The PATRIC Command-Line Interface

Document Conventions

In this document, we observe the following conventions.

Text that you enter or type is shown in a white-background box.

```
This is input.
```

Output is shown in a yellow-background box. In general, you will only see the top portion of the output, since the whole thing could be quite large.

```
This is the top portion
of the output.
```

Output is usually tab-delimited, and you will see columns separated by multiple spaces that don't always line up.

If it is necessary to show multiple excerpts of a single large output stream, the missing parts will be shown with a gray bar.

```
This is the top part.

This is somewhere in the middle.
```

NOTE: we add new genomes to the PATRIC database every week. Your results from the examples in this tutorial may not match ours.

What is the PATRIC Command-line Interface?

PATRIC is an integration of different types of data and software tools that support research on bacterial pathogens. The typical biologist seeking access to the PATRIC data and tools will usually explore the web-based user interface. However, there are many instances in which programatic or command-line interfaces are more suitable. For users that wish command-line access to PATRIC, we provide the tools described in this document. We call these tools the *P3-scripts*. They are intended to run on your machine, going over the network to access the services provided by PATRIC.

Installing the CLI Release

We currently only have a Mac OSX release of the CLI package, but we should soon have a Windows version as well.

The releases are available at the **PATRIC3 github site**.

Download the latest version of the PATRIC dmg (disk image) file. Click on the downloaded file to open it, and drag the PATRIC icon on to the Application folder icon. This will install into your Applications folder.

Then doubleclick on the PATRIC icon in the Applications folder. This will bring up a new Terminal window that is configured for access to the PATRIC command line tools.

Command-Line Help

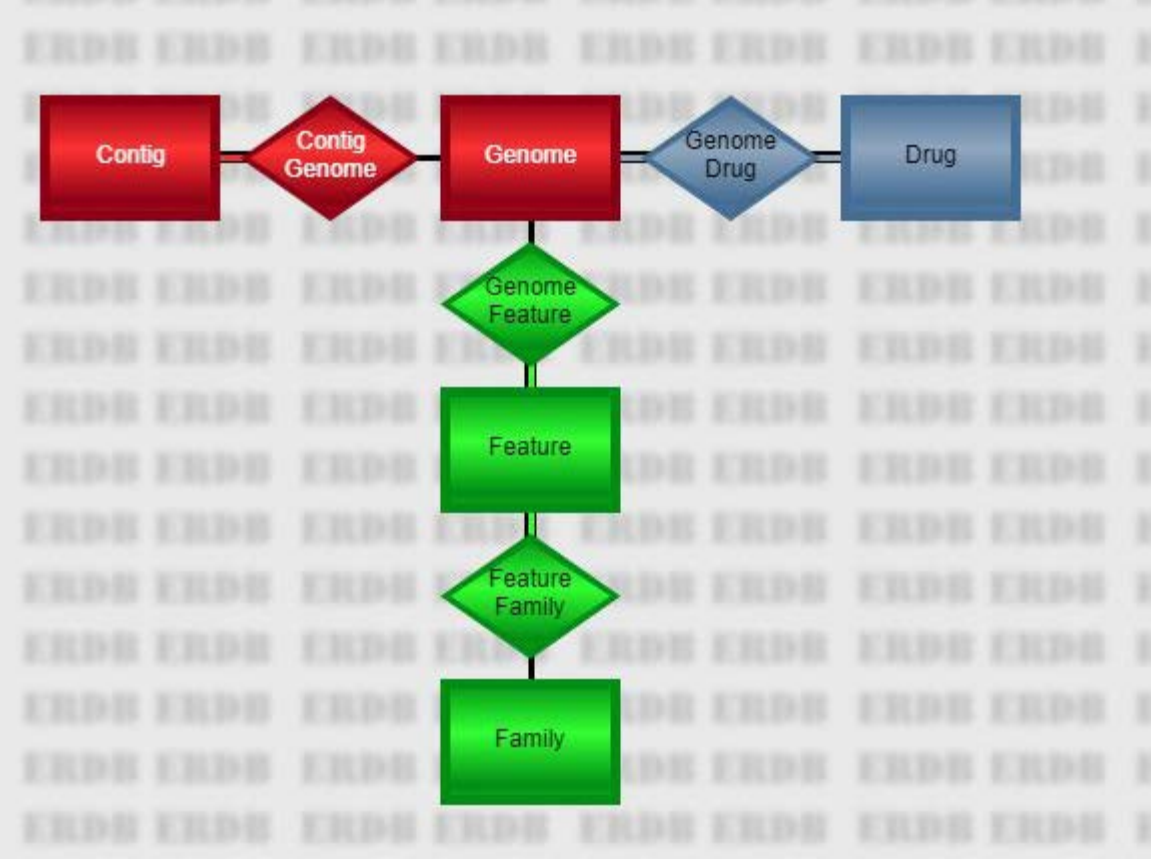
You can specify `--help` as a command-line option on any command to get a summary of the options and parameters, for example

```
p3-match --help
```

```
p3-match.pl [-bchiv] [long options...] match-value
        -i STR --input STR      name of the input file (if not the standard
                                input)
        -c STR --col STR        column number (1-based) or name
        -b INT --batchSize INT  input batch size
        --nohead                file has no headers
        -v --invert --reverse   output non-matching records
        --discards STR          name of file to contain discarded records
        -h --help               display usage information
```

The PATRIC Database

The main PATRIC database is organized as a series of large, heavily-indexed relational tables. From the perspective of the CLI, there are five main tables representing objects of interest, connected by four relationships.



The five entities are as follows.

Genome

A genome is a set of contigs and annotations representing our best estimate of the DNA sequence for an organism. Use **p3-all-genomes** to list all of the genomes or a subset. Given a list of genomes,

- Use **p3-get-genome-data** to retrieve data about the individual genomes.
- Use **p3-get-genome-features** to access the features of the genomes.
- Use **p3-get-genome-contigs** to access the genomes' sequences.
- Use **p3-get-genome-drugs** to access drug resistance data about the genomes.

Fields from the Genome table appear in the output with a heading prefix of `genome`. Thus, the *genome_name* will be in a column named `genome.genome_name`.

Contig

Represents one of the DNA sequences that comprise a genome. A contig can be a chromosome, a plasmid, or a fragment thereof. Contig data can be accessed from genome IDs using **p3-get-genome-contigs**. Fields from the Contig table appear in the output with a heading prefix of `contig`. Thus, the *length* will be in a column named `contig.length`.

Drug

Represents an antimicrobial drug used for therapeutic treatment. This table is the anchor for all antimicrobial resistance data in PATRIC. Use **p3-all-drugs** to get a list of drugs. Use **p3-get-drug-genomes** to get resistance data relating to specific drugs from a list. Fields from the Drug table appear in the output with a heading prefix of `drug`. Thus, the *molecular_formula* will be in a column named `drug.molecular_formula`.

Feature

Represents a region of interest in a genome. This could be a CRISPR array, an RNA site, a protein encoding region, or a regulatory site, among others. A feature can be split across multiple regions, or even multiple contigs, but never multiple genomes. Given a list of genome IDs, use **p3-get-genome-features** to access the features in the genomes. Given a list of family IDs, use **p3-get-family-features** to access the features in the families. Given a list of feature IDs, use **p3-get-feature-data** to access data about those features. **It is important to remember that the ID of the feature is called** *patric_id***, not** *feature_id***.** The internal feature ID is a long string with a lot of data packed into it that may change if the genome is re-annotated (e.g. `PATRIC.269798.23.NC_008255.CDS.22581.24344.fwd`). The *patric_id* value is shorter and more consistent (`fig|269798.23.peg.22`). Fields from the Feature table appear in the output with a heading prefix of `feature`. Thus, the *location* will be in a column named `feature.location`.

Family

Represents a protein family, which is a set of features believed to be isofunctional homologs. Given a list of family IDs, use **p3-get-family-features** to get data about the features in the families or **p3-get-family-data** to get data about the families themselves. Given a list of feature IDs, use **p3-get-feature-data** to get the families to which the features belong. There are three types of protein families supported-- *local* families which are confined to one genus, *global* families which cross the entire database, and *figfams*, which are computed using a different method. Fields from the Family table appear in the output with a heading prefix of `family`. Thus, the *product* will be in a column named `family.product`.

Files and Pipelines

The PATRIC CLI operates on tab-delimited files. That is, each record is divided into fields or columns separated by tab characters. The first record in each file contains the name of each column. Typically, a column name consists of a record name, a dot, and a field name. For example, the following file fragment contains a column from the genome table followed by two columns from the feature table.

```
genome.genome_id    feature.patric_id   feature.product
670.470 fig|670.470.repeat.1    repeat region
670.470 fig|670.470.repeat.2    repeat region
670.470 fig|670.470.repeat.3    repeat region
670.470 fig|670.470.rna.1   tRNA-Ala
670.470 fig|670.470.rna.2   tRNA-Ile
670.470 fig|670.470.repeat.4    repeat region
670.470 fig|670.470.rna.3   16S ribosomal RNA
670.470 fig|670.470.repeat.5    repeat region
670.470 fig|670.470.rna.4   tRNA-Val
670.470 fig|670.470.rna.5   tRNA-Ala
670.470 fig|670.470.repeat.6    repeat region
```

The scripts are designed so they can be chained together in pipelines where the output of one becomes input to the next. For example, the above file was generated by the pipeline

```
p3-all-genomes --eq genus,Methylobacillus | p3-get-genome-features --attr patric_id --attr
product
```

In the first command of this pipeline, the **--eq** command-line option was used to filter a query, while the **--attr** option in the second command was used to specify the output columns and the order in which they appear. These options are available on all of the database scripts.

For get-type scripts (**p3-get-genome-data**, **p3-get-genome-feature-data**, ...), you must supply the id of the object of interest, e.g., the genome id, feature id, etc. By default, the last column in the input file is used as the key field for these get-type scripts. You can modify this behavior using the **--col** command-line option. The special value **0** denotes the last column, but you can also use a 1-based column number (**1** for the first, **2** for the second) or a column name. If the field-name portion of the column name is unique, you can leave off the table-name portion. So, if you want to get location information from the features output by the pipeline above (identified in column **feature.patric_id**, which is the second one), you could use any of the three following commands

```
p3-get-feature-data --col=feature.patric_id --attr sequence_id --attr location <input.tbl
```

```
p3-get-feature-data --col=2 --attr sequence_id --attr location <input.tbl
```

```
p3-get-feature-data --col=patric_id --attr sequence_id --attr location <input.tbl
```

where *input.tbl* is the above output file.

The special script **p3-extract** allows you to select columns from a file and even change the order. Thus, the following pipeline removes the genome ID from our file and puts the feature ID at the end before asking **p3-get-feature-data** for the location information.

```
p3-extract feature.product feature.patric_id <input.tbl | p3-get-feature-data --attr
sequence_id --attr location
```

The same flexibility provided for arguments of the **--col** option is available anywhere you specify column names, including the parameters of **p3-extract**. So, the following invocation is equivalent to the above.

```
p3-extract product 2 <input.tbl | p3-get-feature-data --attr sequence_id --attr location
```

Because of the presence of the headings, many standard file-manipulation commands won't work the way you expect. For example, if you use a standard sort command, the headers will sort somewhere into the middle of the file. We provide p3 scripts for several of the most common needs.

