
- **Dimensions:** structural complexity (off-diagonal complexity, Claussen (2007)) vs. dynamic complexity (compression complexity of the neurons' ouputs, see Li and Vitányi (2008))
- **Left map:** Phenotype-fitness map obtained with the unconstrained encoding (Mouret and Doncieux, 2012). MOLE found 2536 distinct perfect solutions whereas a standard EA found 6 (bright yellow circles).
- **Right map:** Phenotype-fitness map obtained with the more constrained encoding encoding (Kashtan and Alon, 2005). MOLE found 1690 perfect solutions whereas a standard EA found 15.

Conclusions

- Maps illuminate relationships between the dimensions, although the illumination is not flawless, as some perfect solutions found by the standard EA were not located by MOLE.
- Maps allow the exploration of non-trivial dimensions (complexity, modularity, size of solutions, ...).
- Maps allow researchers to compare the potential of different encodings.
- MOLE finds more optimal solutions than standard evolutionary algorithms.

Source code and video

`http://chronos.isir.upmc.fr/~mouret/mole`

Acknowledgments

References

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