

# Metagenomics Taxonomy Reporter

A small little data analytics project's  
journey into the Big Data world

Tin Ho

Title:

Metagenomics Taxonomy Reporter:

A little data analytics project's journey into the Big Data world.

Summary:

This talk is about the journey an HPC sys admin ventures into the data analytics realm. After gathering basic scientific requirements from metagenomics studies, a python program and SQLite database is written to provide a breakdown of the all species found in the study. In order to improve performance, detail storage options are evaluated. Finally, HPC and HDFS+Spark SQL are explored as scale out mechanism for the project.

# Project Origin

- I am a Unix/Storage/HPC geek
- Works at the Scientific Computing group,  
->Provide value-add to the business
- Enlisted local BioInfo head as mentor
- Work on project that is mutually beneficial

# Overview: Input

PH046:198:H760GADXX:1:1211:3745:72353 gi 422933597 ref YP_007003722.1	37.50	32	20	0	97	2	310	341	3.0	28.1
PH046:198:H760GADXX:1:2108:16321:30071 gi 20026759 ref NP_612801.1	55.56	27	9	2	93	19	323	348	3.9	27.7
PH046:198:H760GADXX:1:2116:16937:9584 gi 506498137 ref YP_008003934.1	52.63	19	9	0	38	94	228	246	8.7	26.6

# Overview: Output

Taxonomy report    BLAST - Wikipedia, the free encyclopedia .html

## TAXONOMY REPORT

### GI LEVEL (SUBSPECIES DATA IF AVAILABLE)

Show 10 entries    Search:

Count	Percentage	Rank name	TaxID
761029	26.3165 %	Streptococcus mitis (species)	<a href="#">28037</a>
503011	17.3942 %	unknown (no rank)	-1
278621	9.6348 %	Streptococcus gordonii (species)	<a href="#">1302</a>
235921	8.1582 %	uncultured bacterium (species)	<a href="#">77133</a>
125529	4.3408 %	Mycoplasma hominis (species)	<a href="#">2098</a>
120790	4.1769 %	Streptococcus dysgalactiae subsp. equisimilis (subspecies)	<a href="#">119602</a>
78981	2.7312 %	Streptococcus pneumoniae (species)	<a href="#">1313</a>
68926	2.3835 %	Ureaplasma parvum serovar 3 (no rank)	<a href="#">38504</a>
68459	2.3673 %	Streptococcus sp. VT 162 (species)	<a href="#">1419814</a>
60868	2.1048 %	Streptococcus dentisani 7746 (no rank)	<a href="#">1297534</a>

Showing 1 to 10 of 2,279 entries    Previous    1    2    3    4    5    ...    228    Next

## SPECIES

Show 25 entries    Search:

Count	Percentage	Rank name	TaxID
774290	26.7751 %	Streptococcus mitis	<a href="#">28037</a>
503021	17.3946 %	NoLineageData	-1
278629	9.6350 %	Streptococcus gordonii	<a href="#">1302</a>
235921	8.1582 %	uncultured bacterium	<a href="#">77133</a>

# What does it take?

- BLAST
- Taxonomy
- Database
- Python
- HTML + CSS + jQuery
- Optimization
- Big Data
- Eureka ?!?!

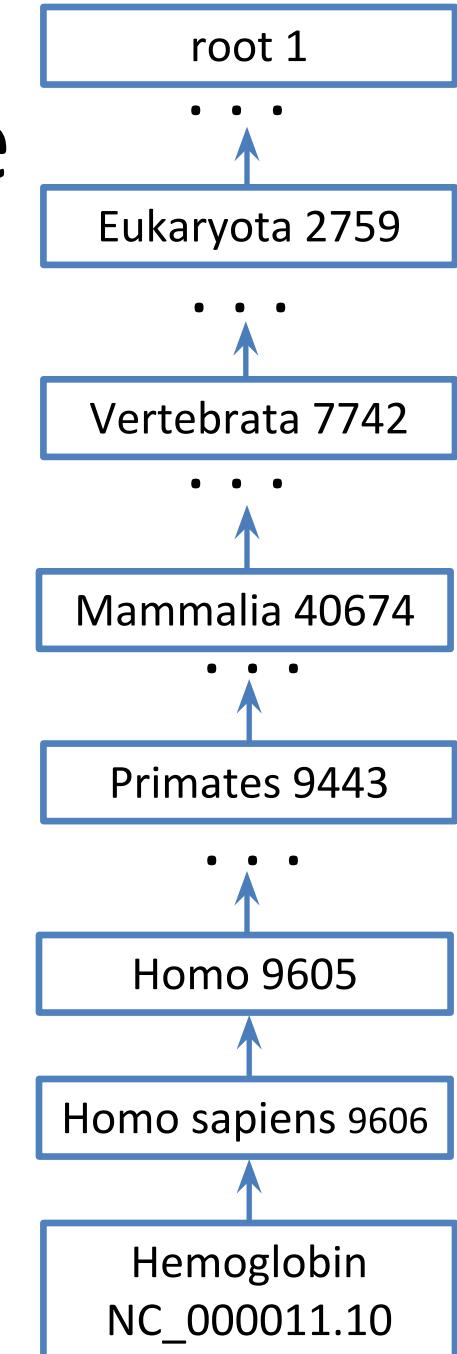
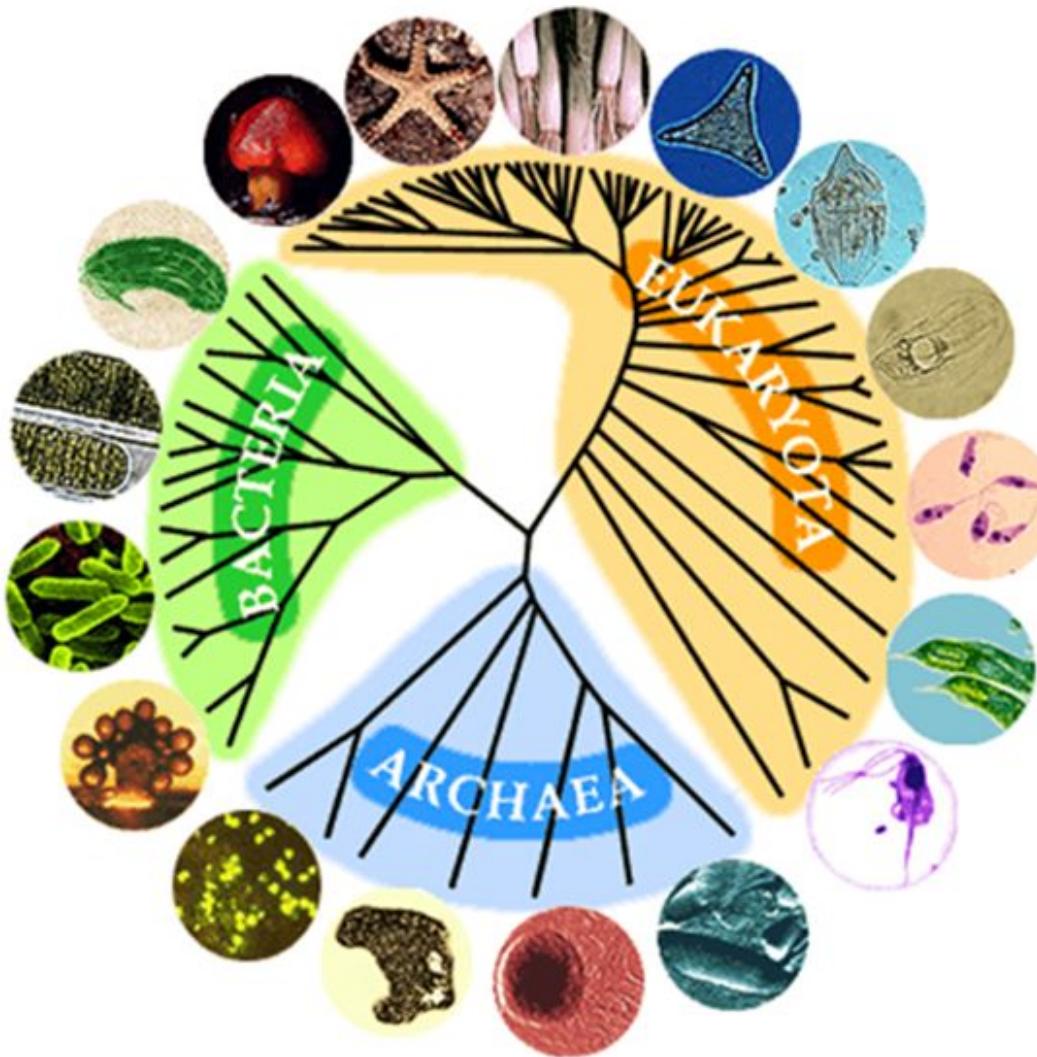
# BLAST

- Basic Local Alignment Search Tool
- Bioinformatics tool to search for similar sequences
- PH30046:198:H760GADXX:1:1211:3745:72353

gi|422933597|ref|YP 007003722.1|  
37.50 32 ↑ 20 0 97 2 310 341  
3.0 28.1 ↑

GI# Accession #

# Taxonomic/Phylogeny Tree



# NCBI Taxonomy Database

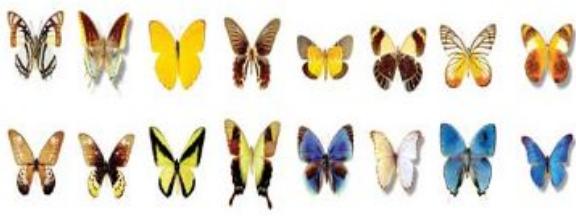
OneFS    DataTables | Table plug-in ...    Home - Taxonomy - NCBI

www.ncbi.nlm.nih.gov/taxonomy    Search

NCBI Resources How To Sign in to NCBI

Taxonomy    Taxonomy    Search

Limits Advanced    Help



## Taxonomy

The Taxonomy Database is a curated classification and nomenclature for all of the organisms in the public sequence databases. This currently represents about 10% of the described species of life on the planet.