P3 Script	Description	Unix Equivalent
p3-extract	Select and re-order specific columns.	cut
p3-sort	Sort by specified columns.	sort
p3-match	Select records that possess (or do not possess) a particular value in a specified column.	grep
p3-join	Horizontally join two files on a single key field.	join
p3-head	Display the first few lines of a file.	head
p3-echo	Create a small file.	echo

These commands do not work precisely like their unix equivalents. Most have fewer options: for example, **p3-match** searches for text in a single column rather than the entire file and does not support regular expressions.

p3-echo

The **p3-echo** command is your most important tool for creating small files that feed into pipes. The `--title` command-line option (abbreviated `-t`) allows you to specify the title for the column you are creating. Each positional parameter forms a single record with a single column.

```
p3-echo -t genome_id 1313.7001 1313.7002 1313.7016
```

```
genome_id
1313.7001
1313.7002
1313.7016
```

You can create a multi-column file by specifying multiple titles. There will be one output column for each title specified. In the example below, there are three titles, so the output table is three columns. Every triple of parameters produces a record.

```
p3-echo -t genome_id -t sequences -t gc_content 1313.7001  52  39.64  1313.7002  45  39.63
1313.7016  58  39.77
```

```
genome_id       sequences       gc_content
1313.7001       52      39.64
1313.7002       45      39.63
1313.7016       58      39.77
```

If a field contains special characters such as spaces or pipe symbols, use double quotes to insure the characters are interpreted correctly.

```
p3-echo -t genome_id -t patric_id -t product 1313.7001 "fig|1313.7001.peg.1362" "hypothetical
 protein"
```

```
genome_id   patric_id   product
1313.7001   fig|1313.7001.peg.1362  hypothetical protein
```

If you leave off the title parameter, the default title `id` is used. This is a handy shortcut when you're in a hurry.

```
p3-echo 1313.7001. 1313.7016
```

```
id
1313.7001
1313.7016
```

Of course, you can only do that for a single-column output.

Database Script Examples

In this section we briefly discuss the main database scripts.

p3-all-genomes

This script lists all genomes with various characteristics. For example,

```
p3-all-genomes --eq genome_name,Streptomyces
```

```
genome.genome_id
284037.4
67257.17
68042.5
68042.6
```

```
1395572.3
68570.5
1160718.3
749414.3
66876.3
249567.6
```

would list all genomes in the genus Streptomyces. (That is, all genomes whose names start with that word.) The **--eq** parameter introduces an equality constraint. In PATRIC, string searches perform a word-based substring match, which allows us to easily do queries of this type. The various database commands all support the **--eq** option. In addition, you can specify output fields using the **--attr** option. Thus,

```
p3-all-genomes --eq genome_name,Streptomyces --attr genome_id --attr
genome_name
```

would output both the ID and name of each genome found, as shown below.

```
genome.genome_id    genome.genome_name
284037.4    Streptomyces sporocinereus strain OsiSh-2
67257.17    Streptomyces albus subsp. albus strain NRRL F-4371
68042.5 Streptomyces hygroscopicus subsp. hygroscopicus strain NBRC 16556
68042.6 Streptomyces hygroscopicus subsp. hygroscopicus strain NBRC 13472
1395572.3   Streptomyces albulus PD-1
68570.5 Streptomyces albulus strain NK660
1160718.3   Streptomyces auratus AGR0001
749414.3    Streptomyces bingchenggensis BCW-1
66876.3 Streptomyces chattanoogensis strain NRRL ISP-5002
249567.6    Streptomyces decoyicus strain NRRL 2666
```

To get a complete list of the available fields, use the **--fields** option. This option is available for all the database scripts described in this section.

```
p3-all-genomes --fields
```

p3-get-genome-data

Given an input file of genome IDs, this script allows you to retrieve additional data and fields. For example, the following pipeline gets all Streptomyces genomes and then appends the genome name, number of contigs, and DNA length.

```
p3-all-genomes --eq genome_name,Streptomyces | p3-get-genome-data --attr
genome_name --attr contigs --attr genome_length
```

```
genome.genome_id    genome.genome_name  genome.contigs  genome.genome_length
284037.4    Streptomyces sporocinereus strain OsiSh-2   125 10242506
67257.17    Streptomyces albus subsp. albus strain NRRL F-4371  307 9246299
68042.5 Streptomyces hygroscopicus subsp. hygroscopicus strain NBRC 16556   133
 10141569
68042.6 Streptomyces hygroscopicus subsp. hygroscopicus strain NBRC 13472   680
 9464604
1395572.3   Streptomyces albulus PD-1   425 9340057
68570.5 Streptomyces albulus strain NK660       9372401
1160718.3   Streptomyces auratus AGR0001    213 7825489
749414.3    Streptomyces bingchenggensis BCW-1  0   11936683
66876.3 Streptomyces chattanoogensis strain NRRL ISP-5002   217 9129105
```

In actual fact, the use of **p3-get-genome-data** in the above pipeline is redundant, since **p3-all-genomes** supports the same command-line options. In practice, you will use **p3-get-genome-data** to process genome ID files created on a separate occasion or via other scripts that don't have the full power of **p3-all-genomes**. If you don't specify any **--attr** values, you get the same output fields as found on the PATRIC genome list tab.

```
```

```
p3-all-genomes --eq genome_name,Streptomyces | p3-get-genome-data
```

```
genome.genome_id    genome.genome_name  genome.genome_id
genome.genome_status    genome.sequences    genome.patric_cds
genome.isolation_country    genome.host_name    genome.disease
genome.collection_year  genome.completion_date
284037.4    Streptomyces sporocinereus strain OsiSh-2   284037.4    WGS 125
9060    China   Rice        2012    2016-08-16T00:00:00Z
67257.17    Streptomyces albus subsp. albus strain NRRL F-4371  67257.17    WGS
 307 8633                   2016-01-26T00:00:00Z
68042.5 Streptomyces hygroscopicus subsp. hygroscopicus strain NBRC 16556
68042.5 WGS 133 8955                    2016-02-05T00:00:00Z
68042.6 Streptomyces hygroscopicus subsp. hygroscopicus strain NBRC 13472
68042.6 WGS 680 8767                    2016-02-05T00:00:00Z
1395572.3   Streptomyces albulus PD-1   1395572.3   WGS 482 8332    China
         2013-12-05T00:00:00Z
68570.5 Streptomyces albulus strain NK660   68570.5 Complete    2   8793
China               2014-06-18T00:00:00Z
1160718.3   Streptomyces auratus AGR0001    1160718.3   WGS 238 6866    China
             2012-07-23T00:00:00Z
749414.3    Streptomyces bingchenggensis BCW-1  749414.3    Complete    1
10313   China               2010-05-28T00:00:00Z
66876.3 Streptomyces chattanoogensis strain NRRL ISP-5002   66876.3 WGS 217
8838    United States               2015-09-18T00:00:00Z
249567.6    Streptomyces decoyicus strain NRRL 2666 249567.6    WGS 304 8231
 United States              2015-08-19T00:00:00Z
1907.4  Streptomyces glaucescens GLA.O  1907.4  Complete    2   6719    India
             2014-10-01T00:00:00Z
1172567.3   Streptomyces globisporus C-1027 1172567.3   WGS 278 6980    China
             2012-05-04T00:00:00Z
```

This is typical of the **p3-get** scripts: the default attributes match what you see on the web site as closely as possible.

p3-get-genome-features

Given a file of genome IDs, return data about the genome's features. So, for example, the following pipeline would return the ID and function (product) of each feature in the Cytophaga genomes.

```
p3-all-genomes --eq genus,Cytophaga | p3-get-genome-features --attr patric_id --attr product
```

```
genome.genome_id    feature.patric_id   feature.product
269798.23   fig|269798.23.peg.1 hypothetical protein
269798.23   fig|269798.23.peg.2 Capsular polysaccharide synthesis enzyme Cap8C;
 Manganese-dependent protein-tyrosine phosphatase (EC 3.1.3.48)
269798.23   fig|269798.23.peg.3 Dihydroflavonol-4-reductase (EC 1.1.1.219)
269798.23   fig|269798.23.peg.4 TPR domain protein
269798.23   fig|269798.23.peg.5 Phosphosulfolactate synthase (EC 4.4.1.19)
269798.23   fig|269798.23.peg.6 DedA protein
269798.23   fig|269798.23.peg.7 Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25)
269798.23   fig|269798.23.peg.8 hypothetical protein
269798.23   fig|269798.23.peg.9 Excinuclease ABC subunit B
269798.23   fig|269798.23.peg.10    DNA polymerase III epsilon subunit
269798.23   fig|269798.23.peg.11    hypothetical protein
269798.23   fig|269798.23.peg.12    putative fatty acid hydroxylase
```

You can use the **--fields** option to list all the fields available in a feature record. In addition, you have access to the usual filtering parameters-- **--eq** as well as **--lt**, **--gt**, **--le**, **--ge**, and **--ne**. So, for example, the following command would restrict the features to CDS features of at least 500 base pairs.

```
p3-all-genomes --eq genus,Cytophaga | p3-get-genome-features --eq
feature_type,CDS --ge na_length,500 --attr patric_id --attr product
```

```
genome.genome_id    feature.patric_id   feature.product
269798.23   fig|269798.23.peg.2 Capsular polysaccharide synthesis enzyme Cap8C;
 Manganese-dependent protein-tyrosine phosphatase (EC 3.1.3.48)
269798.23   fig|269798.23.peg.3 Dihydroflavonol-4-reductase (EC 1.1.1.219)
269798.23   fig|269798.23.peg.4 TPR domain protein
269798.23   fig|269798.23.peg.5 Phosphosulfolactate synthase (EC 4.4.1.19)
269798.23   fig|269798.23.peg.6 DedA protein
269798.23   fig|269798.23.peg.7 Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25)
269798.23   fig|269798.23.peg.8 hypothetical protein
269798.23   fig|269798.23.peg.9 Excinuclease ABC subunit B
269798.23   fig|269798.23.peg.10    DNA polymerase III epsilon subunit
269798.23   fig|269798.23.peg.12    putative fatty acid hydroxylase
269798.23   fig|269798.23.peg.13    Glycosyl transferase
```

p3-get-genome-contigs

Given a file of genome IDs, returns the contigs. The following pipeline returns all the contigs in genome 28903.66.

```
p3-echo -t genome_id 28903.66 | p3-get-genome-contigs --attr sequence_id --attr
 sequence
```

The output will have three columns, including the genome ID, the ID of the contig, and the actual DNA sequence (which can be quite long). Again, use the **--fields** option to see which fields are available for output and filtering in the contig records.

