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Oracle for Research

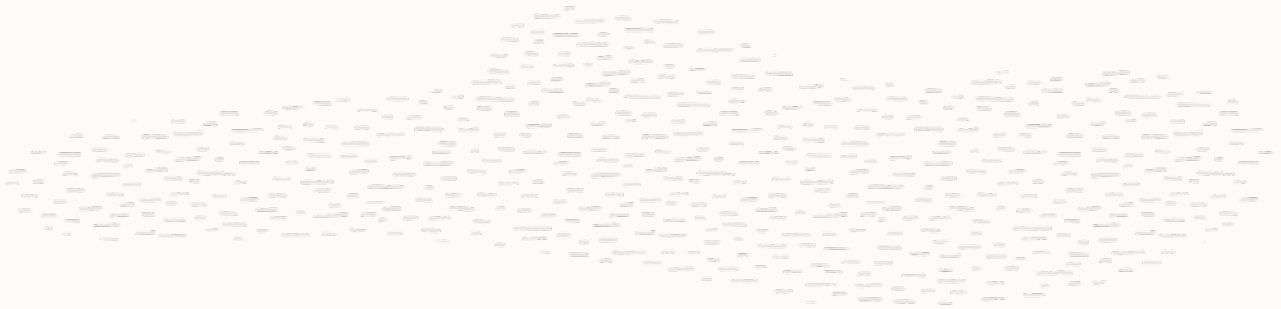
Tech Talk: High Performance Computing for Drug Discovery

Dr. Harinda Rajapaksh, Peter Winn.

April 21, 2021

Agenda

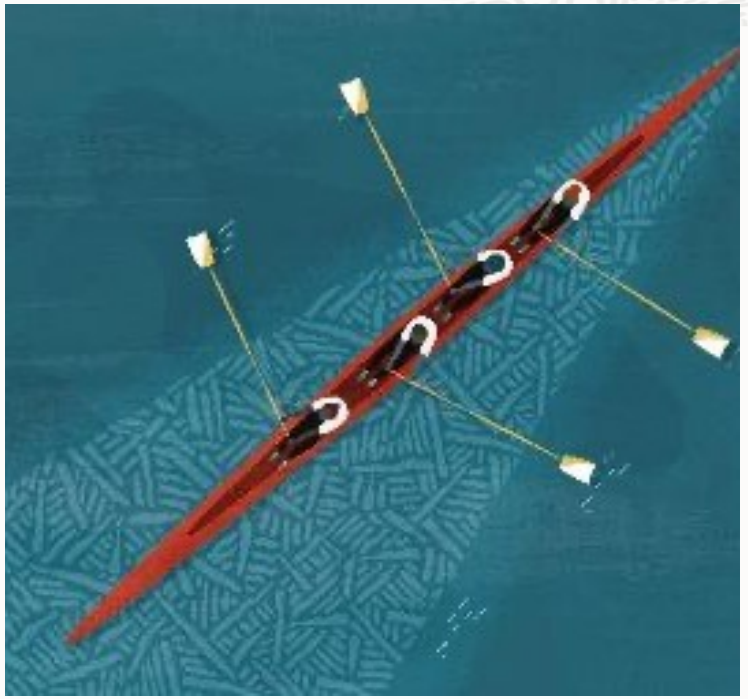
1. Welcome to Oracle for Research
2. A case study in dedicated HPC
3. How did we do it:
   - An introduction to drug discovery
   - Challenges and solutions
   - Oracle HPC Infrastructure
   - How to use OCI Infrastructure for high-throughput drug discovery
   - Useful tips



Digital Research: Asking big questions & sharing big answers

Commodity Super Computing

Automation of Tools and Platforms



Open Collaboration

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Grant Program

Free Credits

Dedicated value of cloud credits to use on what you want, when you want it.

Cloud Expertise

Technical Support and functional supports to make your workloads faster than ever.

Marketing

Collaborative marketing and signal boosting of research and white papers.

Your IP

You remain in control, we’re here to help.

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Case Study

University of New South Wales (UNSW): Drug Screening on dedicated HPC

University of New South Wales – Rapid Drug Discovery

Drug Discovery requires the simulation of hundreds of millions of drug compounds

Growing libraries (200m+) can take years to scan utilizing public compute allocations

Purchases of in-house infrastructure is costly and difficult to justify

Dedicated HPC in OCI could change the game in drug discovery providing answers at predictable low operational costs.

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Warp Speed Pipeline: Outcomes

1 year utilizing ad-hoc allocations on shared compute infrastructure.

~10,000 compounds screened.

