# main

September 7, 2021

# 1 Enrichment in GWAS, TWAS, and DE

```python
[1]: import functools
     import numpy as np
     import pandas as pd
     import collections as cx
     from pybiomart import Dataset
     from gtfparse import read_gtf
     from scipy.stats import fisher_exact
     from statsmodels.stats.multitest import multipletests

     # GO analysis
     from goatools.base import download_go_basic_obo
     from goatools.base import download_ncbi_associations
     from goatools.obo_parser import GODag
     from goatools.anno.genetogo_reader import Gene2GoReader
     from goatools.goea.go_enrichment_ns import GOEnrichmentStudyNS
```

## 1.1 Functions

```python
[2]: @functools.lru_cache()
     def get_gtf_genes_df():
         gtf_df = read_gtf("/ceph/genome/human/gencode25/gtf.CHR/_m/gencode.v25.
      ↪annotation.gtf")
         return gtf_df[gtf_df["feature"] == "gene"][['gene_id', 'gene_name']]


     @functools.lru_cache()
     def get_wgcna_modules():
         return pd.read_csv("../../_m/modules.csv", index_col=0)


     @functools.lru_cache()
     def get_database():
         dataset = Dataset(name="hsapiens_gene_ensembl",
                           host="http://www.ensembl.org",
                           use_cache=True)
```

```python
        db = dataset.query(attributes=["ensembl_gene_id",
                                       "external_gene_name",
                                       "entrezgene_id"],
                           use_attr_names=True).dropna(subset=['entrezgene_id'])
        return db
```

```python
[3]: def fet(a, b, u):
        # a, b, u are sets
        # u is the universe
        yes_a = u.intersection(a)
        yes_b = u.intersection(b)
        no_a = u - a
        no_b = u - b
        m = [[len(yes_a.intersection(yes_b)), len(no_a.intersection(yes_b)) ],
             [len(yes_a.intersection(no_b)), len(no_a.intersection(no_b))]]
        return fisher_exact(m)


    def enrichment_rows():
        mod = get_wgcna_modules().module.unique()
        u = set(get_wgcna_modules().index)
        for ii in range(len(mod)): # for each module
            a = set(get_wgcna_modules()[(get_wgcna_modules().module) == mod[ii]].
     ↪index)
            yield (mod[ii],
                   len(a),
                   *fet(a, gwas_genes, u),
                   *fet(a, twas_genes, u),
                   *fet(a, de_genes, u),
                   )


    def enrichment_rows_nomhc():
        mod = get_wgcna_modules().module.unique()
        u = set(get_wgcna_modules().index) - mhc_genes
        for ii in range(len(mod)): # for each module
            a = set(get_wgcna_modules()[(get_wgcna_modules().module) == mod[ii]].
     ↪index) - mhc_genes
            yield (mod[ii],
                   len(a),
                   *fet(a, gwas_genes - mhc_genes, u),
                   *fet(a, twas_genes - mhc_genes, u),
                   *fet(a, de_genes - mhc_genes, u),
                   )


    def convert2entrez(mod):
```

```python
    df = get_wgcna_modules()[(get_wgcna_modules().module) == mod].copy()
    df["ensemblID"] = df.index.str.replace("\\..*", "", regex=True)
    return df.merge(get_database(), left_on='ensemblID',
                    right_on='ensembl_gene_id')


def obo_annotation(alpha=0.05):
    # database annotation
    fn_obo = download_go_basic_obo()
    fn_gene2go = download_ncbi_associations() # must be gunzip to work
    obodag = GODag(fn_obo) # downloads most up-to-date
    anno_hs = Gene2GoReader(fn_gene2go, taxids=[9606])
    # get associations
    ns2assoc = anno_hs.get_ns2assc()
    for nspc, id2gos in ns2assoc.items():
        print("{NS} {N:,} annotated human genes".format(NS=nspc, N=len(id2gos)))
    goeaobj = GOEnrichmentStudyNS(
        get_database()['entrezgene_id'], # List of human genes with entrez IDs
        ns2assoc, # geneid/GO associations
        obodag, # Ontologies
        propagate_counts = False,
        alpha = alpha, # default significance cut-off
        methods = ['fdr_bh'])
    return goeaobj


def run_goea(mod):
    df = convert2entrez(mod)
    geneids_study = {z[0]:z[1] for z in zip(df['entrezgene_id'],␣
 ↪df['external_gene_name'])}
    goeaobj = obo_annotation()
    goea_results_all = goeaobj.run_study(geneids_study)
    goea_results_sig = [r for r in goea_results_all if r.p_fdr_bh < 0.05]
    ctr = cx.Counter([r.NS for r in goea_results_sig])
    print('Significant results[{TOTAL}] = {BP} BP + {MF} MF + {CC} CC'.format(
        TOTAL=len(goea_results_sig),
        BP=ctr['BP'],  # biological_process
        MF=ctr['MF'],  # molecular_function
        CC=ctr['CC'])) # cellular_component
    goeaobj.wr_xlsx("GO_analysis_module_%s.xlsx" % mod, goea_results_sig)
    goeaobj.wr_txt("GO_analysis_module_%s.txt" % mod, goea_results_sig)
```

