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# **grasp Documentation**

***Release 0.3.0b1***

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**Oct 17, 2016**



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A Simple GRASP ([grasp.nhlbi.nih.gov](http://grasp.nhlbi.nih.gov)) API based on SQLAlchemy and Pandas.

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License	MIT License, made at Stanford, use as you wish.
Version	0.2.0b

For an introduction see the [github readme](#)

For table information see the [wiki](#)



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## Submodules

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### 1.1 grasp.tables

GRASP table descriptions in SQLAlchemy ORM.

These tables do not exist in the GRASP data, which is a single flat file. By separating the data into these tables querying is much more efficient.

This submodule should only be used for querying.

```
class grasp.tables.SNP (**kwargs)
    Bases: sqlalchemy.ext.declarative.api.Base

    An SQLAlchemy Table for GRASP SNPs.

    Study and phenotype information are pushed to other tables to minimize table size and make querying easier.

    Table Name: snps

    Columns: Described in the columns attribute

    int
        The ID number of the SNP, usually the NHLBIkey

    str
        SNP loction expressed as 'chr:pos'

    hvgvs_ids
        A list of HGVS IDs for this SNP

    columns
        A dictionary of all columns 'column_name'=>('type', 'desc')

    ConservPredTFBS

    CreationDate

    Eqt1MethMetabStudy

    HUPfield

    HumanEnhancer

    InGene

    InLincRNA

    InMirNA
```

InMiRNABS

LSSNP

LastCurationDate

NHLBIkey

NearestGene

ORegAnno

PolyPhen2

RNAedit

SIFT

UniProt

chrom

**columns** = `OrderedDict([('id', ('BigInteger', 'NHLBIkey')), ('snpid', ('String', 'SNPid')), ('chrom', ('String', 'chr')), ('p`  
A description of all columns in this table.

**dbSNPClinStatus**

**dbSNPMAF**

**dbSNPfxn**

**dbSNPinfo**

**dbSNPvalidation**

**display\_columns** (*display\_as='table', write=False*)

Return all columns in the table nicely formatted.

**Display choices:** table: A formatted grid-like table tab: A tab delimited non-formatted version of table

list: A string list of column names

#### Parameters

- **display\_as** – {table,tab,list}
- **write** – If true, print output to console, otherwise return string.

**Returns** A formatted string or None

**get\_columns** (*return\_as='list'*)

Return all columns in the table nicely formatted.

**Display choices:** list: A python list of column names dictionary: A python dictionary of name=>desc

long\_dict: A python dictionary of name=>(type, desc)

**Parameters** **return\_as** – {table,tab,list,dictionary,long\_dict,id\_dict}

**Returns** A list or dictionary

**get\_variant\_info** (*fields='dbsnp', pandas=True*)

Use the myvariant API to get info about this SNP.

Note that this service can be very slow. It will be faster to query multiple SNPs.

#### Parameters



- **fields** – Choose fields to display from: ‘[docs.myvariant.info/en/latest/doc/data.html#available-fields](https://docs.myvariant.info/en/latest/doc/data.html#available-fields)’\_ Good choices are ‘dbsnp’, ‘clinvar’, or ‘gwassnps’ Can also use ‘grasp’ to get a different version of this info.
- **pandas** – Return a dataframe instead of dictionary.

**Returns** A dictionary or a dataframe.

**hvg\_ids**

The HVGS ID from myvariant.

**id**

**paper\_loc**

**phenotype\_cats**

**phenotype\_desc**

**population**

**population\_id**

**pos**

**pval**

**snp\_loc**

Return a simple string containing the SNP location.

**snpid**

**study**

**study\_id**

**study\_snpid**

```
class grasp.tables.Phenotype (**kwargs)
    Bases: sqlalchemy.ext.declarative.api.Base
```

An SQLAlchemy table to store the primary phenotype.

**Table Name:** phenos

**Columns:** phenotype: The string phenotype from the GRASP DB, unique. alias: A short representation of the phenotype, not unique. studies: A link to the studies table.

**int**

The ID number.

**str**

The name of the phenotype.