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2 Million top compounds screened on OCI in **2 Hours** for a running cost of ~$100

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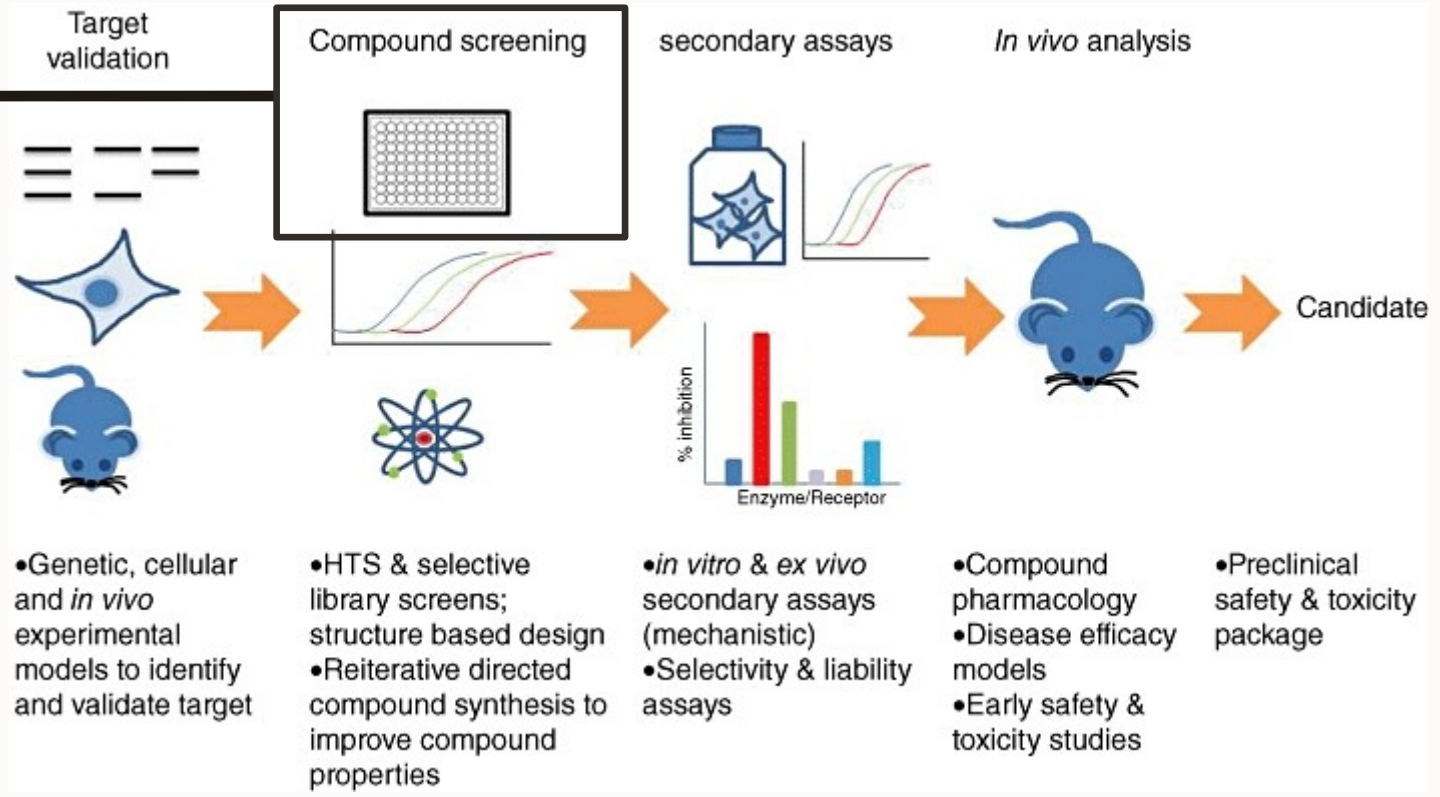
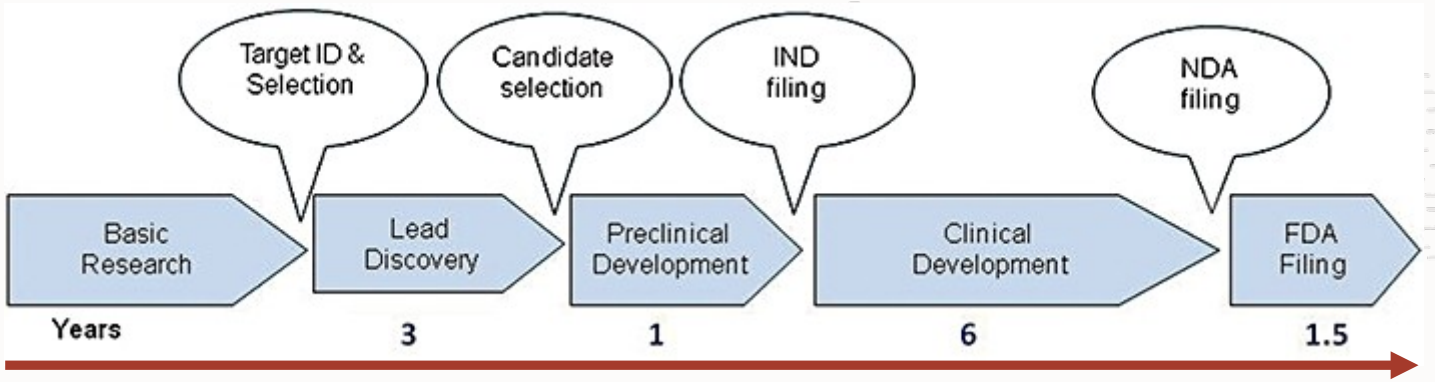
How did we do it