p3-get-genome-drugs

Given a file of genome IDs, output the drug resistance information we have on those genomes. For many genomes, no such data is yet available, so it is not hard to get an empty file output from this command. The following pipeline outputs the default resistance data information for all the Acinetobacter pittii genomes.

```
p3-all-genomes --eq "genome_name,Acinetobacter pittii"" | p3-get-genome-drugs
```

```
genome.genome_id    genome_drug.genome_id   genome_drug.antibiotic
genome_drug.resistant_phenotype
48296.102   48296.102   meropenem   Resistant
48296.102   48296.102   imipenem    Resistant
48296.102   48296.102   ciprofloxacin   Susceptible
48296.102   48296.102   gentamicin  Susceptible
48296.102   48296.102   amikacin    Susceptible
48296.102   48296.102   tigecycline
48296.104   48296.104   imipenem    Resistant
48296.104   48296.104   ciprofloxacin   Susceptible
48296.104   48296.104   gentamicin  Susceptible
```

p3-all-drugs

This script lists anti-microbial drugs from the database. Use the **--fields** option to see a list of all the fields you can select. The default is to simply list the antibiotic name, as shown below.

```
p3-all-drugs
```

```
drug.antibiotic_name
amikacin
amoxicillin
amoxicillin/clavulanic acid
ampicillin
ampicillin/sulbactam
azithromycin
aztreonam
bacitracin
capreomycin
cefaclor
cefazolin
```

p3-get-drug-genomes

Given a file of antibiotic names, display all the resistance data for those antibiotics. The following pipeline lists all the genomes resistant to at least one drug.

```
p3-all-drugs | p3-get-drug-genomes --attr genome_id --attr genome_name --
resistant
```

```
drug.antibiotic_name    genome_drug.genome_id   genome_drug.genome_name
amikacin    1304920.3   Klebsiella pneumoniae 361_1301
amikacin    1427177.3   Mycobacterium tuberculosis XTB13-081
amikacin    1427178.3   Mycobacterium tuberculosis XTB13-082
amikacin    1427180.3   Mycobacterium tuberculosis XTB13-084
amikacin    1427185.3   Mycobacterium tuberculosis XTB13-091
amikacin    1427191.3   Mycobacterium tuberculosis XTB13-097
amikacin    1427192.3   Mycobacterium tuberculosis XTB13-098
amikacin    1427193.3   Mycobacterium tuberculosis XTB13-100
amikacin    1427199.3   Mycobacterium tuberculosis XTB13-107
amikacin    1427200.3   Mycobacterium tuberculosis XTB13-108
amikacin    1427202.3   Mycobacterium tuberculosis XTB13-110
amikacin    1427204.3   Mycobacterium tuberculosis XTB13-112
amikacin    1427207.3   Mycobacterium tuberculosis XTB13-115
```

Rather than typing `--eq resistant_phenotype,resistant`, the **p3-get-drug-genomes** script provides the special command-line options `--resistant` and `--susceptible` to filter for the appropriate resistance phenotypes automatically.

p3-get-family-features

Given a list of protein family IDs, get all the features in the families. PATRIC supports three types of protein families-- `local`, `global`, and `figfam`. The `--ftype` parameter specifies the type of family desired. So, for example, the following pipeline finds the global family for the feature *fig|1105121.3.peg.460* and then lists the ID and product of each family member.

```
p3-echo -t feature_id "fig|1105121.3.peg.460" | p3-get-feature-data --attr
pgfam_id | p3-get-family-features --ftype=global --attr patric_id --attr
product
```

Note that the features found are listed in the column **feature.patric_id**, while the original feature is maintained in the first column **feature_id**.

```
feature_id  feature.pgfam_id    feature.patric_id   feature.product
fig|1105121.3.peg.460   PGF_00112374    fig|1313.8637.peg.2087  hypothetical
protein
fig|1105121.3.peg.460   PGF_00112374    fig|1313.8636.peg.1563  hypothetical
protein
fig|1105121.3.peg.460   PGF_00112374    fig|1313.8645.peg.110   hypothetical
protein
fig|1105121.3.peg.460   PGF_00112374    fig|1313.12423.peg.2037 hypothetical
protein
fig|1105121.3.peg.460   PGF_00112374    fig|1330044.3.peg.533   hypothetical
protein
fig|1105121.3.peg.460   PGF_00112374    fig|1313.5699.peg.1778  hypothetical
protein
fig|1105121.3.peg.460   PGF_00112374    fig|1313.5750.peg.307   hypothetical
protein
fig|1105121.3.peg.460   PGF_00112374    fig|1313.5754.peg.739   hypothetical
protein
fig|1105121.3.peg.460   PGF_00112374    fig|1313.5758.peg.1823  hypothetical
protein
fig|1105121.3.peg.460   PGF_00112374    fig|1313.5781.peg.1819  hypothetical
protein
fig|1105121.3.peg.460   PGF_00112374    fig|1313.5778.peg.686   hypothetical
protein
fig|1105121.3.peg.460   PGF_00112374    fig|1313.5729.peg.1554  hypothetical
protein
```

p3-get-feature-data

Given a file of feature IDs, return data from those features. Again, use the `--fields` option to list the fields you can use for filtering and display. The following pipeline lists the function (product) and protein sequence of each peg of less than 300 base pairs in the genome 1105121.3.

```
p3-echo -t genome_id 1105121.3 | p3-get-genome-features --lt na_length,300 --eq
 feature_type,CDS --attr patric_id | p3-get-feature-data --attr product --attr
aa_sequence
```

```
genome_id   feature.patric_id   feature.product feature.aa_sequence
1105121.3   fig|1105121.3.peg.1487  BOX elements
MKIKEQTRKLAASCSKHCFEVVDKTDEVSYIYNPRRR
1105121.3   fig|1105121.3.peg.1508  hypothetical protein
MISTTYRNHRKRFGLRMNLIAEKVSKTLDKTFDKDVREIPTSQFYQKFVDEMGRTYSGNLILQELITVNGAYKATYIGELS

1105121.3   fig|1105121.3.peg.1557  hypothetical protein
MKREVISNGNDGPSQEILIFTKQIRHWILSDQVISGKRKLFFREDTPKEILDLYENIKSKLDFAYQEVYSNNGLKKYEK
1105121.3   fig|1105121.3.peg.1598  BOX elements
MKIKEQTRKLAAGCSKHCFEVVDRTDEVSNLHTARRR
1105121.3   fig|1105121.3.peg.1776  hypothetical protein
MVASASASSTSTQAQEQVDKSELRALSQELDQRLKALATVSDPKIDATKAVLLDAQKAPEDSALTE
1105121.3   fig|1105121.3.peg.10    hypothetical protein
MENLLDVIEQFLGLSDEKLEELADKNQLLRLQEEKERKNA
1105121.3   fig|1105121.3.peg.94    BOX elements
MKIKEQTRKLAAGCSKHCFEVVDKTDEVSYIYLRQGEADAV
1105121.3   fig|1105121.3.peg.220   Ribonucleotide reductase of class III
(anaerobic), large subunit (EC 1.17.4.2)
MVKRTCGYLGNPQARPMVNGRHKEIAARVKHMNGSTIKIAGHQVTN
1105121.3   fig|1105121.3.peg.228   LSU ribosomal protein L23p (L23Ae)
MNLYDVIKKPVITESSMAQLEAGKYVFEVDTRAHKLLIKQAVEAAFEGVKVANVNTINVKPKAKRVGRYTGFTNKTKKAII

1105121.3   fig|1105121.3.peg.230   SSU ribosomal protein S19p (S15e)
MGRSLKKGPFVDEHLMKKVEAQANDEKKKVIKTWSRRSTIFPSFIGYTIAVYDGRKHVPVYIQEDMVGHKLGEFAPTRTYK
```

The use of **p3-get-feature-data** here is redundant, since you could get the same result by placing the attribute requests directly on **p3-get-genome-features**.

```
p3-echo -t genome_id 1105121.3 | p3-get-genome-features --lt na_length,300 --eq
 feature_type,CDS --attr patric_id --attr product --attr aa_sequence
```

p3-get-feature-data is provided for the situation where you are piping in the feature list from something external or precomputed.

What Is a PATRIC Workspace?

Users of PATRIC have access to a wealth of public data that support interpretation of prokaryotic genomes. The PATRIC team actively integrates newly-sequenced genomes, data relating to antimicrobial resistance, expression data, pathway data and subsystem data into an integrated framework that can be queried using either the PATRIC UI or the CLI.

In the PATRIC UI, your workspace looks a lot like a standard file system, divided into folders full of data. In addition to files you upload, such as FASTA and FASTQ files, there will also be typed objects such as genomes, feature groups, and genome groups. The CLI allows you to move these typed objects between your workspace and your file system so you can manipulate them at will.

Logging In

To access your workspace, you need a PATRIC account. If you do not have one already, go to **https://user.patricbrc.org/register** and register now.

Now that you have a working user name and password, you can use the **p3-login** script to tell the CLI who you are. For example, if your name is `rastuser25`, you would type

```
p3-login rastuser25
```

The script asks you for your password and places a special file on your hard drive that can be used to get authorized access to your workspace data. To log out again, simply use

```
p3-login --logout
```

At any time, you can verify your login status using

```
p3-login --status
```

If you are logged out, it will respond

```
You are currently logged out of PATRIC.
```

If you are logged in, you will get something like

```
You are logged in as rastuser25@patricbrc.org.
```

Working with Genome Groups

Your workspace looks like a full-blown file system, but there are three special folders.

- **Genome Groups** contains named lists of genomes.
- **Feature Groups** contains named lists of features.
- **QuickData** contains folders full of genomes you submitted through the CLI annotation interface.

To create a genome group, you use **p3-put-genome-group**. Say, for example, you want to examine Streptococcus penumoniae genomes that are resistant to penicillin. The following query command will return this list of genomes (we will discuss all query commands in more details later).

```
p3-echo -t antibiotic penicillin | p3-get-drug-genomes --eq "genome_name,Streptococcus
pneumoniae"  --resistant --attr genome_id --attr genome_name >resist.tbl
```

This particular command asks for data from the anti-microbial resistance table. Each record in this table posits a relationship between a genome and an antibiotic drug. We are accessing the table from the direction of taking a drug and finding resistant genomes. To do this, we need a file with a drug name in it. The **p3-echo** command creates this file: the `-t antibiotic` parameter tells it we want a one-column file with a column header of `antibiotic`. We put the single record `penicillin` in that column.

The antibiotic file is then piped into **p3-get-drug-genomes**. Its parameters do the following.

`--eq "genome_name,Streptococcus pneumoniae"`
: Only include records for Streptococcus pneumoniae genomes. Because this is a string field, it does a substring match. A genome name including follow-on strain information (e.g. `Streptococcus pneumoniae strain LMG2888`) will still match.

`--resistant`
: Only include records that state the genome is resistant. This is a special parameter for the **p3-get-drug-genomes** and **p3-get-genome-drugs** commands that is provided for convenience.

`--attr genome_id`
: Output the genome ID.

`--attr genome_name`
: Output the genome name.