## 1.2 Gene annotation

```
[4]: gtf = get_gtf_genes_df()
     gtf.head(2)
```

```
INFO:root:Extracted GTF attributes: ['gene_id', 'gene_type', 'gene_status',
'gene_name', 'level', 'havana_gene', 'transcript_id', 'transcript_type',
'transcript_status', 'transcript_name', 'transcript_support_level', 'tag',
'havana_transcript', 'exon_number', 'exon_id', 'ont', 'protein_id', 'ccdsid']
```

```
[4]:                gene_id gene_name
     0    ENSG00000223972.5   DDX11L1
     12   ENSG00000227232.5    WASH7P
```

## 1.3 GWAS, TWAS and DE enrichment

### 1.3.1 Load DE, TWAS, and GWAS genes

```
[5]: de_genes = set(pd.read_csv('../../../differential_expression/_m/genes/
     ↪diffExpr_szVctl_FDR05.txt',
                                sep='\t', usecols=[0], index_col=0).index)
     len(de_genes)
```

```
[5]: 2701
```

```
[6]: gwas_genes = set(pd.read_csv('/ceph/projects/v3_phase3_paper/inputs/gwas/
     ↪PGC2_CLOZUK/table_s3/hg38/genes/_m/gwas_genes.csv')['gene_id'])
     len(gwas_genes)
```

```
[6]: 2000
```

```
[7]: mhc_genes = set(pd.read_csv('/ceph/projects/v4_phase3_paper/inputs/counts/
     ↪mhc_region_genes/_m/mhc_genes.csv')['gene_id'])
     len(mhc_genes)
```

```
[7]: 383
```

```
[8]: annot = pd.read_csv("/ceph/projects/v4_phase3_paper/inputs/counts/
     ↪text_files_counts/_m/caudate/gene.bed",
                         sep='\t', index_col=0)
     annot["Feature"] = annot.gene_id.str.replace("\\..*", "", regex=True)
     twas = pd.read_csv("../../../twas/feature_comparison/manuscript_supp_data/_m/"+\
                        "BrainSeq_Phase3_Caudate_TWAS_associations_allFeatures.txt.
     ↪gz", sep='\t')
     twas = twas[(twas["FDR"] < 0.05) & (twas["Type"] == "Gene")].merge(annot,␣
     ↪on="Feature")
     twas_genes = set(twas['gene_id'])
     len(twas_genes)
```

```
INFO:numexpr.utils:Note: NumExpr detected 60 cores but "NUMEXPR_MAX_THREADS" not
set, so enforcing safe limit of 8.
INFO:numexpr.utils:NumExpr defaulting to 8 threads.
```

[8]: 684

### 1.3.2  Load WGCNA module

```
[9]: wgcna_df = get_wgcna_modules().merge(gtf, left_index=True, right_on="gene_id",␣
     ↪how="left")
     wgcna_df.head(2)
```

```
[9]:        module          gene_id  gene_name
     12.0     grey  ENSG00000227232.5     WASH7P
     25.0   yellow  ENSG00000278267.1  MIR6859-1
```

```
[10]: wgcna_df[(wgcna_df.gene_id.str.startswith("chr"))]
```

```
[10]:         module                        gene_id gene_name
      NaN  lightgreen  chr11:113412884-113414374(-)       NaN
      NaN  lightgreen  chr11:113412884-113415420(-)       NaN
      NaN  lightgreen  chr11:113414462-113415420(-)       NaN
```

```
[11]: wgcna_df[(wgcna_df.gene_name == 'DRD2')]
```

```
[11]:            module           gene_id gene_name
      1445279.0  lightcyan  ENSG00000149295.13      DRD2
```

```
[12]: wgcna_df[(wgcna_df.gene_name == 'SETD1A')]
```

```
[12]:            module           gene_id gene_name
      1914770.0   yellow  ENSG00000099381.16    SETD1A
```