Deep dive on approach and tips and tricks

Drug discovery

Billions of compounds





Hughes *et al.*, 2011 Br J Pharmacol. 2011 Mar; 162(6): 1239–1249

Drugs screening methods

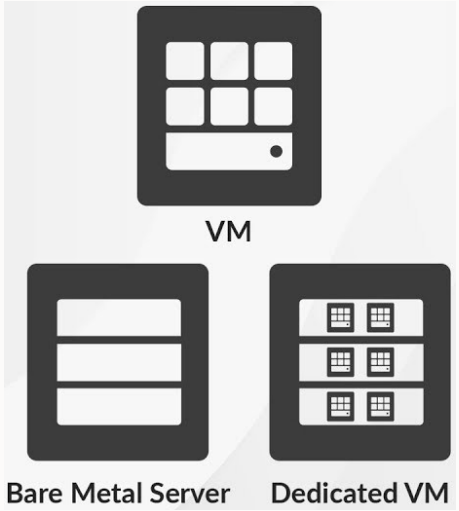
Conventional methods (Wet lab screening)

Computational methods (Molecular docking)

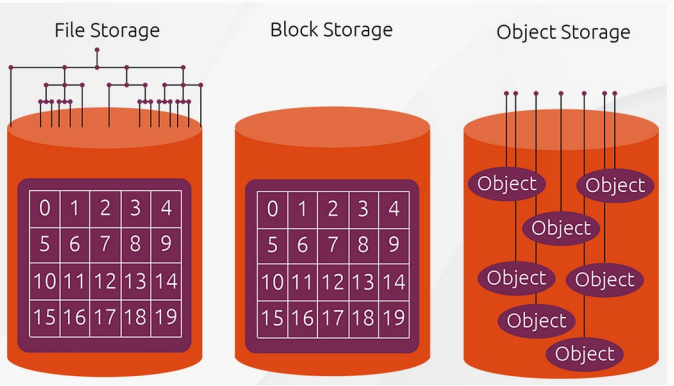
What is molecular docking?

What is molecular docking?

Oracle Infrastructure for Drug Discovery



Computing resources



Storage

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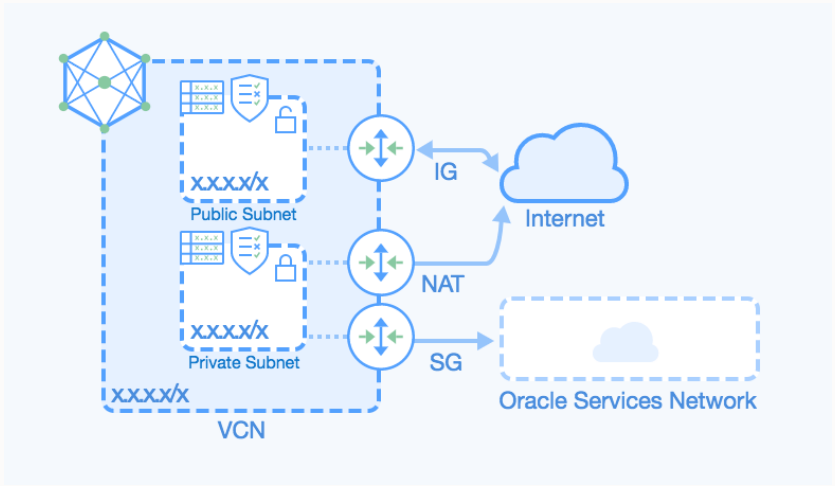
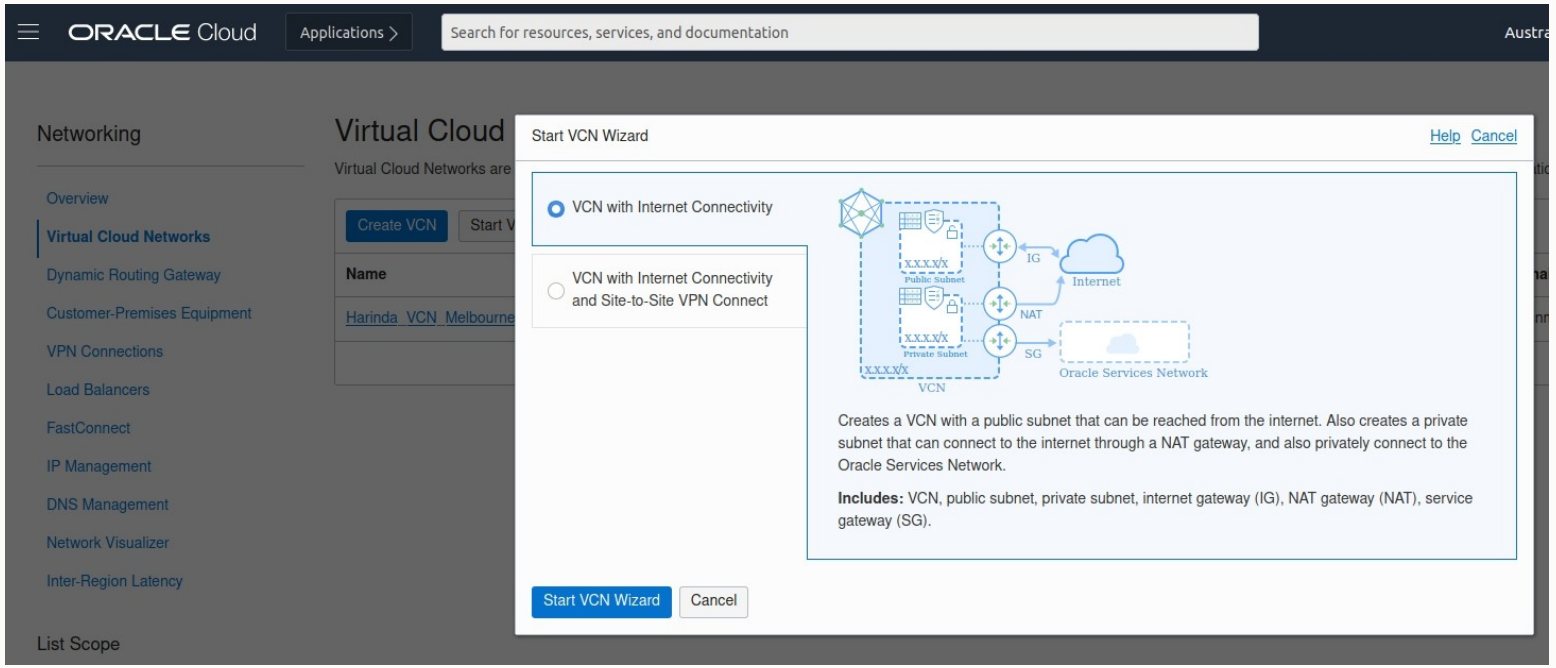
How to use OCI Infrastructure for high-throughput drug discovery