When the command completes, the file **resist.tbl** will contain around 114 lines beginning with the following.

```
antibiotic   genome_drug.genome_id   genome_drug.genome_name
penicillin   1313.7006   Streptococcus pneumoniae P310010-154
penicillin   1313.7016   Streptococcus pneumoniae P310937-212
```

```
penicillin   1313.7018   Streptococcus pneumoniae P311313-217
penicillin   760749.3    Streptococcus pneumoniae GA05248
penicillin   760763.3    Streptococcus pneumoniae GA11304
penicillin   760765.3    Streptococcus pneumoniae GA11663
penicillin   760766.3    Streptococcus pneumoniae GA11856
penicillin   760769.3    Streptococcus pneumoniae GA13338
penicillin   760771.3    Streptococcus pneumoniae GA13455
penicillin   760776.3    Streptococcus pneumoniae GA14373
penicillin   760777.3    Streptococcus pneumoniae GA14688
```

Now we want to create a group for these genomes called **resist_strep**. We use the following command.

```
p3-put-genome-group --col=2 resist_strep <resist.tbl
```

The `--col=2` tells the command that the genome IDs are in the second column. The genome group is simply a set of genome IDs, so the other columns will be ignored by the command. You can read the group back at any time using **p3-get-genome-group**.

```
p3-get-genome-group resist_strep
```

Will output

```
resist_strep.genome_id
1313.7006
1313.7016
1313.7018
760749.3
760763.3
760765.3
760766.3
760769.3
760771.3
```

and so on. Note that if you want to see the names as well, you can use the **p3-get-genome-data** command to add them

```
p3-get-genome-group resist_strep | p3-get-genome-data --attr genome_name
```

```
resist_strep.genome_id  genome.genome_name
1313.7006   Streptococcus pneumoniae P310010-154
1313.7016   Streptococcus pneumoniae P310937-212
1313.7018   Streptococcus pneumoniae P311313-217
760749.3    Streptococcus pneumoniae GA05248
760763.3    Streptococcus pneumoniae GA11304
760765.3    Streptococcus pneumoniae GA11663
760766.3    Streptococcus pneumoniae GA11856
760769.3    Streptococcus pneumoniae GA13338
760771.3    Streptococcus pneumoniae GA13455
760776.3    Streptococcus pneumoniae GA14373
760777.3    Streptococcus pneumoniae GA14688
```

Next we will ask for the genomes that are susceptible to penicillin. We use the same command as before except we put `susceptible` in place of `resistant`. We're going to pipe the results directly into **p3-put-genome-group** to store them in our workspace.

```
p3-echo -t antibiotic penicillin | p3-get-drug-genomes --eq "genome_name,Streptococcus
pneumoniae"  --susceptible --attr genome_id --attr genome_name | p3-put-genome-group --col=2
weak_strep
```

Now when you ask for the group back, you would get something like the following.

```
p3-get-genome-group weak_strep
```

```
weak_strep.genome_id
1313.6939
1313.6941
1313.6942
1313.6944
1313.6947
1313.7001
1313.7002
1313.7007
1313.7009
```

Working with Feature Groups

We want to look at features in the resistant Streptococcus pneumoniae genomes that distinguish them from the susceptible ones. Then we will gather those features into a feature group and store them in our workspace so we can work with them later. We have the genomes we want stored in the genome groups *weak_strep* and *resist_strep*. The command that processes them is called **p3-signature-families**.

p3-signature families compares two genome groups-- group 1 contains genomes that are interesting for some reason, group 2 contains genomes that are not. We can pipe one of the two groups directly into the command, but the other needs to be in a file. We will start by creating a file called *weak.tbl* that contains the *weak_strep* genomes.

```
p3-get-genome-group weak_strep >weak.tbl
```

Now we pipe in *resist_strep* (the interesting set) and specify *weak.tbl* as the source of group 2.

```
p3-get-genome-group resist_strep | p3-signature-families --gs2=weak.tbl >families.tbl
```

The output contains protein families that are common in the interesting set (resistant to penicillin) but not in the other set. If a set file is not specified, it is taken from the standard input. In this case, that would be the interesting set, since there is no **--gs1** parameter.

Our signature families analysis script has no output, because we redirected it to *families.tbl*. We can peek at the results using the `--all` option of **p3-extract**.

```
p3-extract --all <families.tbl
```

```
counts_in_set1  counts_in_set2  family.family_id    family.product
92  10  PGF_00112374    hypothetical protein
92  10  PGF_00303700    hypothetical protein
92  10  PGF_03497231    hypothetical protein
91  10  PGF_03497236    hypothetical protein
```

We found four protein families. The next step is to convert the families into feature IDs. The **p3-get-family-features** script performs that function. We will use the following command.

```
p3-get-family-features --gFile=resist.tbl --gCol=2 --ftype=global --col=family.family_id
<families.tbl
```

The parameters work as follows.

--gFile=resist.tbl
: Only features from the genomes listed in the file *resist.tbl* should be included in the output.

--gCol=2
: The genome IDs in *resist.tbl* are in the second column.

--ftype=global
: The family IDs in the input file are global families. (Local families and FIGfams are also supported, but the **p3-signature-families** script uses global families.)

--col=family.family_id
: The protein family IDs in the input file are in a column named `family.family_id`.

The output looks something like this.

```
counts_in_set1  counts_in_set2  family.family_id    family.product  feature.patric_id
feature.refseq_locus_tag    feature.gene_id feature.plfam_id    feature.pgfam_id
feature.product
92  10  PGF_00112374    hypothetical protein    fig|1105121.3.peg.460   SPAR163_0451    0
PLF_1301_00002060   PGF_00112374    hypothetical protein
92  10  PGF_00112374    hypothetical protein    fig|1069626.3.peg.432   SPAR154_0430    0
PLF_1301_00002060   PGF_00112374    hypothetical protein
92  10  PGF_00112374    hypothetical protein    fig|1313.6771.peg.1961  ERS013947_01920
PLF_1301_00002060   PGF_00112374    hypothetical protein
92  10  PGF_00112374    hypothetical protein    fig|1313.5503.peg.1279  ERS013945_01218
PLF_1301_00002060   PGF_00112374    hypothetical protein
92  10  PGF_00112374    hypothetical protein    fig|1313.5634.peg.1224  ERS013952_01170
PLF_1301_00002060   PGF_00112374    hypothetical protein
92  10  PGF_00112374    hypothetical protein    fig|1069624.3.peg.437   SPAR151_0439    0
PLF_1301_00002060   PGF_00112374    hypothetical protein
92  10  PGF_00112374    hypothetical protein    fig|1069628.3.peg.451   SPAR156_0440    0
PLF_1301_00002060   PGF_00112374    hypothetical protein
92  10  PGF_00112374    hypothetical protein    fig|1313.5669.peg.1163  ERS013960_01123
PLF_1301_00002060   PGF_00112374    hypothetical protein
92  10  PGF_00112374    hypothetical protein    fig|1313.6725.peg.2115  ERS013931_02059
PLF_1301_00002060   PGF_00112374    hypothetical protein
92  10  PGF_00112374    hypothetical protein    fig|1313.5465.peg.1094  ERS013930_01056
PLF_1301_00002060   PGF_00112374    hypothetical protein
92  10  PGF_00112374    hypothetical protein    fig|1313.5418.peg.2058  ERS013923_02003
PLF_1301_00002060   PGF_00112374    hypothetical protein
92  10  PGF_00112374    hypothetical protein    fig|1313.5645.peg.1124  ERS013964_01084
PLF_1301_00002060   PGF_00112374    hypothetical protein
```

We didn't tell **p3-get-family-features** what attributes of the features to display, so it defaulted to the columns normally found on the PATRIC web page *Features* tab. We don't have time to examine these features in detail now, but we can put them in a feature group by piping them into **p3-put-feature-group** as follows.

```
p3-get-family-features --gFile=resist.tbl --gCol=2 --ftype=global --col=family.family_id
<families.tbl | p3-put-feature-group --col=feature.patric_id resist_fids
```

In the **p3-put-feature-group** command, the `--col=feature.patric_id` parameter tells the command that the feature IDs are in the column with that heading, and `resist_fids` is the group name. When you decide to examine the features in greater detail, you can pull back the feature IDs using **p3-get-feature-group**.

```
p3-get-feature-group resist_fids
```

The output will look something like this.

```
resist_fids.patric_id
fig|1105121.3.peg.460
fig|1069626.3.peg.432
fig|1313.6771.peg.1961
fig|1313.5503.peg.1279
fig|1313.5634.peg.1224
fig|1069624.3.peg.437
fig|1069628.3.peg.451
fig|1313.5669.peg.1163
fig|1313.6725.peg.2115
```

At any time, you can get a complete list of the groups in your workspace using the **p3-list-genome-groups** command or the **p3-list-feature-groups** command. So, if you have been following along the above examples and your workspace was empty before you began, you would see the following.

```
p3-list-genome-groups
```

```
resist_strep
weak_strep
```

```
p3-list-feature-groups
```

```
resist_fids
```

Extracting and Mining Genome Typed Objects (GTOs)

Sometimes you want to store a genome on your local hard drive. PATRIC provides a special format for encapsulating all the data from a genome called the *genome typed object* or *GTO*. The **p3-gto** script allows you to download one or more PATRIC genomes in GTO format. The following command downloads two strep genomes -- 1313.7001 and 1313.7016-- in GTO format and stores them in the current directory.

```
p3-gto 1313.7001 1313.7016
```

The GTO files have the same name as the genome ID with a suffix of `.gto`. So, the above command creates **1313.7001.gto** and **1313.7016** in the current directory. If you execute this command and look at **1313.7001.gto**, you will see something like the following (with large portions in the middle removed).

```
{
   "analysis_events" : [],
   "scientific_name" : "Streptococcus pneumoniae P210774-233",
   "source" : "PATRIC",
   "source_id" : "1313.7001",
   "id" : "1313.7001",
   "taxonomy" : [
      "cellular organisms",
      "Bacteria",
      "Terrabacteria group",
      "Firmicutes",
      "Bacilli",
      "Lactobacillales",
      "Streptococcaceae",
      "Streptococcus",
      "Streptococcus pneumoniae"
   ],
   "contigs" : [
      {
         "genetic_code" : "11",
         "dna" :
"gaaaggacaaaatttgtcctttctcaagcttagctgacttcaacccactacagttgacaaagagcctgttttctcaataggattgtactcagg

         "id" : "1313.7001.con.0001"
      },
      {
         "id" : "1313.7001.con.0002",
         "genetic_code" : "11",
         "dna" :
"aaagaagctgttcgaaaagtaggcgatggttatgtctttgaggagaatggagtttctcgttatatcccagccaaggatctttcagcagaaaca

      },

   ],
   "ncbi_taxonomy_id" : "1313",
   "close_genomes" : [],
   "domain" : "Bacteria",
   "genetic_code" : "11",
   "features" : [
      {
         "type" : "repeat_region",
         "family_assignments" : [],
         "annotations" : [
            [
               "Add feature from PATRIC",
               "PATRIC",
               1500218027.10933,
               ""
            ],
            [
               "Set function to repeat region",
               "PATRIC",
```

```
                1500218027.10933,
                ""
             ]
          ],
          "aliases" : [],
          "id" : "fig|1313.7001.repeat.1",
          "function" : "repeat region",
          "location" : [
             [
                "1313.7001.con.0001",
                "67",
                "+",
                413
             ]
          ]
       },
       {
          "location" : [
             [
                "1313.7001.con.0001",
                "567",
                "+",
                539
             ]
          ],
          "function" : "repeat region",
          "id" : "fig|1313.7001.repeat.2",
          "aliases" : [],
          "annotations" : [
             [
                "Add feature from PATRIC",
                "PATRIC",
                1500218027.10944,
                ""
             ],
             [
                "Set function to repeat region",
                "PATRIC",
                1500218027.10944,
                ""
             ]
          ],
          "family_assignments" : [],
          "type" : "repeat_region"
       },

   ]
}
```

This is a JSON-format string, which is to say, it displays an object with fields, some of which are other objects (denoted by curly braces) or lists (denoted by square brackets). JSON is a standard portable data format, described in detail **here** and supported by most programming languages. Without even fully understanding the notation, you can still see in the above listing that various bits of key metadata (scientific name, taxonomy, ID) are present in the file, along with the ID and sequence of each contig and various pertinent data about each feature.