### 1.3.3  Enrichment

```
[13]: edf1 = pd.DataFrame.from_records(enrichment_rows(),
                                      columns=['module_id', 'n_genes', 'gwas_or',␣
      ↪'gwas_p',
                                               'twas_or', 'twas_p', 'de_or', 'de_p'],
                                      index='module_id')
      edf1['twas_fdr_bh'] = multipletests(edf1['twas_p'], method='fdr_bh')[1]
      edf1['gwas_fdr_bh'] = multipletests(edf1['gwas_p'], method='fdr_bh')[1]
      edf1['de_fdr_bh'] = multipletests(edf1['de_p'], method='fdr_bh')[1]
      edf1[['n_genes', 'gwas_or', 'gwas_p', 'gwas_fdr_bh', 'twas_or', 'twas_p',
            'twas_fdr_bh', 'de_or', 'de_p', 'de_fdr_bh']].
      ↪to_csv('wgcna_module_enrichment.csv')
      edf1[['n_genes', 'gwas_or', 'gwas_p', 'gwas_fdr_bh', 'twas_or', 'twas_p',
            'twas_fdr_bh', 'de_or', 'de_p', 'de_fdr_bh']]
```

[13]:

| module_id | n_genes | gwas_or | gwas_p | gwas_fdr_bh | twas_or | twas_p |
|---|---|---|---|---|---|---|
| grey | 3940 | 0.892699 | 0.214026 | 0.523174 | 1.082137 | 0.439890 |
| yellow | 1587 | 1.127312 | 0.308776 | 0.617552 | 1.111805 | 0.444625 |
| turquoise | 3334 | 0.864652 | 0.142167 | 0.390959 | 0.877289 | 0.270678 |
| cyan | 375 | 1.172909 | 0.522217 | 0.691577 | 0.983961 | 1.000000 |
| green | 1568 | 1.245199 | 0.063396 | 0.232452 | 0.889608 | 0.537755 |
| brown | 2253 | 0.767852 | 0.025971 | 0.142843 | 0.864100 | 0.327368 |
| black | 1022 | 1.108971 | 0.480575 | 0.691577 | 1.127104 | 0.509117 |
| midnightblue | 370 | 1.463223 | 0.093245 | 0.293057 | 1.189579 | 0.535008 |
| lightyellow | 226 | 0.908099 | 1.000000 | 1.000000 | 0.584393 | 0.426782 |
| tan | 411 | 1.003817 | 0.903400 | 0.973690 | 1.415578 | 0.184201 |
| royalblue | 217 | 0.728610 | 0.505137 | 0.691577 | 0.609334 | 0.422714 |
| magenta | 679 | 0.623757 | 0.044510 | 0.195843 | 0.528732 | 0.037884 |
| darkred | 204 | 1.879159 | 0.023150 | 0.142843 | 1.688871 | 0.140537 |
| pink | 793 | 1.012345 | 0.929431 | 0.973690 | 1.293422 | 0.167399 |
| blue | 2532 | 1.351950 | 0.001631 | 0.035874 | 1.165965 | 0.192978 |
| lightgreen | 227 | 0.193191 | 0.004850 | 0.053345 | 0.731567 | 0.692431 |
| lightcyan | 339 | 1.014813 | 0.893464 | 0.973690 | 0.784640 | 0.628696 |
| purple | 484 | 1.146919 | 0.499134 | 0.691577 | 0.611986 | 0.174787 |
| red | 1260 | 0.841721 | 0.287101 | 0.617552 | 1.072040 | 0.669600 |
| grey60 | 302 | 1.229691 | 0.394382 | 0.691577 | 1.234897 | 0.492128 |
| salmon | 398 | 1.162782 | 0.534400 | 0.691577 | 0.837017 | 0.764880 |
| greenyellow | 440 | 0.878693 | 0.723219 | 0.883934 | 1.071803 | 0.776149 |

