

ALiBERO

“hands-on” session

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ALiBERO: Evolving a team of complementary pockets rather than a single leader

J. Chem. Inf. Model., 2012, 52 (10), pp 2705–2714.

DOI: 10.1021/ci3001088



What is ALiBERO?

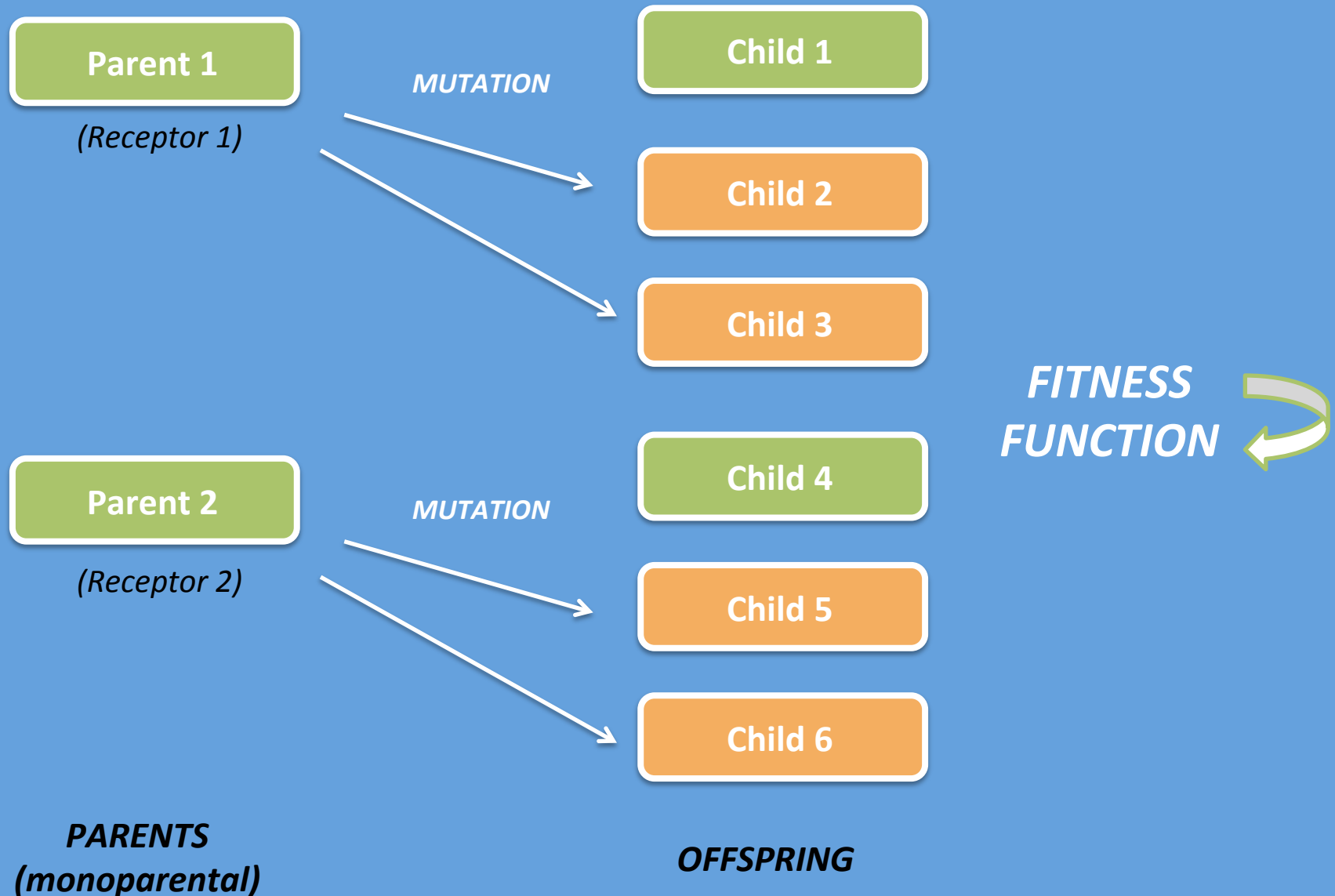
- A computational method that iteratively selects the **combination of pockets** that maximize a fitness function (e.g., AUC)
- **Perl script** (command line) + **ICM-VS**
 - Connected via icm scripts
 - Results come as graphical .icb