**alias**

**id**

**phenotype**

**studies**

```
class grasp.tables.PhenoCats (**kwargs)
    Bases: sqlalchemy.ext.declarative.api.Base

    An SQLAlchemy table to store the lists of phenotype categories.
```

**Table Name:** pheno\_cats

**Columns:** category: The category from the grasp database, unique. alias: An easy to use alias of the category, not unique. snps: A link to all SNPs in this category. studies: A link to all studies in this category.

**int**  
The PhenoCat ID

**str**  
The category name

**alias**

**category**

**id**

**snps**

**studies**

**class** grasp.tables.**Platform**(*platform*)  
Bases: sqlalchemy.ext.declarative.api.Base  
An SQLAlchemy table to store the platform information.

**Table Name:** platforms

**Columns:** platform: The name of the platform from GRASP. studies: A link to all studies using this platform.

**int**  
The ID number of this platform

**str**  
The name of the platform

**id**

**platform**

**studies**

**class** grasp.tables.**Population**(*population*)  
Bases: sqlalchemy.ext.declarative.api.Base  
An SQLAlchemy table to store the platform information.

**Table Name:** populations

**Columns:** population: The name of the population. studies: A link to all studies in this population. snps: A link to all SNPs in this populations.

**int**  
Population ID number

**str**  
The name of the population

**id**

**population**

## 1.2 grasp.db

Functions for managing the GRASP database.

`get_session()` is used everywhere in the module to create a connection to the database. `initialize_database()` is used to build the database from the GRASP file. It takes about an hour 90 minutes to run and will overwrite any existing database.

`grasp.db.get_session(echo=False)`

Return a session and engine, uses config file.

**Parameters** `echo` – Echo all SQL to the console.

**Returns**

A SQLAlchemy session and engine object corresponding to the grasp database for use in querying.

**Return type** session, engine

`grasp.db.initialize_database(study_file, grasp_file, commit_every=250000, progress=False)`

Create the database quickly.

**Study\_file** Tab delimited GRASP study file, available here:  
[github.com/MikeDacre/grasp/blob/master/grasp\\_studies.txt](https://github.com/MikeDacre/grasp/blob/master/grasp_studies.txt)

**Grasp\_file** Tab delimited GRASP file.

**Commit\_every** How many rows to go through before committing to disk.

**Progress** Display a progress bar (db length hard coded).

## 1.3 grasp.config

Manage a persistent configuration for the database.

`grasp.config.config = <configparser.ConfigParser object>`

A globally accessible ConfigParser object, initialized with CONFIG\_FILE.

`grasp.config.CONFIG_FILE = '/Users/dacre/.grasp'`

The PATH to the config file.

`grasp.config.init_config(db_type, db_file='', db_host='', db_user='', db_pass='')`

Create an initial config file.

**Parameters**

- **db\_type** – 'sqlite/mysql/postgresql'
- **db\_file** – PATH to sqlite database file
- **db\_host** – Hostname for mysql or postgresql server
- **db\_user** – Username for mysql or postgresql server
- **db\_pass** – Password for mysql or postgresql server (not secure)

**Returns** NoneType

**Return type** None

`grasp.config.init_config_interactive()`

Interact with the user to create a new config.

Uses readline autocompletion to make setup easier.

`grasp.config.write_config()`

Write the current config to CONFIG\_FILE.

## 1.4 grasp.query

A mix of functions to make querying the database and analyzing the results faster.

```
grasp.query.get_studies(primary_phenotype=None, pheno_cats=None, pheno_cats_alias=None,
                        primary_pop=None, has_disc_pop=None, has_rep_pop=None,
                        only_disc_pop=None, only_rep_pop=None, query=False, count=False,
                        dictionary=False, pandas=False)
```

Return a list of studies filtered by phenotype and population.

There are two ways to query both phenotype and population.

**Phenotype:** GRASP provides a ‘primary phenotype’ for each study, which are fairly poorly curated. They also provide a list of phenotype categories, which are well curated. The problem with the categories is that there are multiple per study and some are to general to be useful. If using categories be sure to post filter the study list.

Note: I have made a list of aliases for the phenotype categories to make them easier to type. Use `pheno_cats_alias` for that.