| module_id | twas_fdr_bh | de_or | de_p | de_fdr_bh |
|---|---|---|---|---|
| grey | 0.739413 | 0.676330 | 2.572857e-11 | 8.086121e-11 |
| yellow | 0.739413 | 0.567600 | 1.189145e-09 | 2.906798e-09 |
| turquoise | 0.739413 | 0.303677 | 3.095585e-57 | 3.405144e-56 |
| cyan | 1.000000 | 1.867858 | 7.274883e-06 | 1.150205e-05 |
| green | 0.739413 | 0.379828 | 4.231908e-21 | 1.862039e-20 |
| brown | 0.739413 | 2.935529 | 7.804697e-79 | 1.717033e-77 |
| black | 0.739413 | 2.301877 | 1.466545e-23 | 8.065996e-23 |
| midnightblue | 0.739413 | 1.491874 | 7.027371e-03 | 8.136956e-03 |
| lightyellow | 0.739413 | 1.826881 | 8.007519e-04 | 9.786968e-04 |
| tan | 0.707588 | 1.956593 | 3.824870e-07 | 7.649741e-07 |
| royalblue | 0.739413 | 0.844996 | 5.253517e-01 | 5.253517e-01 |
| magenta | 0.707588 | 0.449134 | 1.162519e-07 | 2.557542e-07 |
| darkred | 0.707588 | 2.019585 | 1.683286e-04 | 2.178370e-04 |
| pink | 0.707588 | 3.497723 | 1.153651e-46 | 8.460107e-46 |
| blue | 0.707588 | 0.729929 | 7.319488e-06 | 1.150205e-05 |
| lightgreen | 0.801762 | 2.029721 | 4.559218e-05 | 6.686852e-05 |
| lightcyan | 0.801762 | 2.727243 | 1.836597e-13 | 6.734189e-13 |
| purple | 0.707588 | 0.437539 | 4.324439e-06 | 7.928138e-06 |
| red | 0.801762 | 0.683561 | 1.292860e-04 | 1.777682e-04 |
| grey60 | 0.739413 | 0.150158 | 3.957232e-10 | 1.088239e-09 |

```
salmon          0.813108  1.393123  2.245696e-02  2.470266e-02
greenyellow     0.813108  0.767239  1.164459e-01  1.219909e-01
```

### 1.3.4  No MHC region

```
[14]: edf2 = pd.DataFrame.from_records(enrichment_rows_nomhc(),
                            columns=['module_id', 'n_genes', 'gwas_or',␣
      ↪'gwas_p',
                                     'twas_or', 'twas_p', 'de_or', 'de_p'],
                            index='module_id')
      edf2['twas_fdr_bh'] = multipletests(edf2['twas_p'], method='fdr_bh')[1]
      edf2['gwas_fdr_bh'] = multipletests(edf2['gwas_p'], method='fdr_bh')[1]
      edf2['de_fdr_bh'] = multipletests(edf2['de_p'], method='fdr_bh')[1]
      edf2[['n_genes', 'gwas_or', 'gwas_p', 'gwas_fdr_bh', 'twas_or', 'twas_p',
            'twas_fdr_bh', 'de_or', 'de_p', 'de_fdr_bh']].
      ↪to_csv('wgcna_module_enrichment_excluding_mhc_region.csv')
      edf2[['n_genes', 'gwas_or', 'gwas_p', 'gwas_fdr_bh', 'twas_or', 'twas_p',
            'twas_fdr_bh', 'de_or', 'de_p', 'de_fdr_bh']]
```

```
[14]:              n_genes   gwas_or    gwas_p  gwas_fdr_bh   twas_or    twas_p  \
      module_id
      grey            3909  0.850262  0.102202     0.281057  1.032990  0.746956
      yellow          1569  1.025675  0.834775     0.931585  1.103254  0.521159
      turquoise       3313  0.865699  0.177595     0.390709  0.834726  0.150140
      cyan             373  1.256521  0.331638     0.561233  0.976909  1.000000
      green           1563  1.415003  0.006436     0.070794  0.901696  0.629698
      brown           2245  0.829071  0.155947     0.381205  0.916562  0.586088
      black           1014  1.109538  0.494980     0.725971  1.124947  0.491598
      midnightblue     367  1.522798  0.090576     0.281057  1.309193  0.331022
      lightyellow      226  1.087747  0.722394     0.882926  0.636869  0.535715
      tan              408  1.000158  1.000000     1.000000  1.557566  0.089448
      royalblue        214  0.496723  0.199549     0.399097  0.501996  0.293814
      magenta          676  0.628150  0.076511     0.281057  0.471059  0.022054
      darkred          202  1.967530  0.021940     0.120667  1.663843  0.128938
      pink             788  1.038477  0.846895     0.931585  1.372737  0.118340
      blue            2511  1.381774  0.001941     0.042706  1.227438  0.091969
      lightgreen       227  0.231090  0.019341     0.120667  0.797370  0.837113
      lightcyan        338  1.134521  0.660435     0.854680  0.747402  0.612372
      purple           475  0.851828  0.622896     0.854680  0.525295  0.088751
      red             1253  0.857296  0.395329     0.621231  1.148942  0.422294
      grey60           291  0.454860  0.082625     0.281057  0.744392  0.589158
      salmon           397  1.324492  0.225311     0.413070  0.915317  1.000000
      greenyellow      438  0.927932  0.897975     0.940735  1.086932  0.766356

                   twas_fdr_bh     de_or          de_p     de_fdr_bh
      module_id
      grey            0.887359  0.673036  1.788290e-11  5.620340e-11
```

```
yellow            0.814904   0.558072   4.513232e-10   1.241139e-09
turquoise         0.471869   0.305742   2.263035e-56   2.489338e-55
cyan              1.000000   1.880481   6.734897e-06   1.229777e-05
green             0.814904   0.381027   7.589137e-21   3.339220e-20
brown             0.814904   2.945581   6.003082e-79   1.320678e-77
black             0.814904   2.312840   1.036007e-23   5.698037e-23
midnightblue      0.809166   1.506621   5.327744e-03   6.168966e-03
lightyellow       0.814904   1.826750   8.010333e-04   9.790407e-04
tan               0.471869   1.944618   5.322901e-07   1.064580e-06
royalblue         0.807988   0.814611   4.548135e-01   4.548135e-01
magenta           0.471869   0.438756   5.544032e-08   1.219687e-07
darkred           0.471869   1.924064   4.104262e-04   5.311398e-04
pink              0.471869   3.509209   1.168000e-46   8.565331e-46
blue              0.471869   0.729536   7.825853e-06   1.229777e-05
lightgreen        0.920824   2.029600   4.564248e-05   6.694230e-05
lightcyan         0.814904   2.738411   1.682037e-13   6.167469e-13
purple            0.471869   0.446436   7.295151e-06   1.229777e-05
red               0.814904   0.673181   8.420111e-05   1.157765e-04
grey60            0.814904   0.156007   1.187735e-09   2.903353e-09
salmon            1.000000   1.397243   2.227414e-02   2.450156e-02
greenyellow       0.887359   0.771059   1.336408e-01   1.400046e-01
```