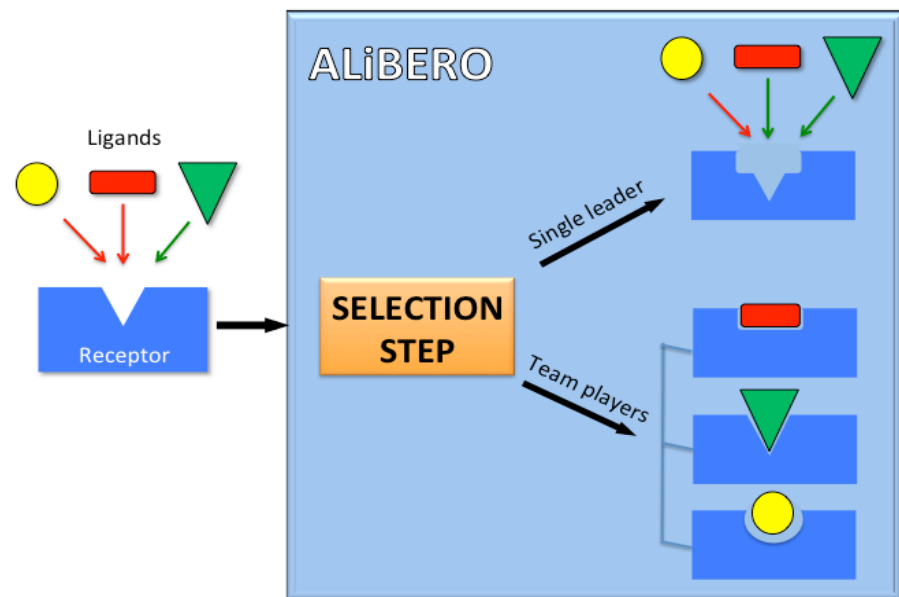
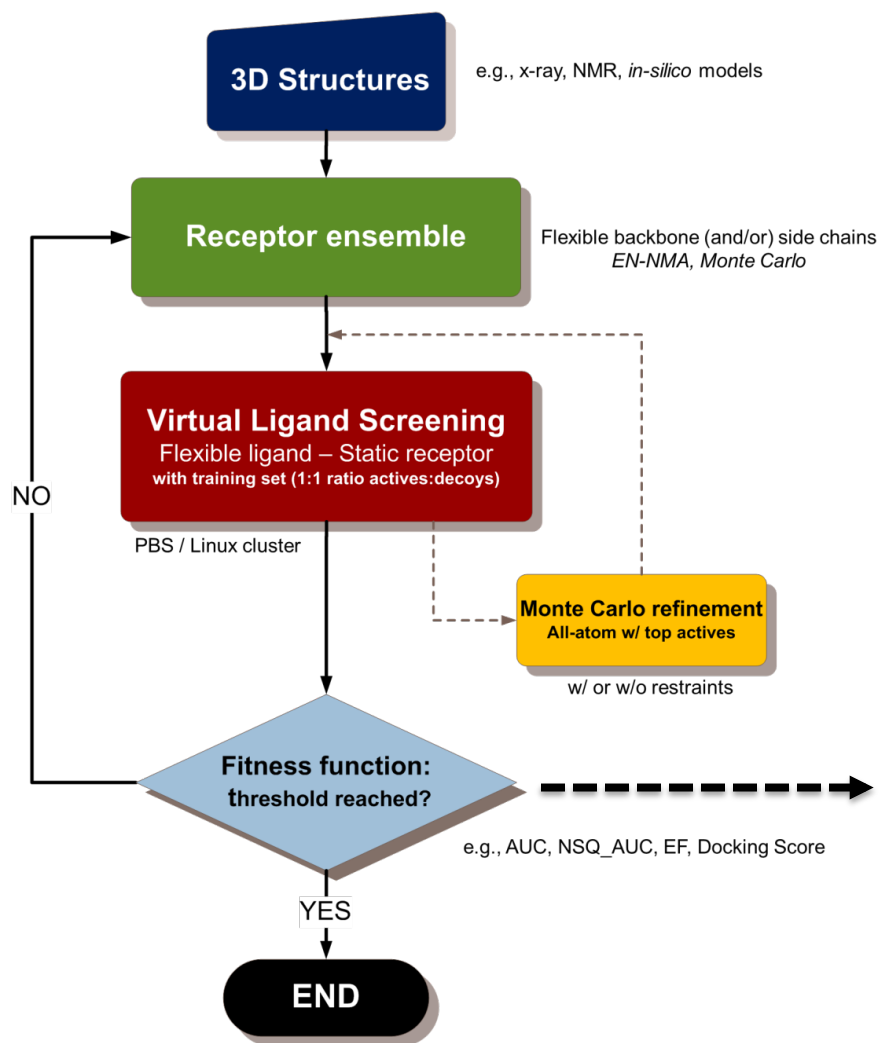
What do I need to run it?