**Population:** Each study has a primary population (list available with ‘get\_populations’) but some studies also have other populations in the cohort. GRASP indexes all population counts, so those can be used to query also. To query these use `has_` or `only_` (exclusive) parameters, you can query either discovery populations or replication populations. Note that you cannot provide both `has_` and `only_` parameters for the same population type.

For doing population specific analyses most of the time you will want the `excl_disc_pop` query.

**Argument Description:** Phenotype Arguments are ‘primary\_phenotype’, ‘pheno\_cats’, and ‘pheno\_cats\_alias’.

Only provide one of `pheno_cats` or `pheno_cats_alias`

Population Arguments are `primary_pop`, `has_disc_pop`, `has_rep_pop`, `only_disc_pop`, `only_rep_pop`.

`primary_pop` is a simple argument, the others use bitwise flags for lookup.

The easiest way to use the following parameters is with the `_ref.PopFlag` object. It uses py-flags. For example:

```
pops = _ref.PopFlag.eur | _ref.PopFlag.afr
```

In addition you can provide a list of strings corresponding to `PopFlag` attributes.

Note: the `only_` parameters work as ANDs, not ORs. So `only_disc_pop='eurlafr'` will return those studies that have BOTH european and african discovery populations, but no other discovery populations. On the other hand, `has_` works as an OR, and will return any study with any of the specified populations.

### Parameters

- **primary\_phenotype** – Phenotype of interest, string or list of strings.
- **pheno\_cats** – Phenotype category of interest.
- **pheno\_cats\_alias** – Phenotype category of interest.
- **primary\_pop** – Query the primary population, string or list of strings.
- **has\_disc\_pop** – Return all studies with these discovery populations
- **has\_rep\_pop** – Return all studies with these replication populations
- **only\_disc\_pop** – Return all studies with ONLY these discovery populations

- **only\_rep\_pop** – Return all studies with ONLY these replication populations
- **query** – Return the query instead of the list of study objects.
- **count** – Return a count of the number of studies.
- **dictionary** – Return a dictionary of title->id for filtering.
- **pandas** – Return a dataframe of study information instead of the list.

**Returns** A list of study objects, a query, or a dataframe.

`grasp.query.get_snps(studies, pandas=True)`

Return a list of SNPs in a single population in a single phenotype.

**Studies** A list of studies.

**Pandas** Return a dataframe instead of a list of SNP objects.

**Returns** Either a DataFrame or list of SNP objects.

`grasp.query.get_variant_info(snp_list, fields='dbsnp', pandas=True)`

Get variant info for a list of SNPs.

#### Parameters

- **snp\_list** – A list of SNP objects or SNP rsIDs
- **fields** – Choose fields to display from: '[docs.myvariant.info/en/latest/doc/data.html#available-fields](https://docs.myvariant.info/en/latest/doc/data.html#available-fields)' Good choices are 'dbsnp', 'clinvar', or 'gwassnps' Can also use 'grasp' to get a different version of this info.
- **pandas** – Return a dataframe instead of dictionary.

**Returns** A dictionary or a dataframe.

`grasp.query.find_intersecting_phenotypes(primary_pops=None, pop_flags=None, check='cat', pop_type='disc', exclusive=False, list_only=False)`

Return a list of phenotypes that are present in all populations.

Can only provide one of primary\_pops or pop\_flags. pop\_flags does a bitwise lookup, primary\_pops queries the primary string only.

By default this function returns a list of phenotype categories, if you want to check primary phenotypes instead, provide check='primary'.

#### Parameters

- **primary\_pops** – A string or list of strings corresponding to the *tables.Study.phenotype* column
- **pop\_flags** – A *ref.PopFlag* object or list of objects.
- **check** – cat/primary either check categories or primary phenos.
- **pop\_type** – disc/rep Use with pop\_flags only, check either discovery or replication populations.
- **exclusive** – Use with pop\_flags only, do an exclusive rather than inclusion population search
- **list\_only** – Return a list of names only, rather than a list of objects

**Returns** A list of *table.Phenotype* or *table.PhenoCat* objects, or a list of names if *list\_only* is specified.

`grasp.query.collapse_dataframe(df, mechanism='median', pvalue_filter=None, protected_columns=None)`

Collapse a dataframe by chrom:location from get\_snps.