You can use a minus sign (`-`) in the parameter list to specify that the genome list come from the standard input. The following creates GTOs for every genome in the genome group *weak_strep*.

```
p3-get-genome-group weak_strep | p3-gto -
```

This capability can be mixed with explicit genome IDs. So the following script creates a GTO for *594.8*, all of the genomes in group *weak_strep*, and then genome *149539.441*.

```
p3-get-genome-group weak_strep | p3-gto 594.8 - 149539.441
```

You can also use the `--outDir` option to specify that the output be put in a different directory. The following creates a new subdirectory **PathogenGTO** in the current directory and puts all the GTOs in it.

```
p3-get-genome-group weak_strep | p3-gto --outDir=PathogenGTO 594.8 - 149539.441
```

You are not required to write code to manipulate GTOs. Instead, we've included some useful scripts in the PATRIC CLI. First and foremost is **p3-gto-scan**. For example, if you run

```
p3-gto-scan 1313.7001.gto
```

you would see the following analysis

```
Processing contigs of 1313.7001.gto.
Processing features of 1313.7001.gto.
All done.
contigs              52
dna              2101113
features            3382
functionAnalyzed    1418
functionRead        3382
functionReused      1964
roleMatch           1492
roleProcessed       3478
```

This rather arcane output tells you several things. First, that there are 52 contigs and 2,101,113 base pairs in the genome. It has 3382 features containing 1418 distinct assigned functions (*functionAnalyzed*). 3382 features had assigned functions (*functionRead*). This means every feature had a valid functional assignment, which is usually the case. 1964 of the features had redundant functions, that is, functions also found earlier in the genome (*functionReused*). 3478 roles were found (*roleProcessed*) of which 1492 were distinct (*roleMatch*).

If you want to see the actual roles, specify the command-line option **`--verbose`**.

```
p3-gto-scan --verbose 1313.7001.gto
```

```
Role name   1313.7001.gto
(2E,6E)-farnesyl diphosphate synthase (EC 2.5.1.10) 1
1,2-diacylglycerol 3-glucosyltransferase (EC 2.4.1.337) 1
1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18)  1
1-phosphofructokinase (EC 2.7.1.56) 1
16S rRNA (cytidine(1402)-2'-O)-methyltransferase (EC 2.1.1.198) 1
16S rRNA (cytosine(1402)-N(4))-methyltransferase EC 2.1.1.199)  1
16S rRNA (cytosine(967)-C(5))-methyltransferase (EC 2.1.1.176)  1
16S rRNA (guanine(1207)-N(2))-methyltransferase (EC 2.1.1.172)  1
16S rRNA (guanine(527)-N(7))-methyltransferase (EC 2.1.1.170)   1
16S rRNA (guanine(966)-N(2))-methyltransferase (EC 2.1.1.171)   1
16S rRNA (uracil(1498)-N(3))-methyltransferase (EC 2.1.1.193)   1
```

In this table, each role name is shown along with the number of times it occurs in the genome. You can see the features as well by adding the **`--features`** command line.

```
p3-gto-scan --verbose --features 1313.7001.gto
```

```
Role name   1313.7001.gto   Features containing role
(2E,6E)-farnesyl diphosphate synthase (EC 2.5.1.10) 1   fig|1313.7001.peg.1606
1,2-diacylglycerol 3-glucosyltransferase (EC 2.4.1.337) 1   fig|1313.7001.peg.679
1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18)  1
fig|1313.7001.peg.595
1-phosphofructokinase (EC 2.7.1.56) 1   fig|1313.7001.peg.227
16S rRNA (cytidine(1402)-2'-O)-methyltransferase (EC 2.1.1.198) 1   fig|1313.7001.peg.1813
16S rRNA (cytosine(1402)-N(4))-methyltransferase EC 2.1.1.199)  1   fig|1313.7001.peg.503
16S rRNA (cytosine(967)-C(5))-methyltransferase (EC 2.1.1.176)  1   fig|1313.7001.peg.1301
16S rRNA (guanine(1207)-N(2))-methyltransferase (EC 2.1.1.172)  1   fig|1313.7001.peg.83
16S rRNA (guanine(527)-N(7))-methyltransferase (EC 2.1.1.170)   1   fig|1313.7001.peg.1682
16S rRNA (guanine(966)-N(2))-methyltransferase (EC 2.1.1.171)   1   fig|1313.7001.peg.145
16S rRNA (uracil(1498)-N(3))-methyltransferase (EC 2.1.1.193)   1   fig|1313.7001.peg.728
```

Later on in this file you can see an example of a role that occurs in multiple features. You will note that a double colon (`::`) is

used to separate the individual feature IDs.

```
6-phospho-beta-galactosidase (EC 3.2.1.85)  1   fig|1313.7001.peg.607
6-phospho-beta-glucosidase (EC 3.2.1.86)    4
fig|1313.7001.peg.1031::fig|1313.7001.peg.1517::fig|1313.7001.peg.443::fig|1313.7001.peg.896
6-phosphofructokinase (EC 2.7.1.11) 1   fig|1313.7001.peg.1372
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) 1   fig|1313.7001.peg.542
```

This is a common convention in the PATRIC CLI-- when a single column contains multiple values, we use a double colon to separate them. You can use the **--delim** option to change this default. Supported alternate delimiters include **space**, **tab**, and **comma**. For example, the following would show if you coded **--delim=space**.

```
6-phospho-beta-galactosidase (EC 3.2.1.85)  1   fig|1313.7001.peg.607
6-phospho-beta-glucosidase (EC 3.2.1.86)    4   fig|1313.7001.peg.1031 fig|1313.7001.peg.1517
 fig|1313.7001.peg.443 fig|1313.7001.peg.896
6-phosphofructokinase (EC 2.7.1.11) 1   fig|1313.7001.peg.1372
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) 1   fig|1313.7001.peg.542
```

The true power in **p3-gto-scan** comes when you use it to compare multiple GTO files. The following command displays a summary of the differences between **1313.7001.gto** and **1313.7016.gto**.

```
p3-gto-scan 1313.7001.gto 1313.7016.gto
```

```
Processing contigs of 1313.7001.gto.
Processing features of 1313.7001.gto.
Processing contigs of 1313.7016.gto.
Processing features of 1313.7016.gto.
Role name   1313.7001.gto   1313.7016.gto
2,3-butanediol dehydrogenase, R-alcohol forming, (R)- and (S)-acetoin-specific (EC 1.1.1.4) 0
   1
2-isopropylmalate synthase (EC 2.3.3.13)    1   2
23S rRNA (adenine(2058)-N(6))-dimethyltransferase (EC 2.1.1.184) => Erm(B)  0   1
4-hydroxybenzoate polyprenyltransferase and related prenyltransferases  0   1
5S rRNA 2   3
6-phospho-beta-galactosidase (EC 3.2.1.85)  1   2
AAA superfamily ATPase  0   1
ABC transporter amino acid-binding protein  0   1
ABC transporter, ATP-binding protein    13  11
ABC transporter, ATP-binding protein (cluster 3, basic aa/glutamine/opines) 3   4
ABC transporter, permease protein (cluster 3, basic aa/glutamine/opines)    5   6
ABC transporter, substrate-binding protein PebA (cluster 3, basic aa/glutamine/opines)  2   1

weak similarity to aminoglycoside phosphotransferase    1   0
* Features  3382    3304
* DNA   2101113 2052306
All done.
contigs              110
dna                4153419
features              6686
functionAnalyzed      1457
functionRead          6686
functionReused        5229
roleMatch             1356
roleMismatch           175
roleProcessed         6877
```

Only roles that differ between the two genomes are shown (175, the number in *roleMismatch*). For each, the role name is shown followed by the number of occurrences in 1313.7001.gto and then the number of occurrences in 1313.7016.gto. So, we can see that *2-isopropylmalate synthase* occurs once in 1313.7001 but twice in 1313.7016. At the end of the role listing, feature and DNA counts are shown. We see that 1313.7016 has 78 fewer features and around 50,000 fewer base pairs (48,807 to be exact). 1356 roles occurred the same number of times in both genomes (*roleMatch*).

You can specify as many GTO file names as you wish in the parameter list for **p3-gto-scan**. As with the single-genome case, **--features** causes the features to be listed in the last column. The **--verbose** option causes even the matching roles to be listed, so you can get counts for everything.

The status and statistical messages are sent to the standard error output, and the role table to the standard output. Thus, if you

redirect these to separate files, the direct output from **p3-gto-scan** can be used to get a convenient list of roles from the script. The file thus created is tab-delimited with headers, just like a normal CLI output file.

The script **p3-gto-fasta** creates FASTA files from a single GTO. Three command-line options (all mutually exclusive) are supported.

--contig
: Output a DNA fasta for the genome's contigs. This is the default.

--protein
: Output a protein fasta for the genome's features. Obviously, only protein-encoding features will be included.

--feature
: Output a DNA fasta for the genome's features. All features are included.

You specify the name of the GTO file as the first parameter of **p3-gto-fasta**.

```
p3-gto-fasta 1313.7001.gto >1313.7001.fna
```

After this script, **1313.7001.fna** will look something like this.

```
>1313.7001.con.0001
gaaaggacaaaatttgtcctttctcaagcttagctgacttcaacccactacagttgacaa
agagcctgttttctcaataggattgtactcaggtgagtagggaggaagaggtaaaagttt
atgcccaaactcttcacacaagagttctagcttacccattctatggaatcttgcattatc
cataataataaccgatggtgtggttaatgttggtaagagaaatttctgaaaccatacttc
aaaaaagtcgctcgtcatcgtctcttcgtaagtcattggagcgattaattcaccatttgt
tagacctgcaaccaaagaaatcctctgatatcttcttccagatactttgcctcttcttaa
ctgacctttaatgagcgaccatattctcgataaaaataagtatcgaatcctgtttcgtc
aatctaaacaggtgctaggtgctttaaactattaaaattcttaagaaataaggctactta
tcgccctgaatatcaaaaaagaaaggacaaaatttgtcctttctcaagcttagctgactt
caacccactacagttgacaaagagcctgttttctcaataggattgtactcaggtgagtag
ggaggaagaggtaaaagtttatgcccaaactcttcacacaagagttctagcttacccatt
```

In the feature-based fasta files, the functional assignment is included as a comment, as shown below.

```
p3-gto-fasta --protein 1313.7001.gto
```

```
>fig|1313.7001.peg.1182 beta-glycosyl hydrolase
MKHEKQQRFSIRKYAVGAASVLIGFAFQAQTVAADGVTTTTENQPTIHTVSDSPQSSENR
TEETPKAELQPETPATDKVASLPKTEEKPQEEVSSTPSDKAEVVTPTSAEKETANKKAEE
ASPKKEEAKEVDSKESNTDKTDKDKPAKKDEAKAEADKPETEAGKERAATVNEKLAKKKI
VSIDAGRKYFSPEQLKEIIDKAKHYGYTDLHLLVGNDGLRFMLDDMSITANGKTYASDDV
KRAIEKGTNDYYNDPNGNHLTESQMTDLINYAKDKGIGLIPTVNSPGHMDAILNAMKELG
IQNPNFSYFGKESARTVNLDNEQAVAFTKALIDKYAAYFAKKTEIFNIGLDEYANDATDA
KGWSVLQADKYYPNEGYPVKGYEKFIAYANDLARIVKSHGLKPMAFNDGIYYNSDTSFGS
FDKDIIVSMWTGGWGGYDVASSKLLAEKGHQILNTNDAWYYVLGRNADGQGWYNLDQGLN
GIKNTPITSVPKTEGADIPIIGGMVAAWADTPSARYSPSRLFKLMRHFANANAEYFAADY
ESAEQALNEVPKDLNRYTAESVAAVKEAEKAIRSLDSNLSRAQQDTIDQAIAKLQETVNN
LTLTPEAQKEEEAKREVEKLAKNKVISIDAGRKYFTLNQLKRIVDKASELGYSDVHLLLG
NDGLRFLLDDMTITANGKTYASDDVKKAIIEGTKAYYDDPNGTTLTQAEVTELIEYAKSK
DIGLIPAINSPGHMDAMLVAMEKLGIKNPQAHFDKVSKTTMDLKNEEAMNFVKALIGKYM
```