- Linux workstation
- Alibero script (from github)
- ICM-VS license
- Optional
 - Linux cluster



ALiBERO is Implemented as an *Evolutionary Algorithm*





- Rueda. M, et al. ALiBERO: evolving a team of complementary pocket conformations rather than a single leader. *J Chem Inf Model.* 2012 Oct 22;52(10):2705-14.



SAMPLING ROUTE
("mutations")

NON-SAMPLING ROUTE

When should I try it?

- You have experimental data for a few *actives* (2D is fine) and...
 - ***Sampling route***: your pocket(s) display bad recognition (AUC, scores) of known actives
 - *Non-sampling route*: you have multiple pockets and want to select the optimum ensemble for VS
 - both

*via Normal Mode Analysis and Monte Carlo side chain refinement

What is the expected performance?

Training Set

AUC: 80-90%

NSQ_AUC: $\geq 60\%$

Homology model

Test Set

NSQ_AUC

15-20%

Great for predicting binding modes

OK, now the bad news...

Overfitting
happens

Prospective VS
sensitive to
false positive
team players ≤ 5

What files do I need?

- One or multiple **converted** receptors embedded as objects in an .icb file
 - Unless there exist sampling reasons, I recommend to delete residues not involved in the pocket
- ICM scripts (provided)
- An *.sdf* file with the ligands to be docked
 - The file must contain a column named “Active” with 1=actives and 0=decoys

Where is ALiBERO exe?

/pro/alibero/alibero
(latest version)

How do I run ALiBERO?

- `$path/alibero -i config_file -n MRCs [-options]`
 - v
 - help
 - man
 - verbose
 - debug

What is the flag `-n`?

- Number of “children”
 - Two modes:
 - Desktop (slow when `-n > ncpu`)
 - Cluster (recommended when `-n 100`)
 - Note that PBS.pm must be updated if outside Abagyan’s lab
 - You’ll need passwordless communication with the cluster

What is the flag `-i`?

- Configuration file

```
pbs      bluefish
inputicb INPUT/RECEPTORS/aliberoMicro.icb
projdir   ESR1_HUMAN_test
cfmdir    /cfs/mrueda/CFS_TEST_ALiBERO
temperature 300 # 1A->300, 1.5A ->600, 2A->1100, 2.5A->1600
function   nsa # NSQ_AUC
nligands   41
sdf        INPUT/LIGANDS/v10actives_w31Decoys.sdf
macrodir   INPUT/MACROS
refinement off # Check the restraints in macro
mrc        5
ntop       3
repeat     1  #
laziness    10 # %
```

ALiBERO has 5 fitness functions

- AUC (auc)
- NSQ_AUC (nsa)
- Average Score for $\frac{1}{2}$ actives (score)
- NSQ_AUC+ (nsaplus) ← recommended
- Consistency of binding mode for actives (con)

What do I need to modify?

- Configuration file (parameters)
- *ase/* for pocket definition
 - @ MakeDock.icm
- Drestraints (if any)
 - @Refine_Hitlist.icm

A few notes about ALiBERO runs

- Remember: It does not modify your input files
- “Parents” & “offspring” compete on each generation. Each parent breeds equal offspring
- Docking **answers** are kept (huge)
- Everything is stored inside project_dir
 - Project_dir/GEN_1
 - Results will appear as Gen_1.icb or Gen_Ref_1.icb (if MC refinement)
 - Gen*icb are browsable

Is there any test I can run?

- Yes, just copy this folder:

`/pro/alibero/test/`

locally, then modify the paths inside the
*in file and you are good to go.

Please, be gentle with the cluster!

Addendum: How do I select the best combination of pockets from a X-ray ensemble, say, from Pocketome?

- `alibero -i config_file -n equal_to_your_npockets_in_ensemble`
- Make sure that you have these parameters on the input file

`maxgen 1`

`refinement off`