### Using Taxonomy

- [Quick Start Guide](#)
- [FAQ](#)
- [Handbook](#)
- [Taxonomy FTP](#)

### Taxonomy Tools

- [Browser](#)
- [Common Tree](#)
- [Statistics](#)
- [Name/ID Status](#)
- [Genetic Codes](#)
- [Linking to Taxonomy](#)
- [Extinct Organisms](#)

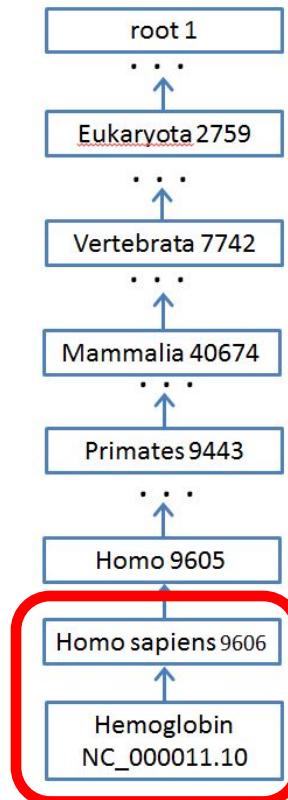
### Other Resources

- [GenBank](#)
- [LinkOut](#)
- [E-Utilities](#)
- [Batch Entrez](#)
- [INSDC](#)

# Accession to Tax-ID

accession	accession.version	taxid	gi
P15711	P15711.1	5875	112670
P18646	P18646.1	3917	112671
P13813	P13813.1	5850	112674
P19084	P19084.1	4232	112676

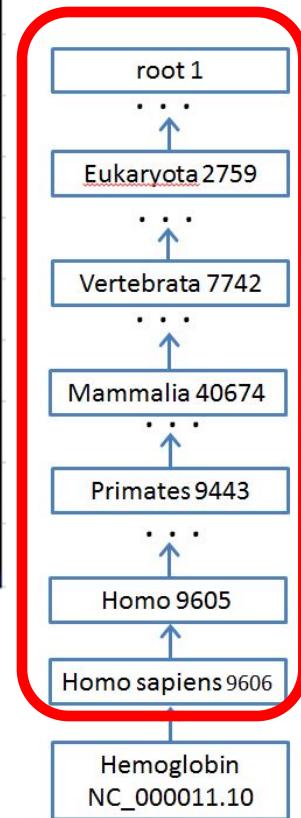
- 818,215,989 rows
- 61 GB



# Tax-ID to Names and Parent

TaxID	Name	Parent TaxID	Rank
9606	Homo sapiens	9605	species
9605	Homo	9604	genus
9604	Homininae	207598	subfamily
207598	Hominidae	314295	family
9443	Primates	314146	order
314146	Euarchontogli	314146	superorder
40674	Mammalia	32524	class
2759	Eukaryota	131567	superkingdom
131567	cellular organisms	1	no rank
1	root	NULL	no rank
378467	Platytheca galloides	4272	species
378464	Elaeocarpus foveolatus	26005	species
378465	Elaeocarpus sericopetalus	26005	species
378462	Elaeocarpus culminicola	26005	species

- 1,438,665 rows
- Source: 213 MB



# Free Python DB Code!

Map NCBI taxonomy and GI

Lazy Bioinformatics get the job done lazily!

Classic Flipcard Magazine Mosaic Sidebar Snapshot

JUL 5 Map NCBI taxonomy and GI into a Sqlite database

This very first technical post is going to be easy but important, for it is the basis of

### Objective

Convert the NCBI taxonomy and GI dumps into a database that can be queried efficiently.

I am going to create a database with two tables. The first table is called "gi\_taxid" which contains the GI number and the taxon it belongs to. The second table is called "tree" and it contains the scientific name, parent taxid and rank. It is called tree because once we build it, we can query the taxonomy with ease. Coupling these two tables, we can do lots of powerful things!

### How

1. Go to <ftp://ftp.ncbi.nih.gov/pub/taxonomy/> and download gi\_taxid\_prot.dmp.gz. This file contains all the taxdmp extracts, we only need names.dmp and nodes.dmp. They are tab-delimited files.
2. Make sure you have sqlite in your computer. Visit [here](#) if you need instructions. If you are using a Mac, it is already there out of the box.

```
dgg32.blogspot.com/2013/07/map-ncbi-taxonomy-and-gi-into-sqlite.html
```

bioinformatics get the job done lazily!

Sidebar Magazine Mosaic Sidebar Snapshot

```
import sys, sqlite3

#taxid : Node
tree = {}

#process the names.dmp
for line in open(sys.argv[1], 'r'):
    fields = line.strip().split("\t")
    notion = fields[6]
    taxid = fields[0]
    name = fields[2]

    if notion == "scientific name":
        if taxid not in tree:
            tree[taxid] = [name, "0", ""]

#process the nodes.dmp
for line in open(sys.argv[2], 'r'):
    fields = line.strip().split("\t")

    taxid = fields[0]
    parent = fields[2]
    rank = fields[4]
```

# DB stat

- Source size: ~61 GB
- SQLite DB file size: ~93G
- Total Rows: ~ 819 Millions
- Load time: 44 min
- Index creation time: 40 min



# DataTables (javascript)

Status - phusem-ion    DataTables | Table plug-in ...

https://datatables.net

bigtable

Search ...

DataTables Editor Your account: Login / Register

DataTables Table plug-in for jQuery

DataTables is a plug-in for the [jQuery](#) Javascript library. It is a highly flexible tool, based upon the foundations of progressive enhancement, and will add advanced interaction controls to any HTML table.

- Pagination, instant search and multi-column ordering
- Supports almost any data source:
  - DOM, Javascript, Ajax and server-side processing
- Easily theme-able: [DataTables](#), [jQuery UI](#), [Bootstrap](#), [Foundation](#)
- Wide variety of [extensions](#) inc. [Editor](#), [Buttons](#), [FixedColumns](#) and [more](#)
- Extensive [options](#) and a beautiful, expressive [API](#)
- Fully [internationalisable](#)
- Professional quality: backed by a suite of 2900+ unit tests
- Free open source software ([MIT license](#))! Commercial support available.
- [Show more features...](#)

How easy is it to use DataTables? Take a peek at the code below: a single `function call` to initialise the table is all it takes!

```
$(document).ready(function() {  
    $('#myTable').DataTable();  
});
```

Getting started with DataTables is as simple as including two files in your web-site, the CSS styling and the DataTables script itself. These two files are available on the [DataTables CDN](#):

CSS //cdn.datatables.net/1.10.12/css/

JS //cdn.datatables.net/1.10.12/js/

An example of DataTables in action is shown below.

Name	Position	Office	Age	Start date	Salary
Airi Satou	Accountant	Tokyo	33	2008/11/28	\$162,700
Angelica Ramos	Chief Executive Officer (CEO)	London	47	2009/10/09	\$1,200,000
Ashton Cox	Junior Technical Author	San Francisco	66	2009/01/12	\$86,000

# HTML without DataTables jQuery

Taxonomy report - taxo\_report\_2016-04-22  
file:///C:/temp/pete2.v7.nojQuery.html

## TAXONOMY REPORT

Job Name: taxo\_report\_2016-04-22  
Job Desc: data from ACUR142\_ATTCCT\_R1\_blastn\_nt.br  
Unique Acc.V Count: 8236  
Total rows processed: 2,521,663  
Rejected rows: 14330  
Jump to: [Accession-level](#) [species](#) [genus](#) [family](#) [superkingdom](#)

### ACCESSION.V TO TAXID (MAPPED RANK)

Count	Percentage	Rank name	TaxID
535942	21.2535 %	Gardnerella vaginalis ATCC 14018 = JCM 11026 (no rank)	<a href="#">585528</a>
430907	17.0882 %	Ureaplasma parvum serovar 3 (no rank)	<a href="#">38504</a>
243629	9.6614 %	Prevotella intermedia (species)	<a href="#">28131</a>
131324	5.2078 %	Prevotella sp. Sc00026 (species)	<a href="#">1231727</a>
127604	5.0603 %	Prevotella sp. oral taxon 299 str. F0039 (no rank)	<a href="#">575614</a>
120582	4.7818 %	uncultured bacterium (species)	<a href="#">77133</a>
116862	4.6343 %	Campylobacter ureolyticus RIGS 9880 (no rank)	<a href="#">1032069</a>
100602	3.9895 %	uncultured Ureaplasma sp. (species)	<a href="#">293430</a>
86298	3.4223 %	Prevotella melaninogenica (species)	<a href="#">28132</a>
83716	3.3199 %	Homo sapiens (species)	<a href="#">9606</a>
30456	1.2078 %	Atopobium vaginae DSM 15829 (no rank)	<a href="#">525256</a>
28575	1.1332 %	Finegoldia magna ATCC 29328 (no rank)	<a href="#">334413</a>
26183	1.0383 %	Ureaplasma diversum (species)	<a href="#">42094</a>
24814	0.9840 %	Pan paniscus (species)	<a href="#">9597</a>
21337	0.8461 %	Prevotella dentalis (species)	<a href="#">52227</a>
20712	0.8214 %	Prevotella enoeca (species)	<a href="#">76123</a>
20450	0.8110 %	Prevotella fusca JCM 17724 (no rank)	<a href="#">1236517</a>
18033	0.7151 %	Anaerococcus prevotii DSM 20548 (no rank)	<a href="#">525919</a>
16796	0.6661 %	Macaca fascicularis (species)	<a href="#">9541</a>

# Using DataTables

```
5      <meta name="viewport" content="width=device-width,initial-scale=1">
6      <title>Taxonomy report </title>
7      <script type="text/javascript" language="javascript"
src="http://code.jquery.com/jquery-1.12.0.min.js">
8          </script>
9      <script type="text/javascript" language="javascript"
src="https://cdn.datatables.net/1.10.11/js/jquery.dataTables.min.js">
10         </script>
11         <script type="text/javascript" class="init">
12             $(document).ready(function() {
13                 $('table.display').DataTable( {           // multi table example use
14                     table.display as selector
15                     lengthMenu: [ [ 10, 25, 50, 100, -1 ], [ 10, 25, 50, 100, "All" ] ],
16                     // all is coded as -1, thus the double array
17                     pageLength: 25,                         // YES, can use -1 to display
18                     all rows by default
19                     order: [ 0, "desc" ],                  // descending order //
20                     https://datatables.net/reference/option/order // def *should* be no
21                     ordering, show data as they are loaded.
22                     } );
23                 } );
24             </script>
25             <link rel="stylesheet" type="text/css"
26 href="https://cdn.datatables.net/1.10.11/css/jquery.dataTables.min.css">
27             <!-- overwrite some css to my liking -->
28             <STYLE>
```

# Bonus: Output

Taxonomy report    BLAST - Wikipedia, the free encyclopedia .html

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120790	4.1769 %	Streptococcus dysgalactiae subsp. equisimilis (subspecies)	<a href="#">119602</a>
78981	2.7312 %	Streptococcus pneumoniae (species)	<a href="#">1313</a>
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## SPECIES

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235921	8.1582 %	uncultured bacterium	<a href="#">77133</a>