Only protein-encoding genes are output with the `--protein` option; however, you see all the features when you use the `--feature` option.

```
p3-gto-fasta --feature 1313.7001.gto
```

```
>fig|1313.7001.repeat.1 repeat region
tgttttctcaataggattgtactcaggtgagtagggaggaagaggtaaaagtttatgccc
aaactcttcacacaagagttctagcttacccattctatggaatcttgcattatccataat
aataaccgatggtgtggttaatgttggtaagagaaatttctgaaaccatacttcaaaaaa
gtcgctcgtcatcgtctcttcgtaagtcattggagcgattaattcaccatttgttagacc
tgcaaccaaagaaatcctctgatatcttcttccagatactttgcctcttcttaactgacc
ttttaatgagcgaccatattctcgataaaaataagtatcgaatcctgtttcgtcaatcta
aacaggtgctaggtgctttaaactattaaaattcttaagaaataaggctactt
```

```
>fig|1313.7001.repeat.2 repeat region
tgttttctcaataggattgtactcaggtgagtagggaggaagaggtaaaagtttatgccc
aaactcttcacacaagagttctagcttacccattctatggaatcttgcattatccataat
```

Using RAST to Create New Genomes

If you have a DNA fasta file and you know the taxonomic ID with a certain degree of confidence, you can use the script **p3-rast** to annotate the DNA and produce a new genome. The standard output of the script is a GTO. In almost every case, you will want to redirect this to a file. In addition, the new genome is stored in your workspace. It will appear in listings from **p3-all-genomes**, and you can find its files via the web interface in your QuickData folders.

To invoke **p3-rast**, you specify a taxonomic ID or the ID of a genome with the same taxonomic ID plus the name to give to the new genome. The contigs should be in the form of a FASTA file via the standard input. All this data is submitted to the PATRIC annotation service. When the service completes, it stores the new genome in your workspace and sends back a GTO. The example below shows a submission of sequences taken from a metagenomic sample named *SRS576036* chosen because they have a high similarity to sequences from Catenibacterium mitsuokai (taxon ID 100886).

```
p3-rast 100886 "Catenibacterium from sample SRS576036" <sample.fna >test.gto 2>test.log
```

Now **test.gto** contains a GTO of the resulting genome and **test.log** contains information about the RAST job. If we use the `--private` option of **p3-all-genomes**, we will see the new genome in the list.

```
p3-all-genomes --private --attr genome_name
```

```
genome.genome_id       genome.genome_name
100886.26       Catenibacterium from sample SRS576036
```

The genome was assigned the ID *100886.26*. We can see this in the GTO file as well.

```
{
   "genetic_code" : "11",

         ],
         "family_assignments" : [],
         "type" : "CDS",
         "id" : "fig|100886.26.peg.1540"
      },
      {
         "protein_translation" :
"MLQIENASIAYGNDILFSGFNLQLERGEIASISGPSGCGKSSLLNAILGFTPLKEGRIVLNGILLDKGNVDVVRKQTAWIPQELALPLEWVKDI

         "aliases" : [],
         "location" : [
            [
               "100886.26.con.0010",
               "23684",
               "-",
               624
            ]

         "type" : "CDS"
      }
   ],
   "id" : "100886.26",
   "contigs" : [
      {
         "id" : "100886.26.con.0001",

}
```

The genome ID appears as a part of every feature ID, as an ID in its own right, and as the first part of every contig ID.

As long as you are signed in, the genomes you create using **p3-rast** will participate in all queries.

```
p3-all-genomes --eq taxon_id,100886 --attr genome_name
```

```
genome.genome_id        genome.genome_name
100886.3        Catenibacterium mitsuokai
100886.26       Catenibacterium from sample SRS576036
```

However, just as you can restrict **p3-all-genomes** to your own private genomes using the `--private` option, you can restrict it to public genomes only using the `--public` option.

```
p3-all-genomes --public --eq taxon_id,100886 --attr genome_name
```

```
genome.genome_id        genome.genome_name
100886.3        Catenibacterium mitsuokai
```

The GTO produced by **p3-rast** has extra information in it describing the annotation process, but it is functionally equivalent to the output were you to re-fetch the genome using the standard script.

```
p3-gto 100886.26
```

A **p3-gto-scan** for **test.gto** would return the same role profile as for **100886.26.gto**.

Customizing Your Toolkit

The set of commands that we support via the p3-scripts offers a fairly broad set of capabilities. For example, say you want the name of a specific genome from the ID. You can do this easily using

```
p3-echo -t genome_id 670.470 | p3-get-genome-data --attr genome_name
```

```
genome_id       genome.genome_name
670.470 Vibrio parahaemolyticus strain S176-10
```

If you do this a lot, you may find the extra typing tedious. It is worth, therefore, a brief discussion of how to create shortcut scripts.

Custom Scripts in the BASH Environment

In BASH (the most popular Unix shell) you can add functions to your **.bashrc** file, using `$`-notation to indicate the incoming command-line variables. So, to create the command

```
gn 670.470
```

You would use the function definition

```
function gn {
    p3-all-genomes --eq=genome_id,$1 --attr genome_name
}
```

You must reload the shell to activate your changes to the **.bashrc** file. Use

```
exec bash
```

to replace your current shell with a new instance.

In the function, the `$1` is replaced by the first parameter on the command, which in our example is `670.470`. If you type

```
gn 1313.7001
```

the `$1` is replaced by `1313.7001`, so the output would be

```
genome_id       genome.genome_name
1313.7001       Streptococcus pneumoniae P210774-233
```

You can have more than one parameter. The second is called `$2`, the third `$3`, and so on. The following function creates a genome group of everything resistant to a particular drug. The drug is the first parameter, the group name the second.

```
function rg {
    p3-echo -t antibiotic $1 | p3-get-drug-genomes --resistant --attr genome_id | p3-put-genome-group $2
}
```

Once the above definition is in place, the following command will put all the methicillin-resistant genomes into the group **meth_resist**.

```
rg methicillin meth_resist
```

Custom Scripts for the Windows CMD Shell

In Windows, you create a file with the extension `.cmd` that has your script in it, and put the file somewhere in your path. The incoming command-line variables use `%`-notation. The special command `@echo off` is normally put at the beginning of the file to prevent the file internals from displaying.

So, to create the command

```
gn 670.470
```

You would create the file

```
@echo off
p3-all-genomes --eq=genome_id,%1 --attr genome_name
```

and save it as **gn.cmd** in your script directory (which should be some directory you have defined and placed on your path).

In the function, the `%1` is replaced by the first parameter on the command, which in our example is `670.470`. If you type

```
gn 1313.7001
```

the `%1` is replaced by `1313.7001`, so the output would be

```
genome_id       genome.genome_name
1313.7001       Streptococcus pneumoniae P210774-233
```

You can have more than one parameter. The second is called `%2`, the third `%3`, and so on. The following function creates a genome group of everything resistant to a particular drug. The drug is the first parameter, the group name the second.

```
@echo off
p3-echo -t antibiotic %1 | p3-get-drug-genomes --resistant --attr genome_id | p3-put-genome-group %2
```

Once the above is saved as **rg.cmd**, the following command will put all the methicillin-resistant genomes into the roup **meth_resist**.

```
rg methicillin meth_resist
```

PATRIC Query Examples

This section posits some typical questions and shows how to answer them. Note that some of the queries could be handled more efficiently using code from someone else. That would, of course, be fine with us.

How many Streptococcus genomes do we have?

```
p3-all-genomes --equal genus,Streptococcus --count
```

```
genome.count
11836
```

Note the use of the `--count` command-line option to produce a count of the results instead of the results themselves.

Which Streptococcus genomes do we have?

```
p3-all-genomes --equal genus,Streptococcus --attr genome_name
```

```
genome.genome_id    genome.genome_name
1302.21 Streptococcus gordonii strain DD07
1303.76 Streptococcus oralis strain DD05
1303.77 Streptococcus oralis strain DD14
1303.78 Streptococcus oralis strain DD15
1303.79 Streptococcus oralis strain DD16
1303.80 Streptococcus oralis strain DD20
1303.81 Streptococcus oralis strain DD21
1303.82 Streptococcus oralis strain DD27
1303.83 Streptococcus oralis strain DD30
```

p3-all-genomes always includes the ID, so all we need for the `--attr` parameter is the name field. If you intend to pipe the results into another script, specify the attributes in the order you want them to appear.

```
p3-all-genomes --equal genus,Streptococcus --attr genome_name --attr genome_id
```

```
genome.genome_name  genome.genome_id
Streptococcus gordonii strain DD07  1302.21
Streptococcus oralis strain DD05    1303.76
Streptococcus oralis strain DD14    1303.77
Streptococcus oralis strain DD15    1303.78
Streptococcus oralis strain DD16    1303.79
Streptococcus oralis strain DD20    1303.80
Streptococcus oralis strain DD21    1303.81
Streptococcus oralis strain DD27    1303.82
Streptococcus oralis strain DD30    1303.83
```

What fraction of the genomes in genus Staphylococcus are resistant to methicillin?

This is a two-step process, since we need two numbers.

```
p3-all-genomes --equal genome_name,Staphylococcus --count
```

We isolate the genus by doing a string match on the genome name, since equality for string fields matches if the value is a substring. We could also use `--equal genus,Staphylococcus` and get an equivalent result.

```
genome.count
10716
```

To get the count of resistant genomes, we need to pipe the drug name into **p3-get-drug-genomes**. Here we don't have the option of using the *genus* field, since only the genome name is present in the drug-genome records, not the entire taxonomy.

```
p3-echo -t antibiotic methicillin | p3-get-drug-genomes --resistant --equal
genome_name,Staphylococcus --count
```

```
antibiotic   genome_drug.count
methicillin  1064
```

The answer is 1064 * 100 / 10716 or 9.93%.

Which global protein family is fig|46170.310.peg.738 in?

```
p3-echo -t patric_id "fig|46170.310.peg.738" | p3-get-feature-data --attr
pgfam_id
```

There are a couple of important things here. We use the *pgfam_id* field to get the global protein family (*plfam_id* would be used to get the local protein family). Also, the feature ID is enclosed in double quotes on the command line so that the vertical bar doesn't confuse the command-line shell.

```
patric_id feature.pgfam_id
fig|46170.310.peg.738 PGF_00040464
```

What function does fig|46170.310.peg.738 implement?