Will use the mechanism defined by 'mechanism' to collapse a dataframe to one indexed by 'chrom:location' with pvalue and count only.

This function is agnostic to all dataframe columns other than:

```
['chrom', 'pos', 'snpid', 'pval']
```

All other columns are collapsed into a comma separated list, a string. 'chrom' and 'pos' are merged to become the new colon-separated index, snpid is maintained, and pval is merged using the function in 'mechanism'.

#### Parameters

- **df** – A pandas dataframe, must have 'chrom', 'pos', 'snpid', and 'pval' columns.
- **mechanism** – A numpy statistical function to use to collapse the pvalue, median or mean are the common ones.
- **pvalue\_filter** – After collapsing the dataframe, filter to only include pvalues less than this cutoff.
- **protected\_columns** – A list of column names that will be maintained as is, although all duplicates will be dropped (randomly). Only makes sense for columns that are identical for all studies of the same SNP.

#### Returns

**Indexed by chr:pos, contains flattened pvalue column, and** all original columns as a comma-separated list. Additionally contains a count and stddev (of pvalues) column. stddev is nan if count is 1.

**Return type** DataFrame

`grasp.query.intersect_overlapping_series(series1, series2, names=None, stats=True, plot=False)`

Plot all SNPs that overlap between two pvalue series.

#### Parameters

- **series** – A pandas series object
- **names** – A list of two names to use for the resultant dataframes
- **stats** – Print some stats on the intersection
- **plot** – Plot the resulting intersection

**Returns** with the two series as columns

**Return type** DataFrame

## 1.5 grasp.info

Little functions to pretty print column lists and category info.

`get_{phenotypes,phenotype_categories,populations}` all display a dump of the whole database.

`get_population_flags` displays available flags from PopFlag.

`display_{study,snp}_columns` displays a list of available columns in those two tables as a formatted string.

`get_{study,snp}_columns` return a list of available columns in those two tables as python objects.

`grasp.info.display_snp_columns (display_as='table', write=False)`

Return all columns in the SNP table as a string.

**Display choices:** table: A formatted grid-like table tab: A tab delimited non-formatted version of table list: A string list of column names

#### Parameters

- **display\_as** – {table,tab,list}
- **write** – If true, print output to console, otherwise return string.

**Returns** A formatted string or None

`grasp.info.display_study_columns (display_as='table', write=False)`

Return all columns in the Study table as a string.

**Display choices:** table: A formatted grid-like table tab: A tab delimited non-formatted version of table list: A string list of column names

#### Parameters

- **display\_as** – {table,tab,list}
- **write** – If true, print output to console, otherwise return string.

**Returns** A formatted string or None

`grasp.info.get_phenotype_categories (list_only=False, dictionary=False, table=False)`

Return all phenotype categories from the PhenoCats table.

**List\_only** Return a simple text list instead of a list of Phenotype objects.

**Dictionary** Return a dictionary of phenotype=>ID

**Table** Return a pretty table for printing.

`grasp.info.get_phenotypes (list_only=False, dictionary=False, table=False)`

Return all phenotypes from the Phenotype table.

**List\_only** Return a simple text list instead of a list of Phenotype objects.

**Dictionary** Return a dictionary of phenotype=>ID

**Table** Return a pretty table for printing.

`grasp.info.get_population_flags (list_only=False, dictionary=False, table=False)`

Return all population flags available in the PopFlags class.

**List\_only** Return a simple text list instead of a list of Phenotype objects.

**Dictionary** Return a dictionary of population=>ID

**Table** Return a pretty table for printing.

`grasp.info.get_populations (list_only=False, dictionary=False, table=False)`

Return all populatons from the Population table.

**List\_only** Return a simple text list instead of a list of Phenotype objects.

**Dictionary** Return a dictionary of population=>ID

**Table** Return a pretty table for printing.

`grasp.info.get_snp_columns (return_as='list')`

Return all columns in the SNP table.

**Display choices:** list: A python list of column names dictionary: A python dictionary of name=>desc long\_dict: A python dictionary of name=>(type, desc)

**Parameters** `return_as` – {table,tab,list,dictionary,long\_dict,id\_dict}

**Returns** A list or dictionary

`grasp.info.get_study_columns (return_as='list')`

Return all columns in the SNP table.