Create the network



VCN with Internet Connectivity



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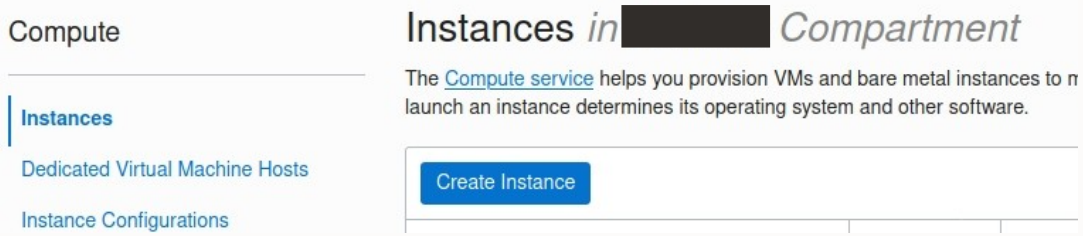
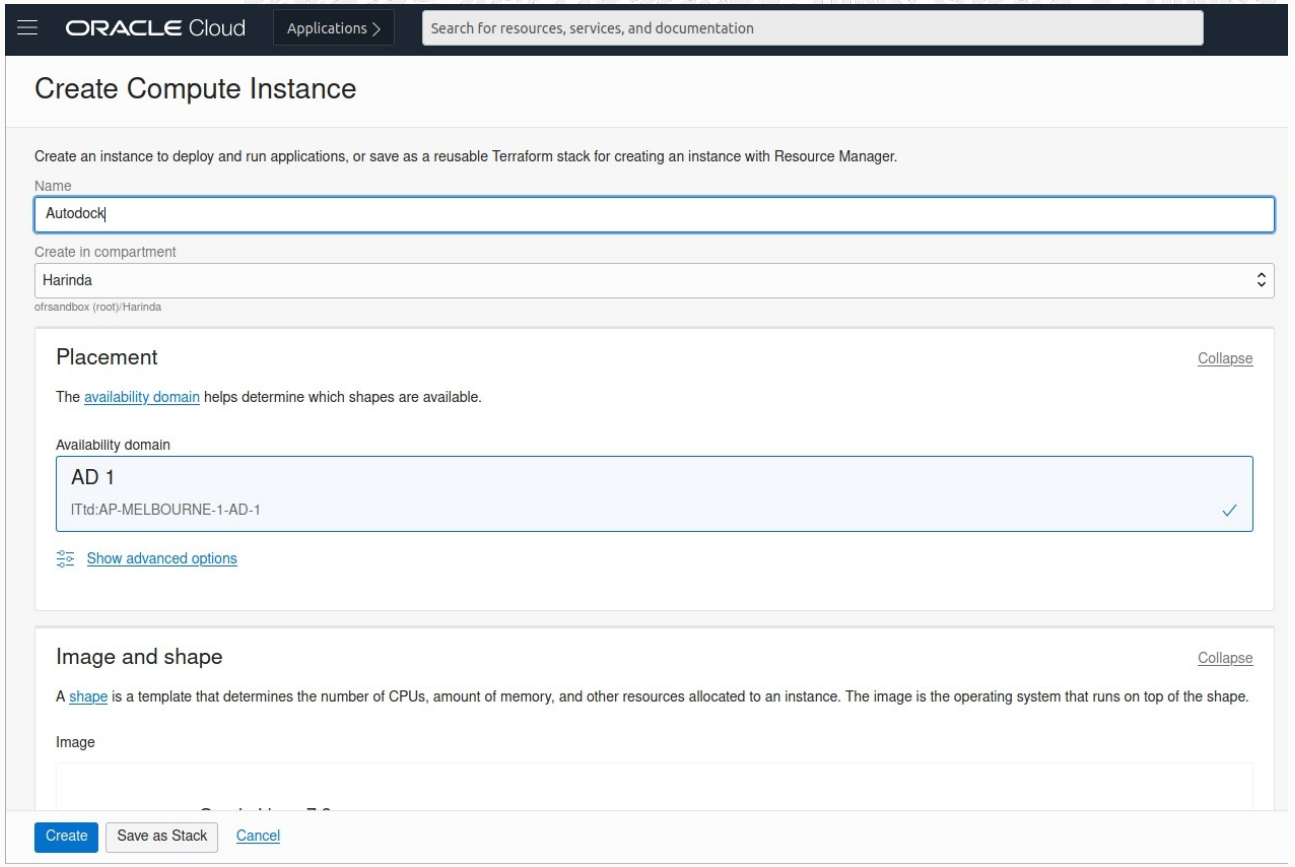
How to use OCI Infrastructure for high-throughput drug discovery