## 1.4 GO enrichment for each cluster

```
[15]: for mod in get_wgcna_modules().module.unique():
          run_goea(mod)
```

requests.get(http://purl.obolibrary.org/obo/go/go-basic.obo, stream=True)
  WROTE: go-basic.obo

FTP RETR ftp.ncbi.nlm.nih.gov gene/DATA gene2go.gz -> gene2go.gz
  gunzip gene2go.gz
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:05.711431 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes

Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association

Load MF Gene Ontology Analysis …

```
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association


Run BP Gene Ontology Analysis: current study set of 2789 IDs … 76%  2,113 of
2,789 study items found in association
100%  2,789 of  2,789 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
   5,611 GO terms are associated with  2,113 of  2,789 study items
  METHOD fdr_bh:
      26 GO terms found significant (< 0.05=alpha) ( 24 enriched +   2
purified): statsmodels fdr_bh
     741 study items associated with significant GO IDs (enriched)
       9 study items associated with significant GO IDs (purified)


Run CC Gene Ontology Analysis: current study set of 2789 IDs … 80%  2,240 of
2,789 study items found in association
100%  2,789 of  2,789 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
     817 GO terms are associated with  2,240 of  2,789 study items
  METHOD fdr_bh:
      20 GO terms found significant (< 0.05=alpha) ( 20 enriched +   0
purified): statsmodels fdr_bh
   2,037 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 2789 IDs … 78%  2,164 of
2,789 study items found in association
100%  2,789 of  2,789 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
   1,750 GO terms are associated with  2,164 of  2,789 study items
  METHOD fdr_bh:
      18 GO terms found significant (< 0.05=alpha) ( 16 enriched +   2
purified): statsmodels fdr_bh
   1,728 study items associated with significant GO IDs (enriched)
       6 study items associated with significant GO IDs (purified)
Significant results[64] = 26 BP + 18 MF + 20 CC
      64 items WROTE: GO_analysis_module_grey.xlsx
      64 GOEA results for  2201 study items. WROTE: GO_analysis_module_grey.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:06.221850 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
```

```
MF 18,194 annotated human genes

Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 1109 IDs … 81%    901 of
1,109 study items found in association
100%  1,109 of  1,109 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
   2,996 GO terms are associated with    901 of  1,109 study items
  METHOD fdr_bh:
      20 GO terms found significant (< 0.05=alpha) ( 18 enriched +   2
purified): statsmodels fdr_bh
     280 study items associated with significant GO IDs (enriched)
      13 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 1109 IDs … 84%    935 of
1,109 study items found in association
100%  1,109 of  1,109 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
     563 GO terms are associated with    935 of  1,109 study items
  METHOD fdr_bh:
      18 GO terms found significant (< 0.05=alpha) ( 18 enriched +   0
purified): statsmodels fdr_bh
     733 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 1109 IDs … 81%    903 of
1,109 study items found in association
100%  1,109 of  1,109 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
     911 GO terms are associated with    903 of  1,109 study items
  METHOD fdr_bh:
      16 GO terms found significant (< 0.05=alpha) ( 14 enriched +   2
purified): statsmodels fdr_bh
     759 study items associated with significant GO IDs (enriched)
```

```
      4 study items associated with significant GO IDs (purified)
Significant results[54] = 20 BP + 16 MF + 18 CC
     54 items WROTE: GO_analysis_module_yellow.xlsx
     54 GOEA results for   884 study items. WROTE: GO_analysis_module_yellow.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:06.852936 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes

Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 1232 IDs … 60%   742 of
1,232 study items found in association
100%  1,232 of  1,232 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
   2,063 GO terms are associated with    742 of  1,232 study items
  METHOD fdr_bh:
       2 GO terms found significant (< 0.05=alpha) (  2 enriched +   0
purified): statsmodels fdr_bh
     135 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 1232 IDs … 64%   792 of
1,232 study items found in association
100%  1,232 of  1,232 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
     474 GO terms are associated with    792 of  1,232 study items
  METHOD fdr_bh:
       4 GO terms found significant (< 0.05=alpha) (  1 enriched +   3
purified): statsmodels fdr_bh
      27 study items associated with significant GO IDs (enriched)
     225 study items associated with significant GO IDs (purified)
```

```
Run MF Gene Ontology Analysis: current study set of 1232 IDs … 59%    723 of
1,232 study items found in association
100%  1,232 of  1,232 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
     718 GO terms are associated with    723 of  1,232 study items
  METHOD fdr_bh:
       6 GO terms found significant (< 0.05=alpha) (  5 enriched +   1