# Text Output

## ===== Taxid at Accession.V =====

count	percentage	Rank name	[ taxid ] (running tally)
5	38.4615 %	Cyprinid herpesvirus 1 (species)	[ 317858 ] ( 5 )
2	15.3846 %	Rous sarcoma virus (species)	[ 11886 ] ( 7 )
1	7.6923 %	Adoxophyes honmai entomopoxvirus 'L' (species)	[ 1293540 ] ( 8 )
1	7.6923 %	Avian leukemia virus (no rank)	[ 11946 ] ( 9 )
1	7.6923 %	Avian leukosis virus (species)	[ 11864 ] ( 10 )
1	7.6923 %	Choristoneura occidentalis granulovirus (species)	[ 364745 ] ( 11 )
1	7.6923 %	Panine herpesvirus 2 (species)	[ 188763 ] ( 12 )
1	7.6923 %	Snake adenovirus 1 (no rank)	[ 189830 ] ( 13 )

## ===== Rank Level: species =====

count	percentage	Rank name	[ taxid ] (running tally)
5	38.4615 %	Cyprinid herpesvirus 1	[ 317858 ] ( 5 )
2	15.3846 %	Avian leukosis virus	[ 11864 ] ( 7 )
2	15.3846 %	Rous sarcoma virus	[ 11886 ] ( 9 )
1	7.6923 %	Adoxophyes honmai entomopoxvirus 'L'	[ 1293540 ] ( 10 )
1	7.6923 %	Choristoneura occidentalis granulovirus	[ 364745 ] ( 11 )
1	7.6923 %	Panine herpesvirus 2	[ 188763 ] ( 12 )
1	7.6923 %	Snake adenovirus A	[ 1146872 ] ( 13 )

## ===== Rank Level: genus =====

count	percentage	Rank name	[ taxid ] (running tally)
5	38.4615 %	Cyprinivirus	[ 692606 ] ( 5 )
4	30.7692 %	Alpharetrovirus	[ 153057 ] ( 9 )
1	7.6923 %	Atadenovirus	[ 100953 ] ( 10 )
1	7.6923 %	Betabaculovirus	[ 558017 ] ( 11 )
1	7.6923 %	Betaentomopoxvirus	[ 10286 ] ( 12 )
1	7.6923 %	Cytomegalovirus	[ 10358 ] ( 13 )

## ===== Rank Level: family =====

count	percentage	Rank name	[ taxid ] (running tally)
5	38.4615 %	Alloherpesviridae	[ 548682 ] ( 5 )
4	30.7692 %	Retroviridae	[ 11632 ] ( 9 )

# CLI (Python argparse)

```
Terminal          Terminal
(local_python_2.7.9)...          taxo > ./taxorpt.py -h
usage: taxorpt.py [-h] [-s IFS] [-c COL] [--db DB] [--html] [--text]
                  [--name JOBNAME] [--desc JOBDESC] [-d] [--version]
                  [infile] [outfile]

Create a taxonomic report for a file with list of GI

positional arguments:
  infile            name of input file to process (def STDIN)
  outfile           name of output file (def STDOUT)

optional arguments:
  -h, --help        show this help message and exit
  -s IFS, --separator IFS, --ifs IFS
                    the column separator character (defualt TAB)
  -c COL, --col COL
                    0-indexed column number containing the Accession.Ver
                    (default 3)
  --db DB          full path to taxonomy db (defualt ./ncbi-taxo-acc.db)
  --html           produce output in html format (default)
  --text            produce output in text format instead of html
  --name JOBNAME   name for this job
  --desc JOBDESC   quoted string describing this job
  -d, --debuglevel Debug mode. Up to -ddd useful for troubleshooting
                     input file parsing. -ddddd intended for coder.
  --version         show program's version number and exit
(local_python_2.7.9)...          taxo >
```

# Bonus: Web-UI

Bookmark Manager × \$ Scriptr

#/scripts/c2c94cca1c20295d64e06922901bb976

# scriptr

ID Bioinformatics Script Runner

Home Scripts History Advanced Support

**taxorpt**

- NGS:QC
- snpDAUG
- checkerboard
- Mobile plasmid sequencing
- MNM
- gBlaster
- The Pub
- NGS:prep
- Beerinformatics

**taxorpt**  
Taxonomy Reporter for Metagenomics BLAST (20160522a)

**Input file** taxorpt\_test\_input.txt  
Location of your NGS read files

160508  
taxorpt  
160425  
160427  
160426  
160505  
160405  
MiSeqF  
160314  
160317  
160328  
160323

**Output file** \$RUN\_OUTPUT\_DIR/taxorpt.html  
File name can be changed from suggestion, but directory should remain \$RUN\_OUTPUT\_DIR

**column\_index** 3  
0-indexed column number containing the Accession.Ver (BLAST OUTPUT use col idx=3)

**separator\_symbol** |

**taxorpt Help**  
[Taxo Report](#)  
[Documentation \(TBA\)](#)

**taxorpt Stats**  
Total runs ever 15  
Average runs per week 15  
Unique users 1

# Code Snapshot

The image shows two terminal windows side-by-side, both titled "Terminal".

The left terminal window displays a large block of Python code, likely from a file named `pyphy.py`. The code consists of numerous function definitions, many of which begin with `def`. Some examples include `getTaxidByName`, `getRankByTaxid`, `getParentByTaxid`, and `getSonsByTaxid`. The code is heavily indented, indicating nested functions or classes.

The right terminal window also displays a block of Python code, likely from a file named `taxorpt.py`. It includes several command-line operations: `> cat taxorpt.py | grep ^def`, `def process_cli()`, `def run_taxo_reporter( args )`, `def main()`, and `> wc -l *py`. Below these, it lists file counts: `743 pyphy_ext.py`, `249 pyphy.py`, `118 taxorpt.py`, and a total of `1110 total`. Further down, it shows `> cat *py | grep ^# | wc -l` resulting in `176`, and ends with `(local_python_2.7.9)...`.

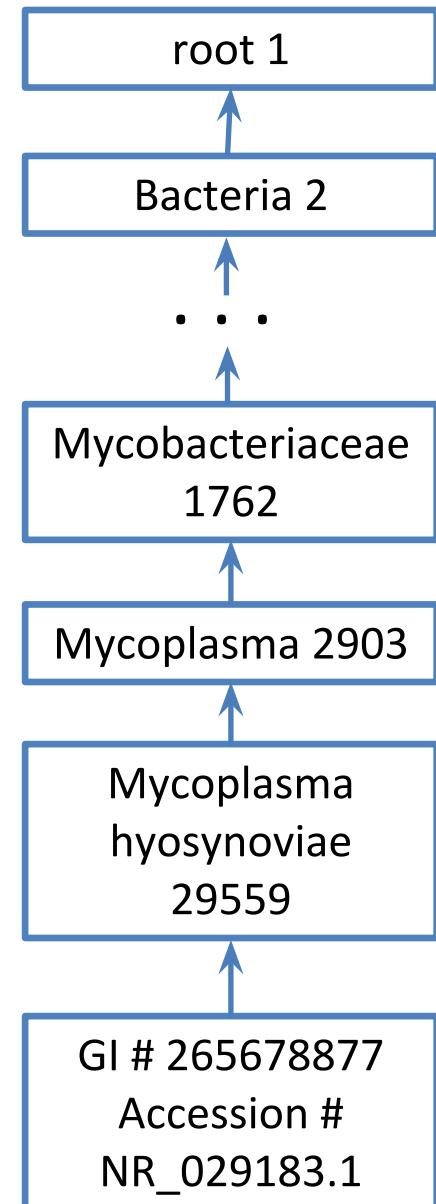
Both terminals have a green prompt at the bottom: `taxo >`.

```
436
437     for rank_item in workingRankSet :                                # this need to be in order, going up taxo tree.
438         dbg( 4, "*** ** rank_item: %s ** ***" % rank_item )
439         currentRank = rank_item
440         childRank = RankSet.getChild( currentRank )
441         parentRank = RankSet.getParent( currentRank )                ## if not topRank
442         if currentRank.name not in resultTable4 :
443             resultTable4.update( {currentRank.name: {}})
444         for childTid in resultTable4[childRank.name] :
445             tid = resultTable4[childRank.name][childTid]['ParentTaxid']
446             dbgMsg = "childtid=%8s : %s (child'sParent=%s)" % (childTid, resultTable4[childRank.name][childTid], tid)
447             dbg( 4, dbgMsg )
448             #print( tid ); print( resultTable4[childRank.name][tid] ) #'Taxid'][['RankName'] )
449             if tid not in resultTable4[currentRank.name] :
450                 parentTaxid = getParentByTaxid( tid )
451                 parentTaxid = getParentByTaxidRank( tid, parentRank.name )
452                 dbg( 4, "for tid: %s got parentTaxid %s" % (tid, parentTaxid) )
453                 rankName = getLineageByTaxid( tid, currentRank.name )
454                 runningCount = resultTable4[childRank.name][childTid]['Tally']
455                 resultTable4[currentRank.name][tid] = { 'ParentTaxid': parentTaxid, 'RankName': rankName, 'Tally': 1 }
456                 #print( "added %s into %s" % (tid, resultTable4[currentRank.name]) )
457                 #print( "added %s into %s" % (tid, resultTable4[currentRank.name]) )
458                 #pass
459                 #print( "bla" )
460             else :
461                 resultTable4[currentRank.name][tid]['Tally'] += resultTable4[childRank.name][childTid]['Tally']
462                 resultTable4[currentRank.name][tid]['Children'].append( childTid )
463                 dbg( 4, 'in else section, updating %s with child %s' % (tid, childTid) )
464
465     ## at this point, need to process the top level domain (superkingdom)
466     ## can probably merge into above with a few if conditions
467     ## but this is easier to read, too many if hides flow of algorithm
468     topRank = RankSet.getHighest()
469     belowTopRank = RankSet.getChild( topRank )
470     dbg( 4, "*** ** rank_item: %s (lower found to be %s) ** ***" % (topRank, belowTopRank) )
471     if topRank.name not in resultTable4 :
472         resultTable4.update( {topRank.name: {} } )
473     for childTid in resultTable4[belowTopRank.name] :
474         tid = resultTable4[belowTopRank.name][childTid]['ParentTaxid']
475         #tid = resultTable4[childRank.name][childTid]['ParentTaxid']
476         dbgMsg = "childtid=%8s : %s (child'sParent=%s)" % (childTid, resultTable4[belowTopRank.name][childTid], tid)
477         dbg( 4, dbgMsg )
478         if tid not in resultTable4[topRank.name] :
479             runningCount = resultTable4[belowTopRank.name][childTid]['Tally']
480             rankName = getLineageByTaxid( tid, topRank.name )
481             # omitting ParentTaxid as no more parent here
482             # this is really the only place it differ from the above block inside the for rank_item loop
483             resultTable4[topRank.name][tid] = { 'RankName': rankName, 'Tally': runningCount, 'Children': [ childTid ] }
484         else :
```

# The Data Analytics Journey...

# Algorithm

- For each BLAST row
- GI#/Accession# ->Tax-ID  
-> parent Tax-ID -> ... root
- For each taxonomy rank level:
- Count unique Tax-ID
  - 29599: 1230
  - 37162: 1680
- Lookup name of each Tax-ID



# Ver 0.1 Performance

	Ver 0.1
Input	5,396,360 line
Process time	12.5 hours (45,135s )
Rate	7174 line/min

Hey, that's 120 line/sec!!  
Can you take that many steps in a sec?!