Launch the computing resources





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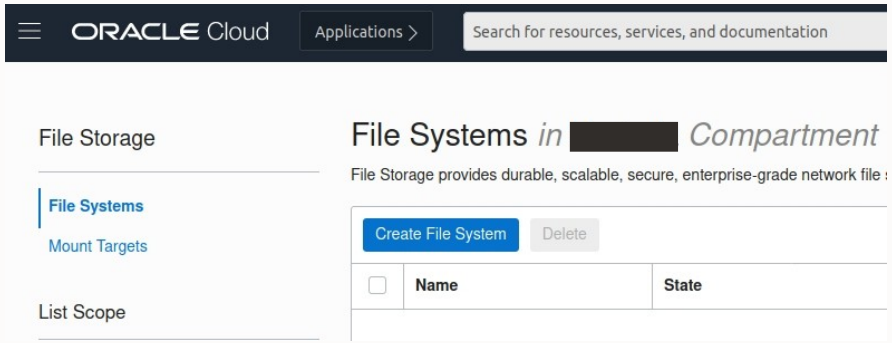
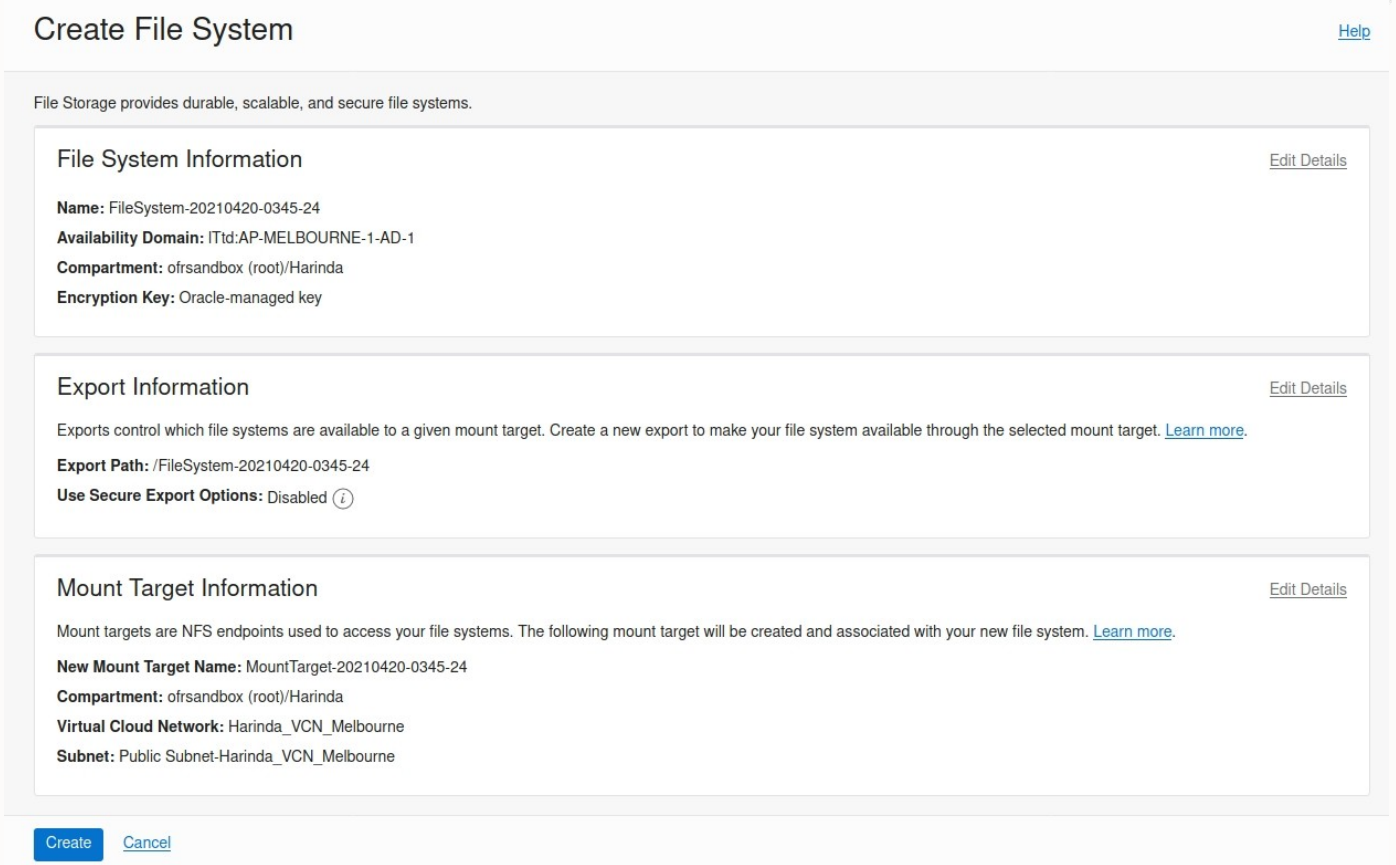
How to use OCI Infrastructure for high-throughput drug discovery