purified): statsmodels fdr_bh
     182 study items associated with significant GO IDs (enriched)
     440 study items associated with significant GO IDs (purified)
Significant results[12] = 2 BP + 6 MF + 4 CC
     12 items WROTE: GO_analysis_module_turquoise.xlsx
     12 GOEA results for   606 study items. WROTE:
GO_analysis_module_turquoise.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:06.340478 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes

Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 349 IDs … 85%    298 of
349 study items found in association
100%    349 of    349 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
   1,384 GO terms are associated with    298 of    349 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
```

```
Run CC Gene Ontology Analysis: current study set of 349 IDs … 91%    317 of
349 study items found in association
100%    349 of    349 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
      323 GO terms are associated with    317 of    349 study items
  METHOD fdr_bh:
        9 GO terms found significant (< 0.05=alpha) (  9 enriched +   0
purified): statsmodels fdr_bh
      222 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 349 IDs … 88%    308 of
349 study items found in association
100%    349 of    349 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
      445 GO terms are associated with    308 of    349 study items
  METHOD fdr_bh:
        2 GO terms found significant (< 0.05=alpha) (  2 enriched +   0
purified): statsmodels fdr_bh
      233 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)
Significant results[11] = 0 BP + 2 MF + 9 CC
      11 items WROTE: GO_analysis_module_cyan.xlsx
      11 GOEA results for   294 study items. WROTE: GO_analysis_module_cyan.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:05.666287 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes

Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association
```

```
Run BP Gene Ontology Analysis: current study set of 909 IDs … 72%     655 of
909 study items found in association
100%     909 of     909 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
   2,226 GO terms are associated with     655 of     909 study items
  METHOD fdr_bh:
       3 GO terms found significant (< 0.05=alpha) (  3 enriched +   0
purified): statsmodels fdr_bh
     122 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 909 IDs … 75%     684 of
909 study items found in association
100%     909 of     909 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
     489 GO terms are associated with     684 of     909 study items
  METHOD fdr_bh:
       6 GO terms found significant (< 0.05=alpha) (  5 enriched +   1
purified): statsmodels fdr_bh
     336 study items associated with significant GO IDs (enriched)
      24 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 909 IDs … 74%     671 of
909 study items found in association
100%     909 of     909 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
     727 GO terms are associated with     671 of     909 study items
  METHOD fdr_bh:
       9 GO terms found significant (< 0.05=alpha) (  8 enriched +   1
purified): statsmodels fdr_bh
     560 study items associated with significant GO IDs (enriched)
       1 study items associated with significant GO IDs (purified)
Significant results[18] = 3 BP + 9 MF + 6 CC
      18 items WROTE: GO_analysis_module_green.xlsx
      18 GOEA results for   605 study items. WROTE: GO_analysis_module_green.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:06.327052 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes

Load BP Gene Ontology Analysis …
```

```
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 2007 IDs … 86%  1,723 of
2,007 study items found in association
100%  2,007 of  2,007 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
   4,742 GO terms are associated with  1,723 of  2,007 study items
  METHOD fdr_bh:
     135 GO terms found significant (< 0.05=alpha) (131 enriched +   4
purified): statsmodels fdr_bh
     988 study items associated with significant GO IDs (enriched)
      20 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 2007 IDs … 91%  1,819 of
2,007 study items found in association
100%  2,007 of  2,007 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
     851 GO terms are associated with  1,819 of  2,007 study items
  METHOD fdr_bh:
     104 GO terms found significant (< 0.05=alpha) (103 enriched +   1
purified): statsmodels fdr_bh
   1,750 study items associated with significant GO IDs (enriched)
      84 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 2007 IDs … 88%  1,759 of
2,007 study items found in association
100%  2,007 of  2,007 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
   1,567 GO terms are associated with  1,759 of  2,007 study items
  METHOD fdr_bh:
      63 GO terms found significant (< 0.05=alpha) ( 61 enriched +   2
purified): statsmodels fdr_bh
   1,512 study items associated with significant GO IDs (enriched)
       3 study items associated with significant GO IDs (purified)
Significant results[302] = 135 BP + 63 MF + 104 CC
     302 items WROTE: GO_analysis_module_brown.xlsx
```

```