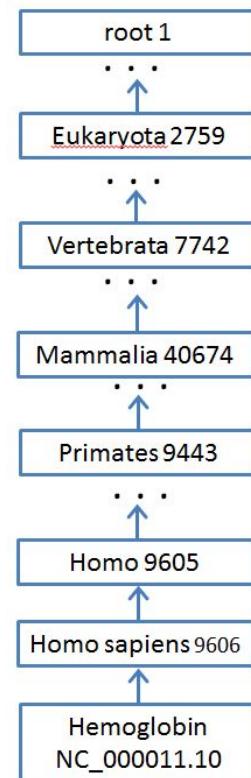
# Improvement #1 (Ver 0.2)

- 5M lines, but not all GI# are unique
- A little sorting, a little bit more coding...
- Reduces to ~ 43k accessions

	Ver 0.2	Ver 0.1
Input lines	5,396,360	5,396,360
Process time	86 min	12.5 hours (45,135 s)
Rate	1,046 line/sec	120 line/sec
Uniq Acc#	42,916	
Rate	<i>8.3 acc#/sec</i>	

# Improvement #2a (Ver 0.3)

- Full Taxonomy Trace, typically ~6-12 ranks:  
('no rank', 'Legionella pneumophila subsp. pneumophila str. Thunder Bay', '1199191'),  
('subspecies', 'Legionella pneumophila subsp. pneumophila', '91891'),  
('species', 'Legionella pneumophila', '446'),  
('genus', 'Legionella', '445'),  
('family', 'Legionellaceae', '444'),  
('order', 'Legionellales', '118969'),  
('class', 'Gammaproteobacteria', '1236'),  
('phylum', 'Proteobacteria', '1224'),  
('superkingdom', 'Bacteria', '2'),  
('no rank', 'cellular organisms', '131567'),  
('no rank', 'root', '1')

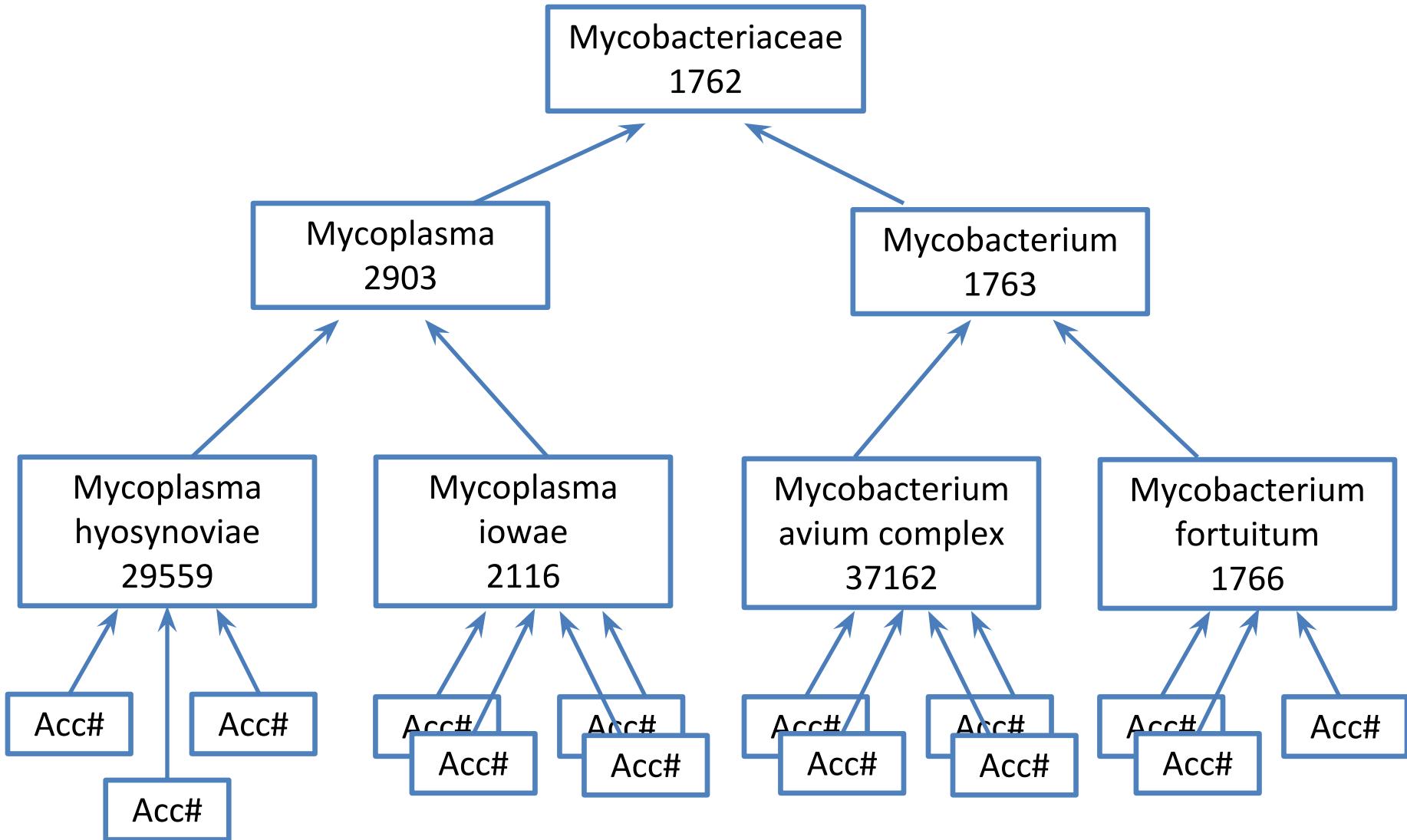


# Improvement #2a (Ver 0.3)

- Full Taxonomy Trace, typically ~6-12 ranks:  
('no rank', 'Legionella pneumophila subsp. pneumophila str. Thunder Bay', '1199191'),  
('subspecies', 'Legionella pneumophila subsp. pneumophila', '91891'),  
('species', 'Legionella pneumophila', '446'),  
('genus', 'Legionella', '445'),  
('family', 'Legionellaceae', '444'),  
('order', 'Legionellales', '118969'),  
('class', 'Gammaproteobacteria', '1236'),  
('phylum', 'Proteobacteria', '1224'),  
('superkingdom', 'Bacteria', '2'),  
('no rank', 'cellular organisms', '131567'),  
('no rank', 'root', '1')
- Reduce to ~4-5 taxonomy rank

# Improvement #2b (Ver 0.3)

- Higher ranks merge -> Reduced DB lookup



# Ver 0.3 Performance

	Ver 0.3	Ver 0.2	Ver 0.1
Input lines	5,396,360	5,396,360	5,396,360
Process time	18 min (1,137s)	86 min	12.5 hours (45,135 s)
Rate	4,746 lines/sec	1,046 line/sec	120 line/sec
Uniq Acc#	42,916	42,916	
<i>Rate</i>	<i>37.7 acc#/sec</i>	<i>8.3 acc#/sec</i>	

Yihaa!!



# How to Further Performance?

- Will local disk be faster than NFS?



VS



image src:

<http://ep.yimg.com/ay/nycewheels/the-birdy-performance-folding-bike-3.png>

# Detour: Isilon File Server

Terminal Sessions View X server Tools Games Settings Macros Help

1.hoti1@c3po status -q

m-ion

Cluster Health: [OK]

Cluster Storage: HDD SSD Storage

Size: 958T (958T Raw) 3.2T (3.2T Raw)

VHS Size: 0

Used: 498T (52%) 88G (3%)

Avail: 459T (48%) 3.2T (97%)

ID	IP Address	Health	DASR	Throughput (bps)	HDD Storage	SSD Storage		
				In	Out	Total	Used / Size	Used / Size
1 1	.90.208	OK		723K	138K	861K	77T/ 130T( 59%)	(No Storage SSDs)
4 1	.90.205	OK		19M	11M	31M	39T/ 65T( 60%)	(No Storage SSDs)
6 1	.90.237	OK		560K	66K	626K	39T/ 65T( 60%)	(No Storage SSDs)
15 1	.90.202	OK		439K	175K	613K	39T/ 65T( 60%)	(No Storage SSDs)
16 1	.90.204	OK		392K	32	392K	39T/ 65T( 60%)	(No Storage SSDs)
17 1	.90.197	OK		20M	221K	20M	74T/ 130T( 57%)	(No Storage SSDs)
18 1	.90.209	OK		2.9K	133K	135K	74T/ 130T( 57%)	(No Storage SSDs)
19 1	.90.212	OK		3.9M	66K	4.0M	74T/ 130T( 57%)	(No Storage SSDs)
20 1	.190	OK		0	32	32	14T/ 60T( 24%)	29G/ 1.1T( 3%)
21 1	.90.199	OK		456K	131K	587K	14T/ 60T( 24%)	29G/ 1.1T( 3%)
22 1	.90.200	OK		277K	131K	408K	14T/ 60T( 24%)	29G/ 1.1T( 3%)
Cluster Totals:				46M	12M	58M	498T/ 958T( 52%)	88G/ 3.2T( 3%)
Health Fields: D = Down, A = Attention, S = Smartfailed, R = Read-Only								
isi version								
Isilon OneFS v7.2.1.1 B_7_2_1_081(RELEASE): 0x702015000100051:Wed Nov 18 11:20:20 GMT 2015 root@sea-build7-02:/b/mnt/obj/b/mnt/src/sys/IQ.amd64.release clang version 3.3 (tags/RELEASE_33/final)								
Sev	Instan...	Start Time	Message	Scope	Actions			
!	28.55291	2016-05-25 15:00:57	SyncIQ is encountering problems with policy sc...	Node 19	<a href="#">View details</a>			
!	20.722248	2016-05-25 12:42:14	AD server missing needed SPN(s) HOST/sync...	Cluster	<a href="#">View details</a>			
!	21.11303...	2016-05-19 14:38:06	Node 19 is online (offline event 21.1130383, Ma...	Node 19	<a href="#">View details</a>			
!	25.3440	2016-05-19 14:37:22	Recurring: The drive in Bay 2 has firmware ver...	Node 19	<a href="#">View details</a>			
!	21.113032	2016-05-19 14:12:21	Node 19 is offline	Node 19	<a href="#">View details</a>			

# Tier Policy

The screenshot shows the OneFS storage management interface. At the top, there's a navigation bar with tabs: DASHBOARD, CLUSTER MANAGEMENT, and FILE. The FILE tab is active, showing sub-links: Storage Pools, SmartQuotas, Deduplication, File System Explorer, and File System Settings. Below this, the main content area is titled "Storage Pools". Under "Storage Pools", there are four tabs: Summary (selected), File Pool Policies, SmartPools, and SmartPools Settings. The "File Pool Policies" tab is currently selected, displaying a list of policies:

Order	Policy Name	Description	Actions
↓	pinned_xtier	Put cscratch and app on X-Tier pool	<a href="#">View / Edit</a> <a href="#">More</a>
↑↓	lowpri_files	Lower Priority files can go to NL-Tier by default	<a href="#">View / Edit</a> <a href="#">More</a>
↑↓	usem_promoting	move recently accessed files to X-Tier	<a href="#">View / Edit</a> <a href="#">More</a>
↑↓	usem_aging_very_first	move files not accessed recently in usem/dlab/ldrive > 1 month to the NL-Tier	<a href="#">View / Edit</a> <a href="#">More</a>
↑↓	usem_aging_first	move files not accessed recently in usem/dlab > 1 month to the NL-Tier	<a href="#">View / Edit</a> <a href="#">More</a>
↑	usem_aging	move files not accessed recently in usem > 1 month to the NL-Tier	<a href="#">View / Edit</a> <a href="#">More</a>
Default Policy This policy applies to all files not selected by higher-priority policies.			