Create the storage





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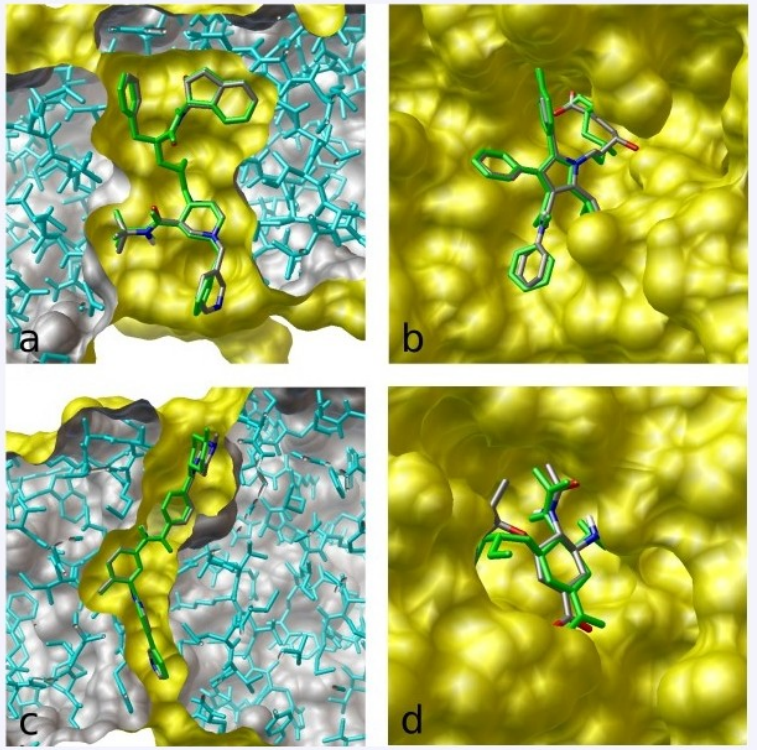
Drugs screening Software



AutoDock Vina

AutoDock Vina is an open-source program for doing molecular docking. It was designed and implemented by Dr. Oleg Trott in the Molecular Graphics Lab at The Scripps Research Institute.

The image on the left illustrates the results of flexible docking (green) superimposed on the crystal structures of (a) indinavir, (b) atorvastatin, (c) imatinib, and (d) oseltamivir bound to their respective targets.

Publication

If you used AutoDock Vina in your work, please cite:

O. Trott, A. J. Olson, AutoDock Vina: improving the speed and accuracy of docking with a new scoring function, efficient optimization and multithreading, *Journal of Computational Chemistry 31 (2010) 455-461*

Drugs screening on your Desktop or Laptop

```
#################################################################
# If you used AutoDock Vina in your work, please cite:          #
#                                                               #
# O. Trott, A. J. Olson,                                        #
# AutoDock Vina: improving the speed and accuracy of docking    #
# with a new scoring function, efficient optimization and       #
# multithreading, Journal of Computational Chemistry 31 (2010)  #
# 455-461                                                       #
#                                                               #
# DOI 10.1002/jcc.21334                                         #
#                                                               #
# Please see http://vina.scripps.edu for more information.      #
#################################################################

WARNING: The search space volume > 27000 Angstrom^3 (See FAQ)
Output will be ZINC000001351167_out.pdbqt
Reading input ... done.
Setting up the scoring function ... done.
Analyzing the binding site ... done.
Using random seed: 914682656
Performing search ...
0%   10   20   30   40   50   60   70   80   90   100%
|----|----|----|----|----|----|----|----|----|----|
**************************************************
done.
Refining results ... done.

mode |   affinity | dist from best mode
     | (kcal/mol) | rmsd l.b.| rmsd u.b.
-----+------------+----------+----------
   1         -6.5      0.000      0.000
   2         -6.4      2.366      2.884
   3         -5.6      3.101      4.031
   4         -5.4      3.755      6.733
   5         -4.3      4.462      7.591
   6         -3.9      5.772      7.075
   7         -3.6      5.697      8.262
Writing output ... done.
```