The function is stored in the feature table's *product* attribute.

```
p3-echo -t patric_id "fig|46170.310.peg.738" | p3-get-feature-data --attr
product
```

```
patric_id      feature.product
fig|46170.310.peg.738   Putative cysteine desulfurase, associated with tRNA 4-
thiouridine synthase
```

Of course, you could ask this question of several features with a single pipe.

```
p3-echo -t patric_id "fig|46170.310.peg.738" "fig|1313.7001.peg.1189"
"fig|66976.18.peg.131" | p3-get-feature-data --attr product
```

```
patric_id   feature.product
fig|46170.310.peg.738   Putative cysteine desulfurase, associated with tRNA 4-
thiouridine synthase
fig|1313.7001.peg.1189  IMP cyclohydrolase (EC 3.5.4.10) /
Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)
fig|66976.18.peg.131    hypothetical protein
```

The **p3-echo** command uses the `--title` command-line option to determine how many parameters to put on each output line. Since our example has only one title, the output file has only a single column, and it can be easily piped to **p3-get-feature-data**.

What drugs is 46170.310 resistant to?

The drug name is in the *antibiotic* attribute of the genome-drug table. We start with a genome ID and use **p3-get-genome-drugs**.

```
p3-echo -t genome_id 46170.310 | p3-get-genome-drugs --resistant --attr
antibiotic
```

```
genome_id   genome_drug.antibiotic
46170.310   ciprofloxacin
46170.310   erythromycin
46170.310   gentamicin
46170.310   methicillin
46170.310   penicillin
```

```
46170.310   trimethoprim/sulfamethoxazole
```

What genomes are resistant to erythromycin?

Here we start with a drug name and use **p3-get-drug-genomes** to get the genome data.

```
p3-echo -t antibiotic erythromycin | p3-get-drug-genomes --resistant --attr
genome_id --attr genome_name
```

```
antibiotic  genome_drug.genome_id   genome_drug.genome_name
erythromycin    1280.4920   Staphylococcus aureus P210110-35
erythromycin    1280.4930   Staphylococcus aureus P210184-226
erythromycin    1280.4940   Staphylococcus aureus P210369-10
erythromycin    1280.4960   Staphylococcus aureus P210464-28
erythromycin    1280.4970   Staphylococcus aureus P310372-198
erythromycin    1280.4990   Staphylococcus aureus P311202-207
erythromycin    1313.6942   Streptococcus pneumoniae P110340-157
erythromycin    1313.7001   Streptococcus pneumoniae P210774-233
erythromycin    1313.7002   Streptococcus pneumoniae P210824-213
erythromycin    1313.7006   Streptococcus pneumoniae P310010-154
erythromycin    1313.7013   Streptococcus pneumoniae P310795-191
```

How close are fig|1302.21.peg.966 and fig|1302.21.peg.1019 on the chromosome?

The script **p3-get-feature-gap** gives us this information. Since it expects two feature IDs on the same input line, we use a **p3-echo** with two titles to put its two parameters on a single line.

```
p3-echo -t f1.patric_id -t f2.patric_id "fig|1302.21.peg.966"
"fig|1302.21.peg.1019" | p3-feature-gap
```

```
f1.patric_id    f2.patric_id    gap
fig|1302.21.peg.966 fig|1302.21.peg.1019    55253
```

Note that if the features are on different contigs, we get a very high number.

```
p3-echo -t f1.patric_id -t f2.patric_id "fig|1313.7001.peg.1159"
"fig|1313.7001.peg.1384" | p3-feature-gap
```

```
f1.patric_id    f2.patric_id    gap
fig|1313.7001.peg.1159  fig|1313.7001.peg.1384  2000000000
```

The very high number makes it easier to simply compare the distance outputs from **p3-feature-gap**. Features on different contigs will always sort as further apart than features on the same contig.

Give me a fasta file of the contigs of genome 1302.21

```
p3-genome-fasta 1302.21
```

```
>1302.21.con.0001 contig
agctcagttggtagtagcgcatgactgttaatcatgatgtcgtaggttcgagtcctactg
ccggagttatatctataagtaagacaagaaattcttgtctttttatatttattgtgtttt
tgcaatttaatttttaagttcttatttaataaaaagcttgaagattattcttcaagcttt
ttatgtttattaaagaatgcttcatagagggctttaatagctgctttttcttgttcagag
tttactacgagcatgatagaaacttcgctagatccttgagagatcatttgaatattaatt
ttgctgtctgatagagcctttgtagccgtagcagtcagaccgatatgacttttcatttgc
```

Give me the protein sequences for the pegs in genome 1302.21.

```
p3-genome-fasta --protein 1302.21
```

```
>fig|1302.21.peg.966 putative Zn-dependent protease
MRFLLNLFRFIWRMFWRLVWAGIVAFIILVSVLYLTNPSQTGLTAVRQAVQTAVNQLDTF
LDQQGIHTGLGQNVQNLGEHLTDQHVASSDGARWENARATVYIETENSTFRAAYQEAIKS
WNATGAFTFQLVEDKSQANIIATEMNDSTITAAGEAESQTNVLTKRFTKVTVRLNAYYLL
NNYYGYSHERIVNTASHELGHAIGLDHNESESVMQSAGSFYSIQPIDIQAVKELYQD
>fig|1302.21.peg.969 Putative metallopeptidase (Zinc) SprT family
MNLNEYIKQVSLEDFGWEFRHQAFWNKRLRTTGGRFFPKDGHLDFNPKIYETFGLETFRK
IVRHELAHYHLYYQGKGYRHKDRDFKELLKQVGGLRYAPGLPAKKLKLHYQCRSCCTDFY
RQRRIEIKKYRCGRCKGKLRLLKQER
```

Given a list of genomes, produce a list of pairs of roles that are implemented by pegs that are close on the chromosome, sorted by number of occurrences.

Here we assume our list of genomes is in the file **genomes.tbl**. The content of this file is shown below.

```
genome_id
1310696.14
66976.17
91890.5
316273.25
186497.12
1353158.3
135461.13
1173954.3
1176728.3
```

We use **p3-get-genome-features** to get the feature and location data, **p3-function-to-role** to convert the functions to roles, and **p3-generate-close-roles** to compute the physically close roles. Because we only want protein-encoding genes (pegs), we filter the genome features by type. (If we didn't do this, the output would start with a whole bunch of generic roles involving ribosomes and CRISPR repeats.) The output is automatically sorted by decreasing number of occurrences.

```
p3-get-genome-features --eq feature_type,CDS --attr sequence_id --attr location
 --attr product <genomes.tbl | p3-function-to-role | p3-generate-close-roles
```

```
role1   role2   count
Transposase, IS3/IS911 family   Mobile element protein  33
Mobile element protein  Mobile element protein  29
Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5)
 Copper-translocating P-type ATPase (EC 3.6.3.4) 25
Potassium efflux system KefA protein    Small-conductance mechanosensitive
channel  13
Cobalt-zinc-cadmium resistance protein CzcA Cation efflux system protein CusA
 13
Gamma-glutamyltranspeptidase (EC 2.3.2.2)   Glutathione hydrolase (EC
3.4.19.13)    13
Efflux ABC transporter, ATP-binding protein Efflux ABC transporter, permease
protein    11
```

Note that the occurrence counts are shown in the last column of the output.

What genomes in a list have GC content values greater than 60%.

For this exercise we will use the **genomes.tbl** file as input.

```
genome_id
1310696.14
66976.17
91890.5
316273.25
186497.12
1353158.3
135461.13
1173954.3
1176728.3
```

The GC content percentage is found in the *gc_content* attribute, as shown in the example below (we use **p3-sort** to sort the results by the content percentage).

```
p3-get-genome-data --attr gc_content --attr genome_name <genomes.tbl | p3-sort
gc_content/n
```

```
genome_id       genome.gc_content       genome.genome_name
91890.5 38.19   Legionella pneumophila subsp. pascullei strain D-7158
66976.17        38.28   Legionella pneumophila serogroup 1 strain Lp01_666
186497.12       40.8    Pyrococcus furiosus DSM 3638
1353158.3       43.41   Methanococcoides vulcani strain SLH 33
135461.13       43.88   Bacillus subtilis subsp. subtilis strain BSD-2
1173954.3       45.1    Vibrio parahaemolyticus O4:K12 str. K1203
1176728.3       50.67   Escherichia coli K71
316273.25       64.56   Xanthomonas campestris pv. vesicatoria str. 85-10
```

As you can see, there is only one genome in this set with a GC content over 60%. To get only that genome, we use the **--gt** parameter to filter for specific values of that field.

```
p3-get-genome-data --attr gc_content --attr genome_name --gt gc_content,60
<genomes.tbl
```

```
genome_id   genome.gc_content   genome.genome_name
316273.25   64.56   Xanthomonas campestris pv. vesicatoria str. 85-10
```

What roles are found in Vibrio campbellii but not Vibrio alginolyticus?

To answer this question, we need a file of roles from Vibrio alginolyticus and use it to filter out roles from Vibrio campbellii. The following pipe gets all the roles from Vibrio alginolyticus genomes and puts them in the file **aRoles.tbl**.

```
p3-all-genomes --eq "genome_name,Vibrio alginolyticus" | p3-get-genome-features
 --attr product | p3-function-to-role | p3-sort --count feature.role
>aRoles.tbl
```

There are a lot of pieces to this pipe. First, **p3-all-genomes** gets all the genome IDs for Vibrio alginolyticus. Then **p3-get-genome-features** finds all the features for those genomes and outputs the functional assignment (product). **p3-function-to-role** converts the functions to roles and eliminates the hypotheticals. Finally, **p3-sort** with the **--count** option counts the number of occurrences of each role. It takes a while, but the output looks something like this.

```
feature.role    count
(2E,6E)-farnesyl diphosphate synthase (EC 2.5.1.10) 34
(3R)-hydroxymyristoyl-[ACP] dehydratase (EC 4.2.1.-)    34
1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18)  37
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) 34
1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74)  34
1,4-dihydroxy-2-naphthoyl-CoA hydrolase (EC 3.1.2.28) in menaquinone
biosynthesis   34
1,6-anhydro-N-acetylmuramyl-L-alanine amidase   35
1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)  34
1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)    35
1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase (EC 1.17.7.1)   38
1-phosphofructokinase (EC 2.7.1.56) 34
```

Now we perform the same exercise with Vibrio campbellii.

```
p3-all-genomes --eq "genome_name,Vibrio campbellii" | p3-get-genome-features --
attr product | p3-function-to-role | p3-sort --count feature.role >cRoles.tbl
```

```
feature.role    count
```

```
(2E,6E)-farnesyl diphosphate synthase (EC 2.5.1.10) 25
1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18)  27
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) 25
1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74)  27
1,4-dihydroxy-2-naphthoyl-CoA hydrolase (EC 3.1.2.28) in menaquinone
biosynthesis   28
1,6-anhydro-N-acetylmuramyl-L-alanine amidase   25
1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)  30
1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)    27
1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase (EC 1.17.7.1)   26
1-phosphofructokinase (EC 2.7.1.56) 33
16 kDa heat shock protein A 25
```

Now we filter **cRoles.tbl** by removing records that match **aRoles.tbl**. Note that we are matching on the key column ONLY. We don't care about the counts, only which roles are in campbellii but not alginolyticus. The **p3-file-filter** command performs this task.

```
p3-file-filter --reverse --col=feature.role aRoles.tbl <cRoles.tbl
```

The `--reverse` option tells us we want roles that are in the standard input file (**cRoles.tbl**) but not the filter file (**aRoles.tbl**). The `--col` option tells us we are comparing values in the *feature.role* column. Both files are the same format; if the formats were different, we could specify a different key column identifier for the filter file by appending it as a positional parameter. So, another way to code the same thing would be

```
p3-file-filter --reverse --col=feature.role aRoles.tbl feature.role <cRoles.tbl
```

The output looks something like this

```
feature.role    count
2,3-dihydroxybenzoate-AMP ligase (EC 2.7.7.58) of siderophore biosynthesis  33
2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase (EC 1.14.13.-)  1
2-pyrone-4,6-dicarboxylic acid hydrolase (EC 3.1.1.57)  14
23S ribosomal RNA rRNA prediction is too short  1
3-polyprenyl-4-hydroxybenzoate carboxy-lyase UbiX (EC 4.1.1.-)  1
4-amino-4-deoxy-L-arabinose transferase 26
4-carboxy-2-hydroxymuconate-6-semialdehyde dehydrogenase    17
4-carboxy-4-hydroxy-2-oxoadipate aldolase (EC 4.1.3.17) 16
4-hydroxy-2-oxovalerate aldolase (EC 4.1.3.39)  7
4-oxalmesaconate hydratase (EC 4.2.1.83)    14
4-oxalocrotonate tautomerase    1
```

What is the average length of proteins in family PGF_00112374?