At the bottom right of the interface, there's a link to "Create a File Pool Policy". Above the interface, there's a terminal window showing the command "isi storagepool nodepools list" and its output, which includes storage pool names like "n400\_72tb\_12gb-ram" and "n400\_144tb\_48gb", their sizes, protection levels, and manual status.

```
1. /home/mobaxterm 2. /home/mobaxterm/psx 3. hoti1@c3po 4. /drives/c/temp +  
isi filepool policies list --verbose  
    Name: pinned_xtier  
    Description: Put clscratches and app on X-Tier pool  
    Apply Order: 1  
    File Matching Pattern: Path == usem/clscratches (case sensitive)  
    Set Requested Protection: default  
        Data Access Pattern: -  
        Enable Coalescer: -  
        Data Storage Target: X-Tier  
        Data SSD Strategy: metadata  
    Snapshot Storage Target: X-Tier  
    Snapshot SSD Strategy: metadata  
        Cloud Pool: -  
    Cloud Compression Enabled: -  
    Cloud Encryption Enabled: -  
        Cloud Data Retention: -  
Cloud Incremental Backup Retention: -  
    Cloud Full Backup Retention: -  
        Cloud Accessibility: -  
        Cloud Readahead: -  
    Cloud Cache Expiration: -  
    Cloud Writeback Frequency: -  
-----  
    Name: usem_promoting  
    Description: move recently accessed files to X-Tier  
    Apply Order: 3  
    File Matching Pattern: Path == usem (case sensitive) AND Accessed Time < 1W  
    Set Requested Protection: default  
        Data Access Pattern: -  
        Enable Coalescer: -  
        Data Storage Target: X-Tier  
        Data SSD Strategy: metadata  
    Snapshot Storage Target: X-Tier  
    Snapshot SSD Strategy: metadata  
-----  
    Name: usem_aging_first  
    Description: move files not accessed recently in usem/dlab > 1 month to the NL-Tier  
    Apply Order: 5  
    File Matching Pattern: Accessed Time > 1M AND Path == usem/dlab (case sensitive)  
    Set Requested Protection: -  
        Data Access Pattern: -  
        Enable Coalescer: -  
        Data Storage Target: NL-Tier  
        Data SSD Strategy: metadata  
    Snapshot Storage Target: NL-Tier  
    Snapshot SSD Strategy: avoid
```

# Local Disk

- SAS
- 6 Gbps
- 15,000 rpm

	NFS (Isilon)	Local HD
iozone benchmark	2,012.9 Mbps	823.2 Mbps



./iozone -i 0 -c -e -w -r 1024k -s 16g -t 4 -+n -b result.xls

# Detour: Local Disk vs NFS

	Ver 0.3 NFS	Ver 0.3 Local HD
lozone write (Mbps)	2,012.9	823.2
lozone read (Mbps)	2542.3	67,178
Input lines	5,396,360	5,396,360
Process time	920 s (15.3 min)	91.36 s (*) (1.5 min)
Rate (lines/sec)	5,866	59,067
cp time	-	970.17 s
Total time	920 s	1,062 s
Rate (lines/sec)	5,866	5,081

# Detour: NFS vs Local Disk vs RAMdisk

	Ver 0.3 NFS	Ver 0.3 Local HD <code>/dev/sda</code>	Ver 0.3 RAMdisk <code>/dev/shm</code>
lozone write (Mbps)	2,012.9	823.2	56,873
lozone read (Mbps)	2542.3	67,178	66,632
Input lines	5,396,360	5,396,360	5,396,360
Process time	920 s (15.3 min)	91.36 s (*) (1.5 min)	94.88 s (1.6 min)
Rate (lines/sec)	5,866	59,067	56,876
cp time	-	970.17 s	475.35 s
Total time	920 s	1,062 s	570 s
Rate (lines/sec)	5,866	5,081	9,467

# Larger Performance Question

- How to run 100 or 1000 jobs?
- Other Bioinformatics job would use much larger dataset
- Further performance improvement?



image sources:

<http://fm.cnbc.com/applications/cnbc.com/resources/img/editorial/2013/02/20/100475233-gallery.530x298.jpeg?v=1361374656>

# HPC to the Rescue

## RESOURCES

- My Clusters
- r2d2
  - Switches
    - switch01
  - Networks
    - externalnet
    - globalnet
    - ibnet
    - internalnet
    - ipnet
  - Power Distribution Units
  - Software Images
    - default-image
    - sciComp-SBL-RHEL6.5
    - sciComp-SBL-RHEL6.5...
    - sciComp-SBL-RHEL6.6...
    - tin-test
  - Node Categories
    - default
    - sciComp-Default
    - sciComp-Default-8\_slots
    - scicomp-gpu
  - Head Nodes
    - r2d2
  - Racks
  - Chassis
    - chassis-skywalker
  - Virtual SMP Nodes
  - Nodes
    - c3po
    - skywalker-1-10
    - skywalker-1-11
    - skywalker-1-12

## EVENT VIEWER

## All Events

	Time	Cluster	Source	Message
1	31/May/2016 02:31:00	r2d2	skywalker-3-8	Check 'smart' is in state UNKNOWN on skywalker-3-8
1	31/May/2016 01:31:01	r2d2	skywalker-3-8	Check 'smart' is in state PASS on skywalker-3-8
1	31/May/2016 01:01:00	r2d2	skywalker-3-6	Check 'smart' is in state UNKNOWN on skywalker-3-6
1	31/May/2016 01:01:00	r2d2	skywalker-3-8	Check 'smart' is in state UNKNOWN on skywalker-3-8
1	31/May/2016 00:30:15	r2d2	skywalker-3-8	Check 'smart' is in state PASS on skywalker-3-8
1	31/May/2016 00:30:15	r2d2	skywalker-3-6	Check 'smart' is in state PASS on skywalker-3-6

# High Throughput Computing

- Mixed generations (Nehalem, Haswell)
- A few large memory SMP nodes
- A few GPU nodes
- IB QDR interconnect
- All nodes have full NFS access to “HPC NAS”

# TaxoRpt on HPC

- qsub taxorpt.py for parallel run
- DB is SQLite.
  - All job queries same DB file from NFS
  - Copy to local disk
  - RAMdisk availability challenge

# Future Directions: Lustre?

- Place SQLite DB file in Lustre
  - Lustre as a dedicated file server
  - 10 Gbps connection? -> “Faster NFS”
  - IB connection?
  - May need to copy DB
  - Storage “embedded” within HPC?
- HDFS ??

# HDFS

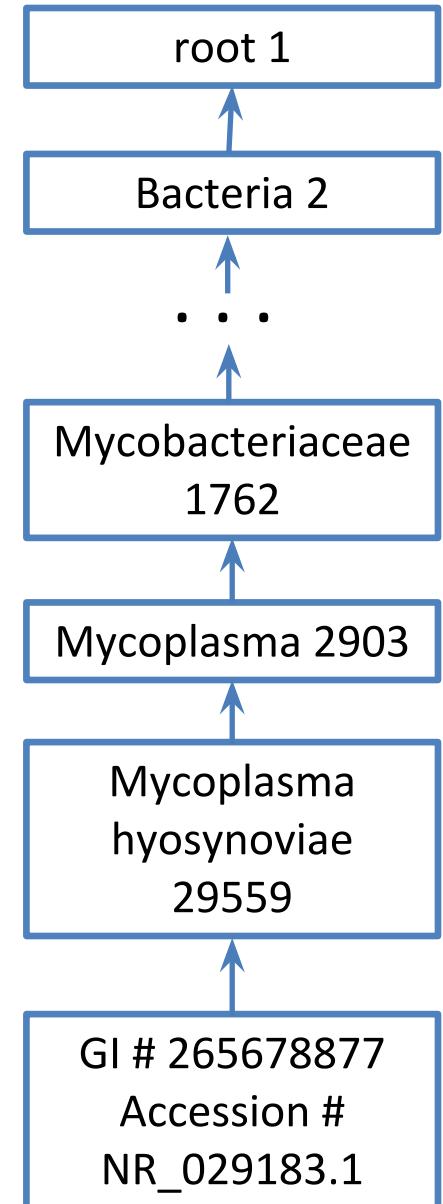
- Hadoop Distributed File System
- Data distributed on server nodes with many disks
- Processing of data is to be dispatched to the server node containing local portion of data
  - 20 data nodes in Hadoop -> 20 active workers
  - 20 hpc nodes->19 idle workers!!
- Especially useful if want single summary result from the 100 jobs.