Drugs screening on OCI

- Single node screening
- Multi-node screening

Drugs screening on OCI

- Single node screening
- **Multi-node screening**

ORACLE Cloud Marketplace | Oracle Cloud Home

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High Performance Computing

HPC Cluster

High Performance Computing - RDMA cluster network

Oracle Cloud Infrastructur | High Performance Computing

Improving the performance

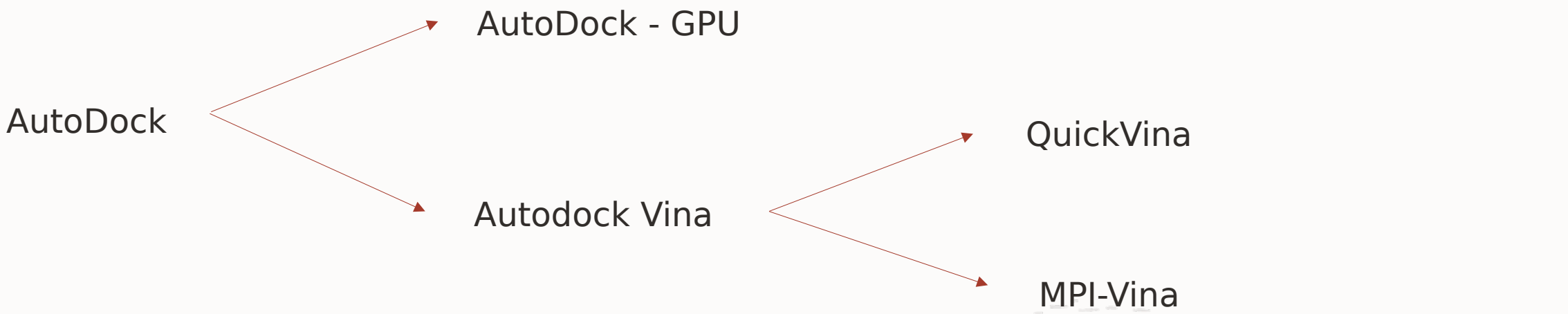
Filtering compounds before docking

Analyze the receptor

1. Molecular weight
2. xlogP
3. Net Charge
4. Number of rotatable bonds
5. Polar surface area
6. Hydrogen donors
7. Hydrogen acceptors
8. Polar desolvation
9. Apolar desolvation