**Display choices:** list: A python list of column names dictionary: A python dictionary of name=>desc long\_dict: A python dictionary of name=>(type, desc)

**Parameters** `return_as` – {table,tab,list,dictionary,long\_dict,id\_dict}

**Returns** A list or dictionary

## 1.6 grasp.ref

*ref.py* holds some simple lookups and the *PopFlags* classes that don't really go anywhere else. Holds reference objects for use elsewhere in the module.

**class** `grasp.ref.PopFlag`

Bases: `flags.Flags`

A simplified bitwise flag system for tracking populations.



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## Console Script

---

A Simple GRASP ([grasp.nhlbi.nih.gov](http://grasp.nhlbi.nih.gov)) API based on SQLAlchemy and Pandas

Author	Michael D Dacre < <a href="mailto:mike.dacre@gmail.com">mike.dacre@gmail.com</a> >
Organization	Stanford University
License	MIT License, use as you wish
Created	2016-10-08
Version	0.3.0b1

Last modified: 2016-10-17 00:18

This is the front-end to a python grasp api, intended to allow easy database creation and simple querying. For most of the functions of this module, you will need to call the module directly.

```
usage: grasp [-h] {search,conf,info,init} ...
```

### Sub-commands:

**search (s, lookup)** Query database for variants by location or id

Query for SNPs in the database. By default returns a tab-delimited list of SNPs with the following columns: 'id', 'snpid', 'study\_snpid', 'chrom', 'pos', 'phenotype', 'pval'

The `--extra` flag adds these columns: 'InGene', 'InMiRNA', 'inLincRNA', 'LSSNP'

The `--study-info` flag adds these columns: 'study\_id (PMID)', 'title'

The `--db-snp` flag uses the myvariant API to pull additional data from db\_snp.

```
usage: grasp search [-h] [--extra] [--study-info] [--db-snp] [--pandas] [-o]
                    [--path]
                    query
```

### Positional arguments:

**query** rsID, chrom:loc or chrom:start-end

### Options:

**--extra** Add some extra columns to output

**--study-info** Include study title and PMID

**--db-snp** Add dbSNP info to output

**--pandas** Write output as a pandas dataframe

**-o, --out** File to write to, default STDOUT.

**--path** PATH to write files to

**conf (config)** Manage local config

```
usage: grasp conf [-h]
                  [--db {sqlite,postgresql,mysql} | --get-path | --set-path_
↪PATH | --init]
```

**Options:**

**--db** Set the current database platform.  
Possible choices: sqlite, postgresql, mysql

**--get-path** Change the sqlite file path

**--set-path** Change the sqlite file path

**--init** Initialize the config with default settings. Will ERASE your old config!

**info** Display database info

Write data summaries (also found on the wiki) to a file or the console.

Choices: all: Will write everything to separate rst files, ignores all other flags except ‘-path’ phenotypes: All primary phenotypes. phenotype\_categories: All phenotype categories. populations: All primary populations. population\_flags: All population flags. snp\_columns: All SNP columns. study\_columns: All Study columns.

```
usage: grasp info [-h] [-o] [--path]
                  {study_columns,populations,population_flags,snp_columns,
↪phenotypes,all,phenotype_categories}
```

**Positional arguments:**

**display** Choice of item to display, if all, results are written to independant rst files, and optional args are ignored  
Possible choices: study\_columns, populations, population\_flags, snp\_columns, phenotypes, all, phenotype\_categories

**Options:**

**-o, --out** File to write to, default STDOUT.

**--path** PATH to write files to

**init** Initialize the database

```
usage: grasp init [-h] [-n] study_file grasp_file
```

**Positional arguments:**

**study\_file** GRASP study file from: [github.com/MikeDacre/grasp/blob/master/grasp2\\_studies.txt](https://github.com/MikeDacre/grasp/blob/master/grasp2_studies.txt)

**grasp\_file** GRASP tab delimited file

**Options:**

**-n, --no-progress** Do not display a progress bar

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## Indices and tables

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