# HDFS/Spark SQL HW

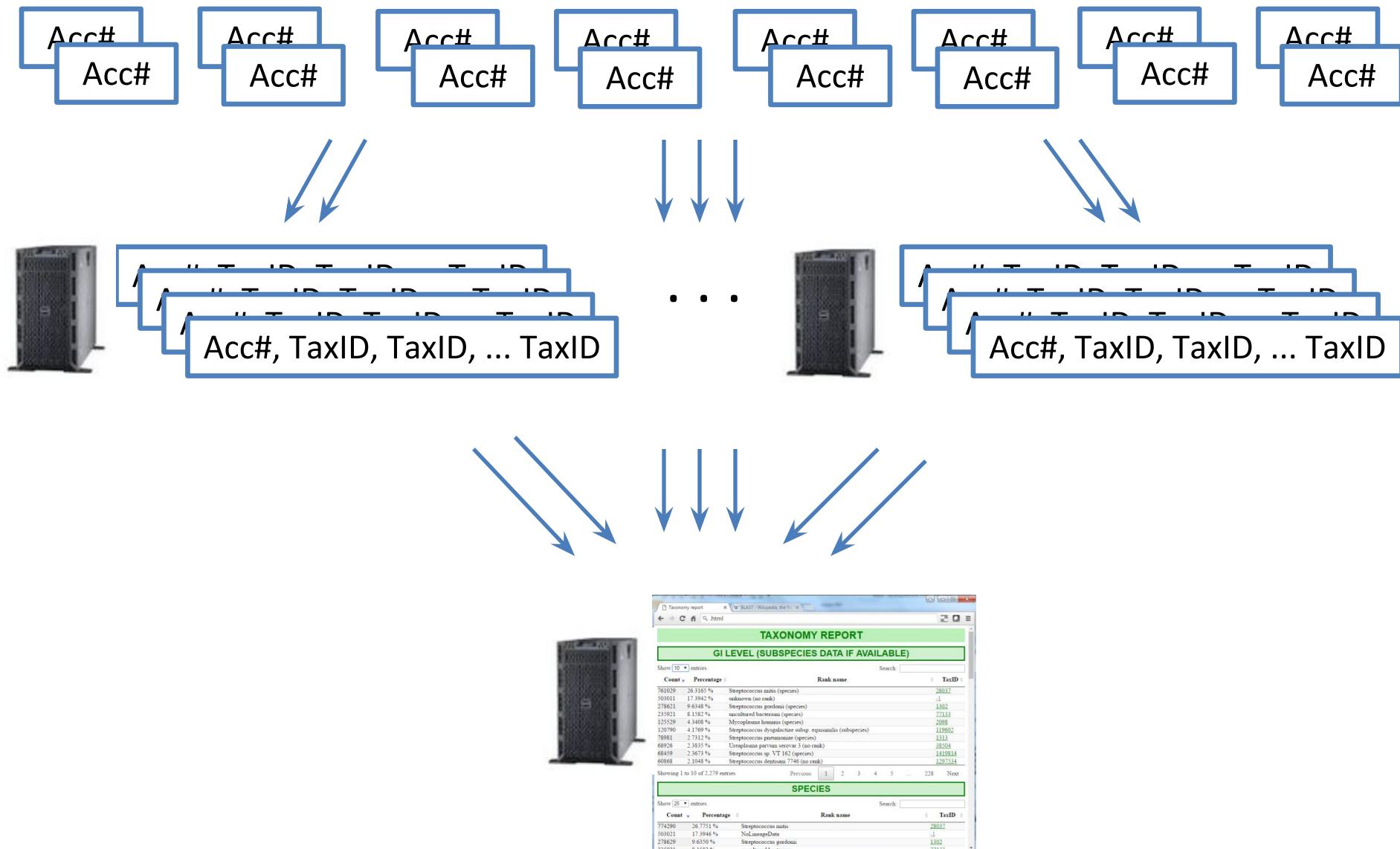
- HDFS background
- 2 name nodes (Lustre MDS)
- 1 journal node
- 8 data nodes (Lustre OSS)
  - 26 disks
  - each a /hdfs/dataX
  - 512 TB of space

# Spark SQL

- Distributed storage in HDFS
  - > Distributed processing
    - Spark
    - Spark SQL
- Create Taxonomy DB in Hadoop cluster
- Optimization #1 using Spark SQL
  - Modify TaxoRpt to use Spark SQL instead of SQLite
- Optimization #2 using Spark



# Optimization #2: Scatter, Gather



# Where is your bet?

- Lustre?
- HDFS/Spark SQL?
- Dedicated server with:
  - Lot of RAM?
  - Fusion IO card?

# Summary

- Data analytics can be tricky
- Be sure to pick the right combination of technologies
- Have a clear goal in mind
- Be ready for eureka moments that send you down a new path



*"It's a poor craftsman, son, who blames his tools."*

**Thank You!!**

?

# Backup Slides...

# Ipsilon NFS Export

OneFS

https://:8080/OneFS#NFS/NFSExports

NFS Exports

Select an action

Export ID / Path	Description	
103 Path: /	Home Directory	<a href="#">View details</a>   <a href="#">Delete</a>
102 Path: /	InsightIQ FSA - SYSTEM EXPORT	<a href="#">View details</a>   <a href="#">Delete</a>
101 Path: /	...e...	<a href="#">Hide details</a>   <a href="#">Delete</a>

NFS Export Details

Export ID:

Description:

Clients:

Always Read-Write Clients:

Always Read-Only Clients:

Root Clients:

Unresolved Clients:

Directory Paths:

[...and 3 more](#)

[Edit](#)

Permissions: **Read-write access ENABLED** [Edit](#)  
**Mount access to sub-directories DISABLED**

Map Root User: **Using custom value of:**  
User : Map root users to user nobody  
Primary Group : No primary group  
Secondary Groups: No secondary groups [Edit](#)

Map Non Root User: **Using default value of:**  
disabled [Edit](#)

Map Failure User: **Using default value of:**  
disabled [Edit](#)

Security Type(s): **Default: UNIX** [Edit](#)

**[+] Advanced Export Settings**

# Isilon Jobs

OneFS x

https:// 3:8080/OneFS#Operations/Types

Logged in as root | Review recent events | Log out | Help ?

Cluster Name: phusem-ion (OneFS Version: 7.2.1.1)

DASHBOARD CLUSTER MANAGEMENT FILE SYSTEM DATA PROTECTION ACCESS PROTOCOLS

General Settings Network Configuration Hardware Configuration Job Operations Auditing Diagnostics

## Job Operations

Job Summary Job Types Job Reports Job Events Impact Policies

### Job Types

Name	State	Priority	Impact	Schedule	Actions
Collect <i>Create a list of changes between two consecutive SyncIQ snapshots.</i>	Enabled	4	LOW	Manual	<a href="#">View / Edit</a> <a href="#">More ▾</a>
Dedupe <i>Scan a directory for redundant data blocks and deduplicate all redundant data stored in the directory. This job requires a SmartDedupe license.</i>	Enabled	4	LOW	Manual	<a href="#">View / Edit</a> <a href="#">More ▾</a>
DedupeAssessment <i>Scan a directory for redundant data blocks and report an estimate of the amount of space that could be saved by deduplicating the directory. This job does not require a SmartDedupe license.</i>	Enabled	6	LOW	Manual	<a href="#">View / Edit</a> <a href="#">More ▾</a>
DomainMark <i>Associate a path and its contents with a domain.</i>	Enabled	5	LOW	Manual	<a href="#">View / Edit</a> <a href="#">More ▾</a>

# Isilon Jobs (cont'd)

3080/OneFS#Operations/Types					
Job Name	Status	Priority	Protection Level	Last Run	Action
DomainMark <i>Associate a path and its contents with a domain.</i>	Enabled	5	LOW	Manual	<a href="#">View / Edit</a> <a href="#">More</a>
FSAnalyze <i>Gather information about the file system.</i>	Enabled	6	LOW	Every day at 22:00	<a href="#">View / Edit</a> <a href="#">More</a>
FlexProtect <i>Scan the file system after a device failure to ensure that all files remain protected. FlexProtect is most efficient in clusters that contain only HDDs.</i>	Enabled	1	MEDIUM	Manual	<a href="#">View / Edit</a> <a href="#">More</a>
FlexProtectLin <i>Following a node failure, scan the file system to ensure that all files remain protected. FlexProtectLin is most efficient if file system metadata is stored on SSDs.</i>	Enabled	1	MEDIUM	Manual	<a href="#">View / Edit</a> <a href="#">More</a>
IntegrityScan <i>Verify file system integrity.</i>	Enabled	1	MEDIUM	Manual	<a href="#">View / Edit</a> <a href="#">More</a>
MediaScan <i>Locate and clear media-level errors from disks.</i>	Enabled	8	LOW	The 1st saturday of every month at 12:00	<a href="#">View / Edit</a> <a href="#">More</a>
MultiScan <i>Perform the work of the AutoBalance and Collect jobs simultaneously.</i>	Enabled	5	OFF_HO...	Manual	<a href="#">View / Edit</a> <a href="#">More</a>
PermissionRepair <i>Correct file and directory permissions in the /ifs directory.</i>	Enabled	5	LOW	Manual	<a href="#">View / Edit</a> <a href="#">More</a>
QuotaScan <i>Update quota accounting for domains created on an existing file tree. This job requires a SmartQuotas license.</i>	Enabled	6	LOW	Manual	<a href="#">View / Edit</a> <a href="#">More</a>
SetProtectPlus <i>Apply a default file policy across the cluster. This job runs only if the Isilon SmartPools software module is not licensed.</i>	Enabled	6	LOW	Manual	<a href="#">View / Edit</a> <a href="#">More</a>
ShadowStoreDelete <i>Free space that is associated with a shadow store.</i>	Enabled	2	LOW	Every sunday at 12:00am	<a href="#">View / Edit</a> <a href="#">More</a>
ShadowStoreProtect <i>Protect shadow stores which are referenced by a lin with a higher requested protection</i>	Enabled	6	LOW	Every day every 16 hours from 4:00am	<a href="#">View / Edit</a> <a href="#">More</a>
SmartPools <i>Enforce SmartPools file policies. This job requires a SmartPools license.</i>	Enabled	6	LOW	Every 1 days at 18:00	<a href="#">View / Edit</a> <a href="#">More</a>
SnapRevert <i>Revert an entire snapshot back to head.</i>	Enabled	5	LOW	Manual	<a href="#">View / Edit</a> <a href="#">More</a>
SnapshotDelete <i>Free space associated with deleted snapshots.</i>	Enabled	2	MEDIUM	Manual	<a href="#">View / Edit</a> <a href="#">More</a>
TreeDelete <i>Delete a specified file path in the /ifs directory.</i>	Enabled	4	MEDIUM	Manual	<a href="#">View / Edit</a> <a href="#">More</a>
WormQueue <i>Scan the SmartLock LIN queue.</i>	Enabled	6	LOW	Every day at 02:00	<a href="#">View / Edit</a> <a href="#">More</a>

# Isilon SyncIQ (DR)

OneFS

https:// 8080/OneFS#SyncIQ/Policies

OneFS STORAGE ADMINISTRATION Cluster Name: phusem-ion (OneFS Version: 7.2.1.1)

DASHBOARD CLUSTER MANAGEMENT FILE SYSTEM DATA PROTECTION ACCESS PROTOCOLS

SnapshotIQ SyncIQ Backup Antivirus

SyncIQ

Summary Policies

SyncIQ Policies

Select a bulk action

Policy Name	State
home_mirror	Enabled
iso_mirror	Enabled
ldrive_mirror	Enabled
medchem-dev-sl...	Enabled
ngs_mirror	Enabled
plp_mirror	Enabled
nron2_mirror	Enabled