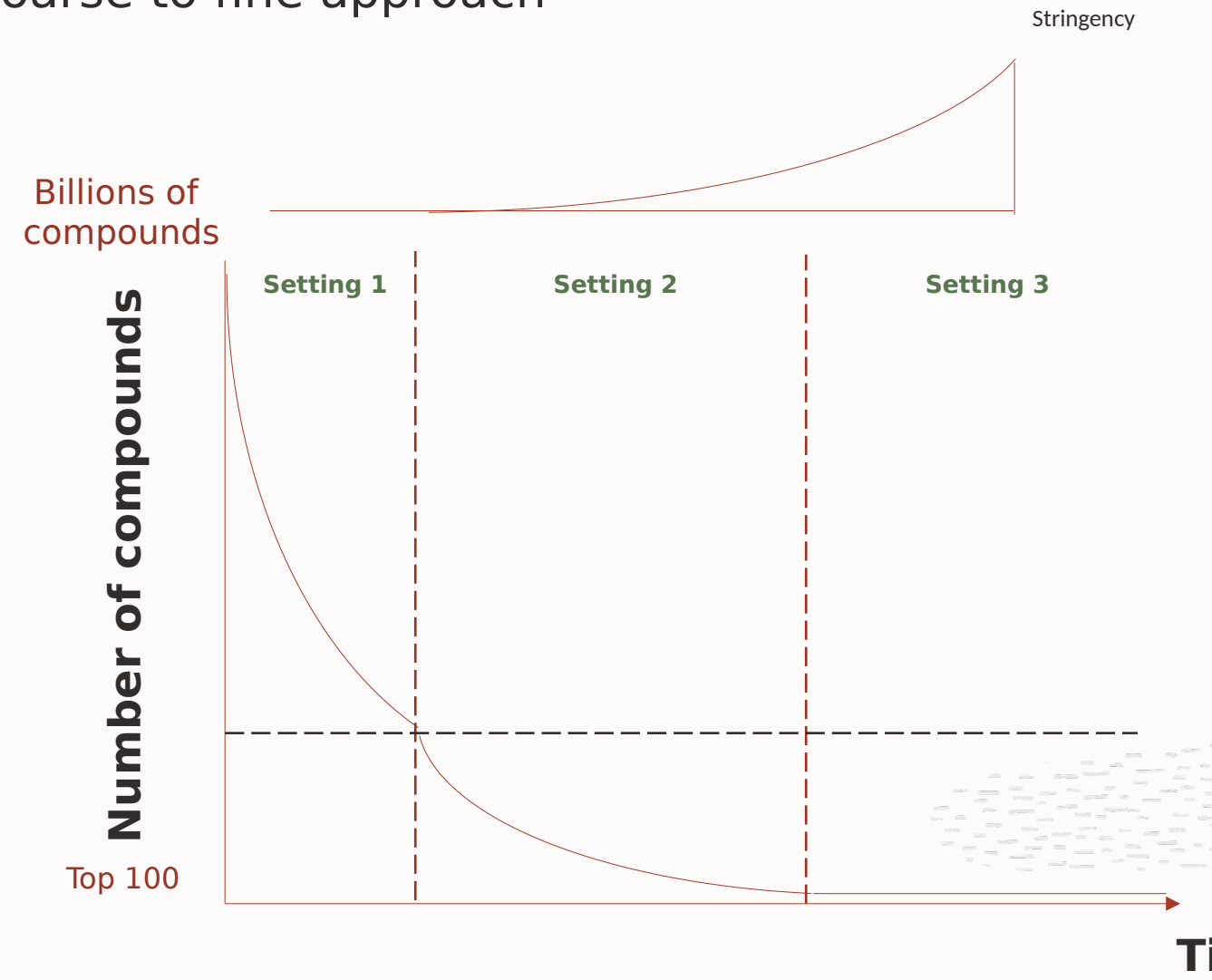
Improving the performance

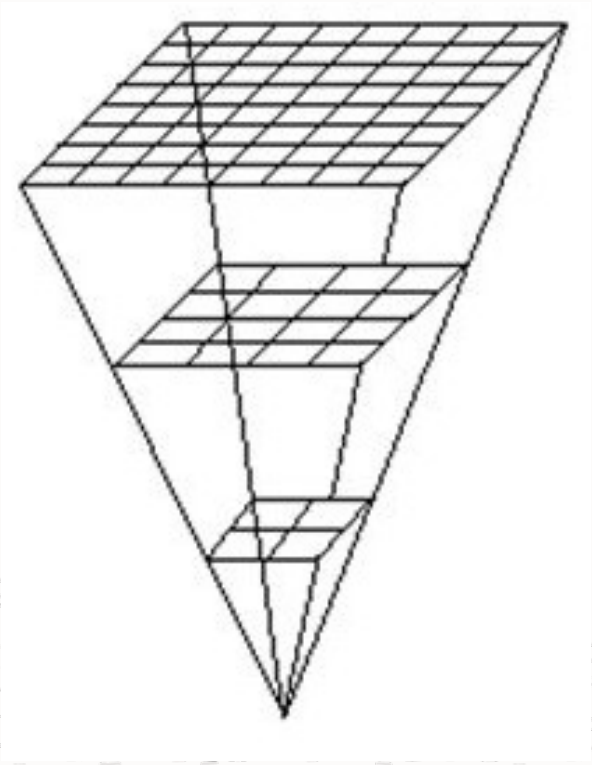
Choice of the software / algorithm



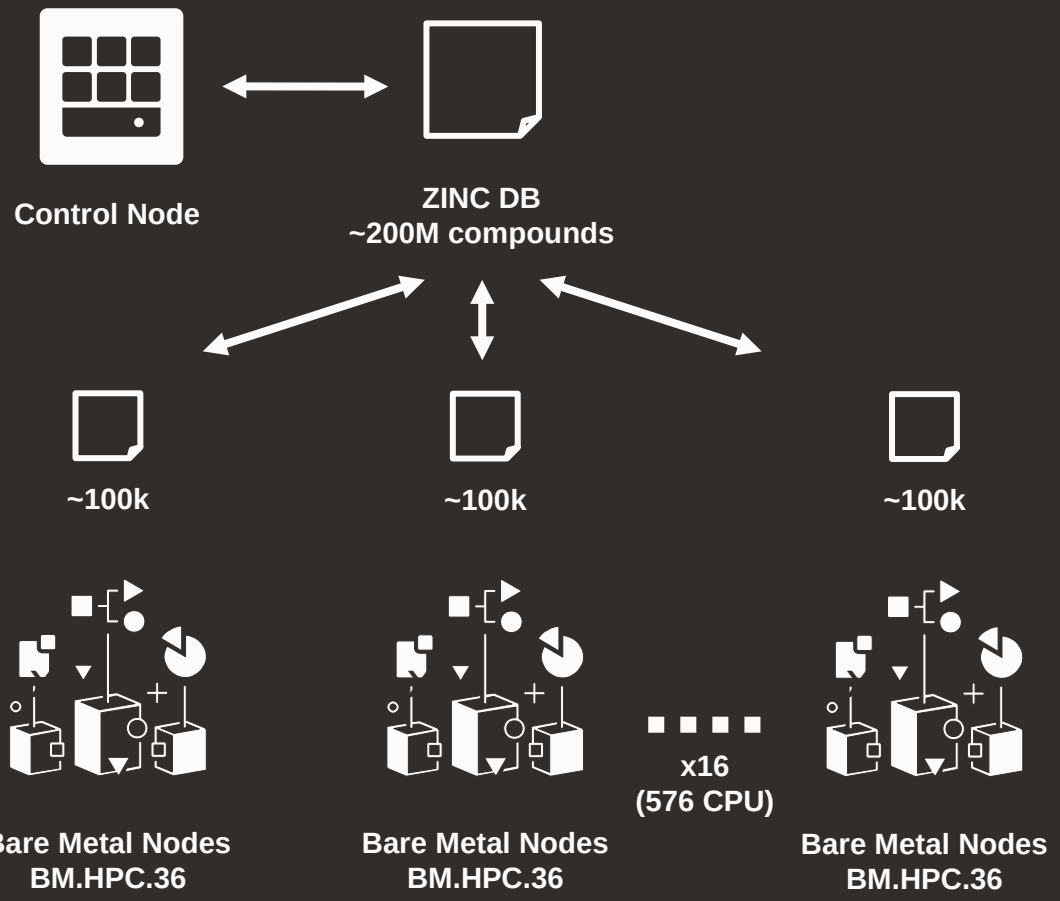
Improving the performance

Coarse to fine approach





Warp Speed Pipeline



- Drug database is filtered to prioritize top 2M compounds from >750M possible.
- Control nodes serve drug batches, optimizing for utilization, to dedicated HPC nodes.
- Autodock Vina codebase customized for Oracle HPC shapes to utilize in-memory disks and BM CPU architecture for high performance.
- Pipeline is embarrassingly parallelized to avoid network communication and scale linearly for maximum performance.
- HPC nodes are destroyed on completion with results saved to shared storage to manage costs.

Questions?

w: oracle.com/oracle-for-research

e: oracleforresearch_ww@oracle.com

Our mission is to help people
see data in new ways, discover
insights,
unlock endless possibilities.

Thank You