If we had a file of protein family names with the amino acid length of each protein in the family, we can use the script **p3-stats** to output the mean length as well as the minimum, count, maximum, and standard deviation. The following pipe does the trick.

```
p3-echo -t family PGF_00112374 | p3-get-family-features --ftype=global --attr
aa_length | p3-stats --col=family feature.aa_length
```

```
family  count   average min max stdev
PGF_00112374    3414    818.125659050967    31  901 193.491091039707
```

The **p3-echo** command creates a one-line file with the family ID in it. We use **p3-get-family-features** to get all the features in this family. The `--ftype=global` parameter indicates that this is a global protein family (there are also families of type *local* and *figfam*). For each feature, we want the amino acid length. This value is stored in the *aa_length* attribute. Finally, we have **p3-stats**. The `--col=family` parameter tells us the input file records are to be grouped by the content of the *family* column. The positional `feature.aa_length` parameter tells us the numbers to analyze can be found in the *aa_length* column from the *feature* record. The output tells us there are 3414 pegs in the family. The average length is a little over 818 amino acids with a standard deviation of well over 193. The total range is 31 amino acids to 901 amino acids.

Display the CDS and RNA features for genome 1313.7001 sorted by location on the chromosome.

```
p3-echo -t genome_id 1313.7001 | p3-get-genome-features --in
feature_type,CDS,rna --attr patric_id --attr sequence_id --attr start --attr
strand --attr product | p3-sort feature.sequence_id feature.start/n
feature.strand
```

We start by useing **p3-echo** to create a file that has our single genome ID in it. The bulk of the retrieval work is performed by **p3-get-genome-features**. The `--in` parameter allows us to specify a list of values for a specific field. In this case, we want *feature_type* to equal either `CDS` or `rna`. To sort by location, we need the contig ID (*sequence_id*) and the start location (*start*). The start location is always the leftmost location on the contig, so it is perfect for sorting. Finally, we add the strand (`+` or `i`) and then the functional assignment (*product*) so we can see what the feature does. The **p3-sort** gets the file records in the proper order. Because one of the fields is numeric, we put a `/n` after the field name. This tells the sorter that for the *feature.start* column, the value `20` comes before, not after, the value `100`. The output will look something like this.

```
genome_id   feature.patric_id   feature.sequence_id feature.start
feature.strand  feature.product
1313.7001   fig|1313.7001.peg.1 1313.7001.con.0001  40  -   Mobile element
protein
1313.7001   fig|1313.7001.peg.2 1313.7001.con.0001  540 -   Mobile element
protein
1313.7001   fig|1313.7001.peg.3 1313.7001.con.0001  994 -   Mobile element
protein
1313.7001   fig|1313.7001.peg.4 1313.7001.con.0002  1   +   Streptococcal
histidine triad protein
1313.7001   fig|1313.7001.peg.5 1313.7001.con.0003  1   +   Endo-beta-N-
acetylglucosaminidase (EC 3.2.1.96)
1313.7001   fig|1313.7001.peg.6 1313.7001.con.0003  1120    -
Fibronectin/fibrinogen-binding protein
1313.7001   fig|1313.7001.peg.7 1313.7001.con.0003  2880    +   Metal-dependent
 hydrolase YbeY, involved in rRNA and/or ribosome maturation and assembly
1313.7001   fig|1313.7001.peg.8 1313.7001.con.0003  3358    +   Diacylglycerol
kinase (EC 2.7.1.107)
1313.7001   fig|1313.7001.peg.9 1313.7001.con.0003  3770    +   GTP-binding
protein Era
1313.7001   fig|1313.7001.peg.10    1313.7001.con.0003  4684    +
Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23)
1313.7001   fig|1313.7001.peg.11    1313.7001.con.0003  5541    +   Dephospho-
CoA kinase (EC 2.7.1.24)
1313.7001   fig|1313.7001.peg.12    1313.7001.con.0003  6133    +   Multidrug
resistance efflux pump PmrA
1313.7001   fig|1313.7001.peg.13    1313.7001.con.0003  7521    +   Protein
translocase membrane subunit SecG
1313.7001   fig|1313.7001.peg.14    1313.7001.con.0003  7856    +   3'-to-5'
exoribonuclease RNase R
1313.7001   fig|1313.7001.peg.15    1313.7001.con.0003  10173   +   tmRNA-
binding protein SmpB
1313.7001   fig|1313.7001.peg.16    1313.7001.con.0003  10656   +   Tellurite
methyltransferase (EC 2.1.1.265)
```

Compute the upstream regions for the protein-encoding genes in genome 1313.7001.

We get upstream regions from the **p3-feature-upstream** script, but to use it we need an input list of feature IDs. We will produce feature IDs and functional assignments, then append the upstream sequences.

```
p3-echo -t genome_id 1313.7001 | p3-get-genome-features --eq feature_type,CDS -
-attr patric_id --attr product | p3-feature-upstream --col=feature.patric_id
```

The `-eq feature_type,CDS` insures we only see protein-encoding features. Because we are not putting the feature ID in the last column, we use `--col=feature.patric_id` to direct **p3-feature-upstream** to the correct input column. The output will look something like this. Note the upstream DNA is in the last column.

```
genome_id   feature.patric_id   feature.product upstream
```

```
1313.7001   fig|1313.7001.peg.1182  beta-glycosyl hydrolase
ttgtcatctcctcttgactctcgttaatataagaaataaaataagggcgttgatttatataatcgctatcaatataacaat

1313.7001   fig|1313.7001.peg.1189  IMP cyclohydrolase (EC 3.5.4.10) /
Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)
gatcaatatcttaggtatgcttagccttggttttgcttatcttgttttactgttactgcatttaattggtgtttaactaat

1313.7001   fig|1313.7001.peg.1191  Phosphoribosylglycinamide formyltransferase
 (EC 2.1.2.2)
tcagccctgaaaatgtagagcgtgtaaaagaattgttggatgaagcagtctatgaaattggtcgcatcgtcaagaaagaaa

1313.7001   fig|1313.7001.peg.1192  Phosphoribosylformylglycinamidine cyclo-
ligase (EC 6.3.3.1)
tctctatgactacgaagaagactatcgtagaagtttggaagaaaagaccagtttttacaagtaggcgacagattctccatt

1313.7001   fig|1313.7001.peg.1199  hypothetical protein
aaggtggcggatgcaattggggagattttgccaaagcaggtgttggaggaggagctatacttggaggtgtggcctatgcag

1313.7001   fig|1313.7001.peg.1211  hypothetical protein
ttggcgattaccaacaatggacaggaaaaccatctggttaagatggcattcttggaattaaaaaatacagagaaaccagca

1313.7001   fig|1313.7001.peg.1259  Acetyl xylan esterase 1; Cephalosporin-C
deacetylase (EC 3.1.1.41)
aaagaatctaaattcactttctatttacccttctttcttgcattgattacatagatatgctacagttgtggtaacgattac

1313.7001   fig|1313.7001.peg.1278  Helicase loader DnaB
acgttttgctagtgtctatcgtagttttaaggatgtcagtgagttagagagcttgctccaacaaatcacccagtcctctaa

1313.7001   fig|1313.7001.peg.1288  Fructokinase (EC 2.7.1.4)
ttattagatagtaagatttacagaggaaaatctaaaaaatagagacatttagactttcgaagtatgctataataaagaaaa
```

You can use the `--len` parameter of **p3-feature-upstream** to change the number of base pairs displayed (the default is 100). If the feature is at the edge of the contig, you may see less than the specified length or even nothing at all, since the script stops at the contig boundary. To see downstream regions instead, use the `--downstream` option. This pipe shows the 10 base pairs downstream of each gene.

```
p3-echo -t genome_id 1313.7001 | p3-get-genome-features --eq feature_type,CDS -
-attr patric_id --attr product | p3-feature-upstream --col=feature.patric_id --
downstream --len=10
```

```
genome_id   feature.patric_id   feature.product downstream
1313.7001   fig|1313.7001.peg.1182  beta-glycosyl hydrolase    gtcttttcga
1313.7001   fig|1313.7001.peg.1189  IMP cyclohydrolase (EC 3.5.4.10) /
Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)
gaagataaaa
1313.7001   fig|1313.7001.peg.1191  Phosphoribosylglycinamide formyltransferase
 (EC 2.1.2.2)    ctttttgatg
1313.7001   fig|1313.7001.peg.1192  Phosphoribosylformylglycinamidine cyclo-
ligase (EC 6.3.3.1)     aaaaaatagc
1313.7001   fig|1313.7001.peg.1199  hypothetical protein    tcaaaactat
1313.7001   fig|1313.7001.peg.1211  hypothetical protein    tcaactacat
1313.7001   fig|1313.7001.peg.1259  Acetyl xylan esterase 1; Cephalosporin-C
deacetylase (EC 3.1.1.41)  ggagtcgact
1313.7001   fig|1313.7001.peg.1278  Helicase loader DnaB    atggaaagtg
```

What is the codon usage in genome 186497.12?

The **p3-sequence-profile** script counts the number of occurrences of each letter in a sequence field. To use it, we need to create a file that has the sequences we want to analyze in the last column. We start with the genome ID, then use **p3-get-genome-features** to get the feature data. The *aa_sequence* field contains the protein sequences, which are then processed by **p3-sequence-profile**.

```
p3-echo -t genome_id 186497.12 | p3-get-genome-features --attr aa_sequence |
p3-sequence-profile
```

By default, **p3-sequence-profile** works on the last input column, which in this case is the amino acid sequence. The output will look something like this.

```
letter  count
L   58114
E   51852
I   50270
K   46874
V   45417
G   41210
A   38057
R   30791
S   28102
F   25399
T   25375
D   25340
P   24706
Y   23048
N   19998
M   12966
Q   10045
H   8653
W   7104
C   3359
```

Note that the output is sorted from most common to least. The same trick works for DNA sequences, which are in the *na_sequence* field.

```
p3-echo -t genome_id 186497.12 | p3-get-genome-features --attr na_sequence |
p3-sequence-profile
```

```
letter  count
A   597286
T   465185
G   440197
C   305118
```