View SyncIQ Policy Details

\* = Required field

**Settings**

\* Policy Name **home\_mirror**

Description **No value**

Enabled **Yes, policy is enabled**

Action **Synchronize**

Run Job **Every 1 days every 1 hours between 12:00 AM and 11:59 PM**

Last Successful Run **01:00 PM**

Last Started **2016-05-30 13:09:58-0700**

**Source Cluster**

\* Source Root Directory **/ifs/usem/home**

Included Directories **No value**

Excluded Directories **No value**

File Matching Criteria **No value**

**Close** **Edit Policy**

# Isilon SMB

OneFS X

https://10.80.1.1080/OneFS#SMB/Shares

OneFS STORAGE ADMINISTRATION

DASHBOARD CLUSTER MANAGEMENT FILE SYSTEM DATA P

Windows Sharing (SMB) UNIX Sharing (NFS) FTP Settings HTTP Settings ACLs

Windows Sharing (SMB) Current Access Zone: System

SMB Shares Default Share Settings SMB Server Settings

SMB Shares

SMB Service Status: Enabled [SMB Settings](#)  
SMB Shares: 42

SMB Shares

Name / Path

[Edit](#)

Advanced Settings: [+](#) [Advanced SMB Share Settings](#)

Setting Value

Create Permissions Use custom Use create mask and mode [Edit](#)

Setting	Default/Custom	User [R W X]	Group [R W X]
Other [R W X]			
Create Mask (Dir)	Use custom	✓ ✓ ✓	✓ ✓ ✓
Create Mode (Dir)	Use custom	✓ ✓ ✓	✓ ✓ ✓
Create Mask (File)	Use custom	✓ ✓	✓ ✓
Create Mode (File)	Use custom	✓ ✓	✓ ✓

Performance Settings

Setting Value

Change Notify Use default Norecurse

Olocks Use default Yes

Security Settings

Setting Value

Impersonate Guest Use default Never

Impersonate User Use custom Sys\_usem\_ngs [Edit](#)

NTFS ACL Use custom No [Edit](#)

Access Based Enumeration Use default No

HOST ACL Use custom No value [Edit](#)

[Edit](#)

DASHBOARD

CLUSTER MANAGEMENT

FILE SYSTEM

DATA PROTECTION

ACCESS

PROTOCOLS

[General Settings](#)**Network Configuration**[Hardware Configuration](#)[Job Operations](#)[Auditing](#)[Diagnostics](#)

## Network Configuration

### External Network Settings

#### Subnets [Add subnet](#)

[ninety](#)

Subnet:

Netmask:

Gateway:

SmartConnect zone:

[eight](#) – HPC storage

Subnet:

Netmask:

Gateway:

SmartConnect zone:

#### DNS Settings [Edit](#)

Domain name servers:

DNS search list:

DNS resolver options:

#### Provisioning Rules [Add rule](#)

[basic](#) [Delete](#)

If node type is Storage-I, then assign ext-1 to pool pool90 in subnet ninety

### Internal Network Settings

#### InfiniBand Interfaces

[int-a](#)

State: Enabled

Netmask: 255.255.255.0

IP ranges: 192.168.1.1 – 192.168.1.100

[int-b / Failover](#)

State: Enabled

Netmask: 255.255.255.0

IP ranges: 192.168.2.1 – 192.168.2.100

int-b

IP ranges: 192.168.3.1 – 192.168.3.100

Failover

# Isilon Networks

# Isilon 2x10 GigE Conf

Network Settings - phuse X

https://:8080/NetworkEdit?subnet=eight&init=true

**OneFS** STORAGE ADMINISTRATION

DASHBOARD CLUSTER MANAGER

General Settings Network Configuration

## Network Configuration

**eight** – HPC storage VLAN [Delete subnet](#)

**Settings** [Edit](#)

Subnet:	10.
Netmask:	255.
MTU:	1500
Gateway:	10.
SmartConnect service IP:	10.
VLAN tagging (802.1Q):	Disabled
VLAN ID:	not set
Hardware load balancing IPs:	not set

### IP Address Pools [Add pool](#)

- + **eight** [Delete pool](#)
- + **SyncIQ** [Delete pool](#)

### IP Address Pools [Add pool](#)

- **eight** [Delete pool](#)

**Basic settings** [Edit](#)

IP range (low-high): 10. 30

Access zone: System

**SmartConnect settings** [Edit](#)

Zone name:	synciq
Connection policy:	Round Robin
SmartConnect service subnet:	eight
IP allocation method:	Static

### Pool members [Edit](#)

Aggregation mode: Round-Robin Tx

- 10gige-2, Node 01
- 10gige-2, Node 04
- 10gige-2, Node 06
- 10gige-2, Node 15
- 10gige-2, Node 16
- 10gige-2, Node 17
- 10gige-2, Node 18
- 10gige-2, Node 19
- 10gige-2, Node 20
- 10gige-2, Node 21
- 10gige-2, Node 22

### IP Address Pools [Add pool](#)

- + **SyncIQ** [Delete pool](#)

## IP Address Pools [Add pool](#)

+ **eight** [Delete pool](#)

- **SyncIQ** [Delete pool](#)

### Basic settings [Edit](#)

IP range (low-high): 10. 99

Access zone: System

### SmartConnect settings [Edit](#)

Zone name: synciq  
Connection policy: Round Robin  
SmartConnect service subnet: eight  
IP allocation method: Static

### Pool members [Edit](#)

Aggregation mode: Round-Robin Tx

- 10gige-2, Node 01
- 10gige-2, Node 04
- 10gige-2, Node 06
- 10gige-2, Node 15
- 10gige-2, Node 16
- 10gige-2, Node 17
- 10gige-2, Node 18
- 10gige-2, Node 19
- 10gige-2, Node 20
- 10gige-2, Node 21
- 10gige-2, Node 22

# Isilon 2x 1GigE config

Network Settings - phusem-ion

https://8080/Net

Settings [Edit](#)

Subnet: 255.255.255.0  
Netmask: 1500  
MTU:  
Gateway: Priority 1  
SmartConnect service IP:  
VLAN tagging (802.1Q): Disabled  
VLAN ID: not set  
Hardware load balancing IPs: not set

IP Address Pools [Add pool](#)

pool90 — phusem-ion [Delete pool](#)

Basic settings [Edit](#)  
IP range (low-high): 165.100.100.100 - 165.100.100.105  
Access zone: System

SmartConnect settings [Edit](#)  
Zone name: phusem-ion.nibr.novartis.net  
Connection policy: Connection Count  
SmartConnect service subnet: ninety  
IP allocation method: Dynamic  
Rebalance policy: Automatic Failback  
IP failover policy: Round Robin

Pool members [Edit](#)  
Aggregation mode: Legacy FEC mode

- ext-1, Node 01
- ext-2, Node 01
- ext-1, Node 04
- ext-2, Node 04
- ext-1, Node 06
- ext-2, Node 06
- ext-1, Node 15
- ext-2, Node 15
- ext-1, Node 16
- ext-2, Node 16
- ext-1, Node 17
- ext-2, Node 17
- ext-1, Node 18
- ext-2, Node 18
- ext-1, Node 19
- ext-2, Node 19
- ext-1, Node 20
- ext-2, Node 20
- ext-1, Node 21
- ext-2, Node 21
- ext-1, Node 22
- ext-2, Node 22

# Silicon Tier Pools

OneFS

https:// 8080/OneFS#StoragePools/SmartPools

DASHBOARD CLUSTER MANAGEMENT FILE SYSTEM DATA PROCAGE 3 of 4

Storage Pools SmartQuotas Deduplication File System Explorer File System Settings

## Storage Pools

Summary File Pool Policies SmartPools SmartPools Settings

### Tiers & Node Pools

+ Create a Tier

Name	State	Nodes	Requested Protection	SSD/L3	HDD % Used	SSD % Used	Actions
X-Tier	Good	20-22	--	Has SSDs	23.9%	2.7%	<a href="#">View / Edit</a> <a href="#">More ▾</a>
x400_66tb_1.2tb-ssd_24gb	Good	20-22	+2d:1n	Has SSDs	23.9%	2.7%	<a href="#">View / Edit</a> <a href="#">More ▾</a>
NL-Tier	Good	1, 4, 6, 15-19	--	--	58.4%	--	<a href="#">View / Edit</a> <a href="#">More ▾</a>
n400_72tb_12gb-ram	Good	4, 6, 15-16	+2d:1n	--	60.3%	--	<a href="#">View / Edit</a> <a href="#">More ▾</a>
n400_144tb_48gb	Good	1, 17-19	+2d:1n	--	57.4%	--	<a href="#">View / Edit</a> <a href="#">More ▾</a>

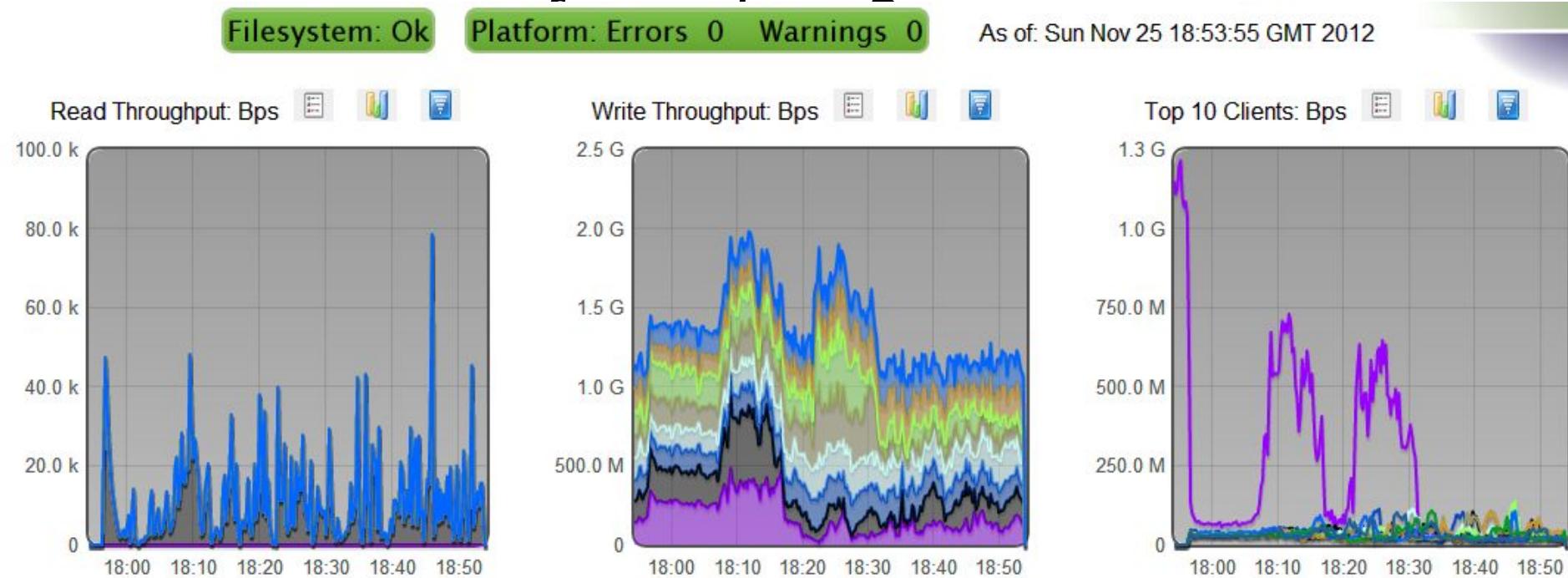
 = Tier  = Node Pool  = Manual Node Pool  = Unprovisioned Node

```
# isi filepool policies list
```

Name	Description
pinned_xtier	Put clscratch and app on X-Tier pool
lowpri_files	Lower Priority files can go to NL-Tier by default
usem_promoting	move recently accessed files to X-Tier
usem_aging_very_first	move files not accessed recently in usem/dlab/ldrive > 1 month to the NL-Tier
usem_aging_first	move files not accessed recently in usem/dlab > 1 month to the NL-Tier
usem_aging	move files not accessed recently in usem > 1 month to the NL-Tier

```
Total: 6
```

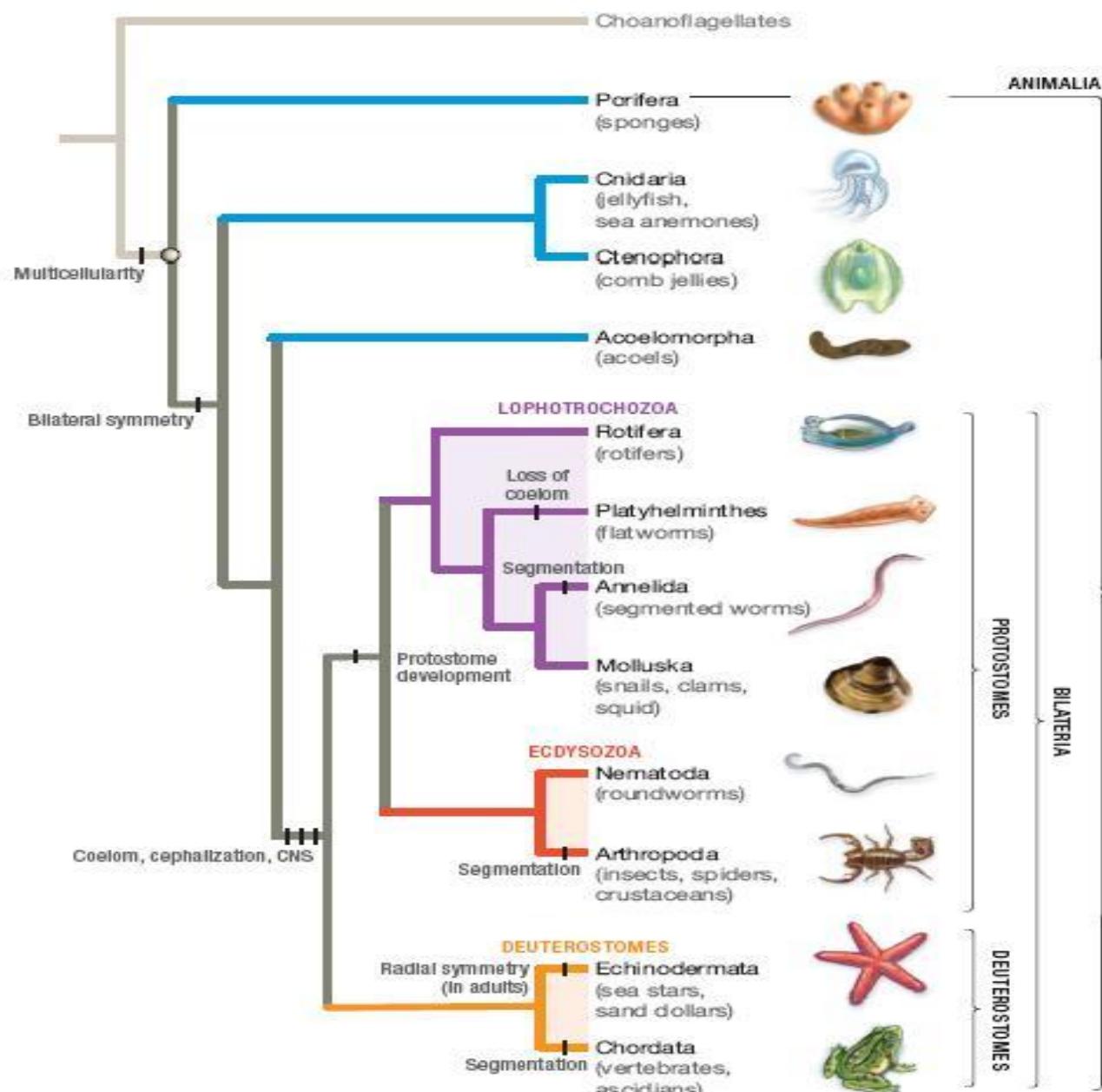
# Lustre ??

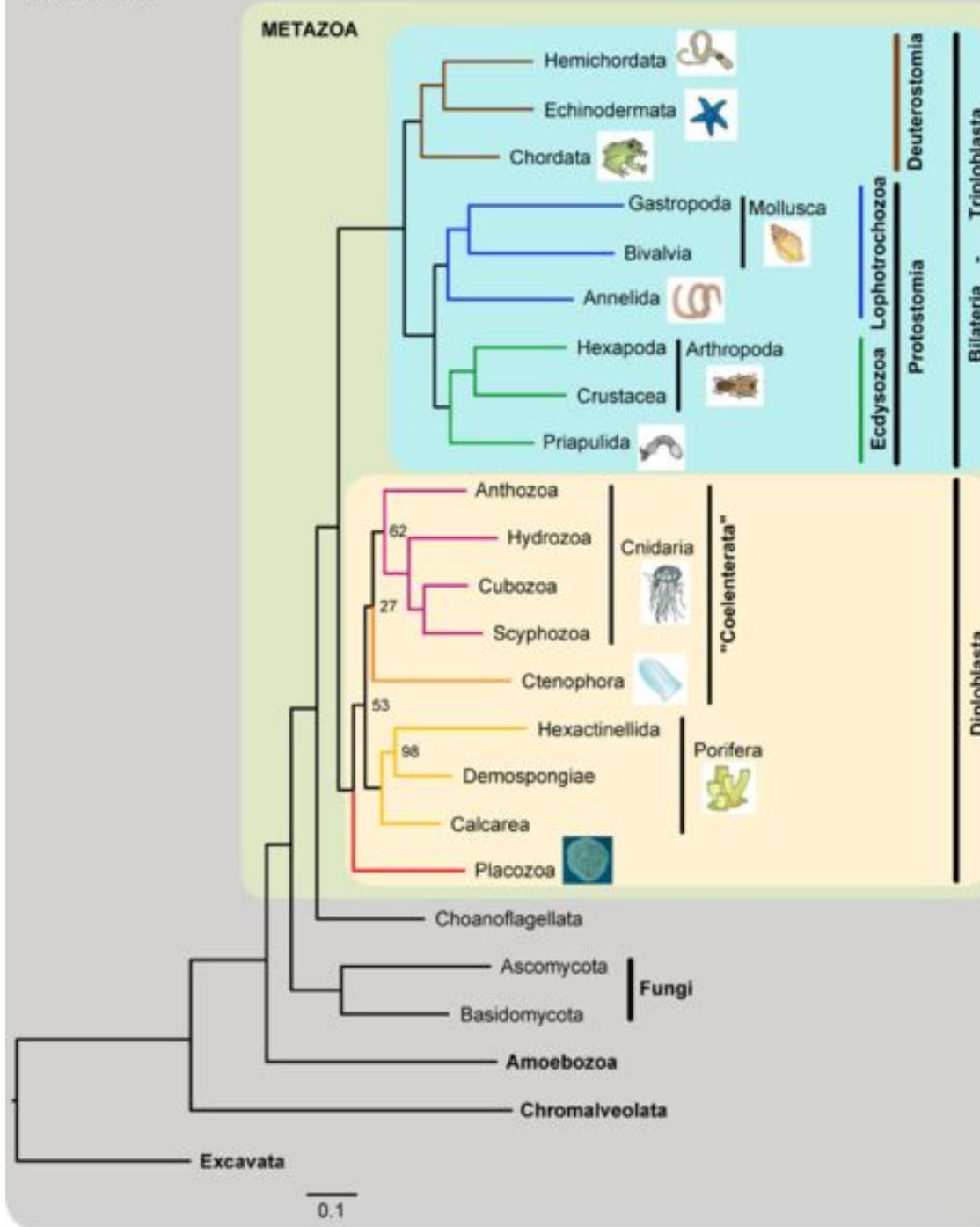


Terascala Lustre: ~ 14-20 Gbits/sec throughput.  
Isilon IQ-10000x-ssd: ~ 7-9 Gbits/sec throughput.

# Detour: HDFS data node perf

- Is it better to have 26 jbod mounts?
- RAID?
- RAID done the wrong way can have race conditions?





# iozone

- Simple file system-load generator
- `./iozone -i 0 -i 1 -c -e -w -r 1024k -s 16g -t 4 -+n -b result.xls`
  - -i 0 = write/rewrite
  - -i 1 = read/re-read
  - -i 2 = random-read/write
  - -c include close in timing
  - -e include flush
  - -w don't unlink temp file
  - -r record size in 1024k
  - -s the created IOZONE.DUMMY file size
  - -t number of threads (too low may not saturate device)
  - -+n no retest
  - -b create excel result file (kinda useless)

# Detour: Local Disk vs NFS (tstNum 0 = write test only)

	Ver 0.3 NFS#1	Ver 0.3 NFS#2	Ver 0.3 Local Host 1 Run 1	Ver 0.3 Local Host 1 Run 2	Ver 0.3 Local Host 2 Run 1 Sk41	Ver 0.3 Local Host 2 Run 2 sk41
lozone (Mbps)	2149	2092	686	695	813 (sda) (1701 nfs)	(2433 nfs)
Input lines	5,396,360					
Process time	1,137s (18min)	920s (15.3min)	102.28s (1.7min)	41.26s	224.70 (3.8min)	91.36 (1.5min)
Rate	4,746 lines/sec	line/sec				
Cp time				786.16		970.17
Total ...						