    302 GOEA results for  1858 study items. WROTE: GO_analysis_module_brown.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:05.482915 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes


Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association


Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association


Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association


Run BP Gene Ontology Analysis: current study set of 859 IDs … 81%    695 of
859 study items found in association
100%    859 of    859 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
   2,852 GO terms are associated with    695 of    859 study items
  METHOD fdr_bh:
      17 GO terms found significant (< 0.05=alpha) ( 15 enriched +   2
purified): statsmodels fdr_bh
     216 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 859 IDs … 84%    725 of
859 study items found in association
100%    859 of    859 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
     515 GO terms are associated with    725 of    859 study items
  METHOD fdr_bh:
      20 GO terms found significant (< 0.05=alpha) ( 20 enriched +   0
purified): statsmodels fdr_bh
     608 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 859 IDs … 84%    722 of
859 study items found in association
```

```
100%    859 of    859 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
     861 GO terms are associated with    722 of    859 study items
  METHOD fdr_bh:
      22 GO terms found significant (< 0.05=alpha) ( 20 enriched +   2
purified): statsmodels fdr_bh
     617 study items associated with significant GO IDs (enriched)
       4 study items associated with significant GO IDs (purified)
Significant results[59] = 17 BP + 22 MF + 20 CC
     59 items WROTE: GO_analysis_module_black.xlsx
     59 GOEA results for   705 study items. WROTE: GO_analysis_module_black.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:05.462110 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes

Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 348 IDs … 87%    304 of
348 study items found in association
100%    348 of    348 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
   1,619 GO terms are associated with    304 of    348 study items
  METHOD fdr_bh:
       1 GO terms found significant (< 0.05=alpha) (  1 enriched +   0
purified): statsmodels fdr_bh
      18 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 348 IDs … 90%    314 of
348 study items found in association
100%    348 of    348 study items found in population(29107)
```

```
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
     389 GO terms are associated with    314 of    348 study items
  METHOD fdr_bh:
      20 GO terms found significant (< 0.05=alpha) ( 20 enriched +   0
purified): statsmodels fdr_bh
     251 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 348 IDs … 89%    309 of
348 study items found in association
100%    348 of    348 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
     496 GO terms are associated with    309 of    348 study items
  METHOD fdr_bh:
       5 GO terms found significant (< 0.05=alpha) (  5 enriched +   0
purified): statsmodels fdr_bh
     250 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[26] = 1 BP + 5 MF + 20 CC
     26 items WROTE: GO_analysis_module_midnightblue.xlsx
     26 GOEA results for   306 study items. WROTE:
GO_analysis_module_midnightblue.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:06.162584 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes

Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 220 IDs … 90%    198 of
220 study items found in association
100%    220 of    220 study items found in population(29107)
```

```
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
     965 GO terms are associated with    198 of    220 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 220 IDs … 94%    206 of
220 study items found in association
100%    220 of    220 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
     255 GO terms are associated with    206 of    220 study items
  METHOD fdr_bh:
       3 GO terms found significant (< 0.05=alpha) (  3 enriched +   0
purified): statsmodels fdr_bh
     107 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 220 IDs … 93%    204 of
220 study items found in association
100%    220 of    220 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
     347 GO terms are associated with    204 of    220 study items
  METHOD fdr_bh:
       3 GO terms found significant (< 0.05=alpha) (  3 enriched +   0
purified): statsmodels fdr_bh
     174 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[6] = 0 BP + 3 MF + 3 CC
       6 items WROTE: GO_analysis_module_lightyellow.xlsx
       6 GOEA results for   196 study items. WROTE:
GO_analysis_module_lightyellow.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:06.574018 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes

Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association
```

```
Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 346 IDs … 84%    292 of
346 study items found in association
100%    346 of    346 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
   1,441 GO terms are associated with    292 of    346 study items
  METHOD fdr_bh:
       7 GO terms found significant (< 0.05=alpha) (  7 enriched +   0
purified): statsmodels fdr_bh
      42 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 346 IDs … 88%    305 of
346 study items found in association
100%    346 of    346 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
     333 GO terms are associated with    305 of    346 study items
  METHOD fdr_bh:
      17 GO terms found significant (< 0.05=alpha) ( 17 enriched +   0
purified): statsmodels fdr_bh
     249 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 346 IDs … 86%    296 of
346 study items found in association
100%    346 of    346 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
     487 GO terms are associated with    296 of    346 study items
  METHOD fdr_bh:
       9 GO terms found significant (< 0.05=alpha) (  9 enriched +   0
purified): statsmodels fdr_bh
     240 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[33] = 7 BP + 9 MF + 17 CC
      33 items WROTE: GO_analysis_module_tan.xlsx
      33 GOEA results for   295 study items. WROTE: GO_analysis_module_tan.txt
  EXISTS: go-basic.obo
```

```
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:05.420147 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes

Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 197 IDs … 85%    167 of
197 study items found in association
100%    197 of    197 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
     994 GO terms are associated with    167 of    197 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 197 IDs … 91%    179 of
197 study items found in association
100%    197 of    197 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
     251 GO terms are associated with    179 of    197 study items
  METHOD fdr_bh:
       4 GO terms found significant (< 0.05=alpha) (  4 enriched +   0
purified): statsmodels fdr_bh
     130 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 197 IDs … 94%    185 of
197 study items found in association
100%    197 of    197 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
```

```
   4,418 GO terms are associated with 17,841 of 29,107 population items
     348 GO terms are associated with    185 of    197 study items
  METHOD fdr_bh:
       2 GO terms found significant (< 0.05=alpha) (  2 enriched +   0
purified): statsmodels fdr_bh
     157 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[6] = 0 BP + 2 MF + 4 CC
      6 items WROTE: GO_analysis_module_royalblue.xlsx
      6 GOEA results for   176 study items. WROTE:
GO_analysis_module_royalblue.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:06.293213 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes

Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 625 IDs … 75%    471 of
625 study items found in association
100%    625 of    625 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
   2,050 GO terms are associated with    471 of    625 study items
  METHOD fdr_bh:
      30 GO terms found significant (< 0.05=alpha) ( 30 enriched +   0
purified): statsmodels fdr_bh
     170 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 625 IDs … 81%    507 of
625 study items found in association
100%    625 of    625 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
```

```
    1,752 GO terms are associated with 18,721 of 29,107 population items
      370 GO terms are associated with    507 of    625 study items
  METHOD fdr_bh:
       31 GO terms found significant (< 0.05=alpha) ( 30 enriched +   1
purified): statsmodels fdr_bh
      353 study items associated with significant GO IDs (enriched)
        8 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 625 IDs … 77%    480 of
625 study items found in association
100%    625 of    625 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
      563 GO terms are associated with    480 of    625 study items
  METHOD fdr_bh:
       15 GO terms found significant (< 0.05=alpha) ( 14 enriched +   1
purified): statsmodels fdr_bh
      367 study items associated with significant GO IDs (enriched)
        8 study items associated with significant GO IDs (purified)
Significant results[76] = 30 BP + 15 MF + 31 CC
       76 items WROTE: GO_analysis_module_magenta.xlsx
       76 GOEA results for   465 study items. WROTE:
GO_analysis_module_magenta.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:06.139482 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes

Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 193 IDs … 82%    159 of
193 study items found in association
100%    193 of    193 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
```

```
  12,416 GO terms are associated with 17,843 of 29,107 population items
     924 GO terms are associated with    159 of    193 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 193 IDs … 91%    176 of
193 study items found in association
100%    193 of    193 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
     233 GO terms are associated with    176 of    193 study items
  METHOD fdr_bh:
       7 GO terms found significant (< 0.05=alpha) (  7 enriched +   0
purified): statsmodels fdr_bh
      79 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 193 IDs … 88%    169 of
193 study items found in association
100%    193 of    193 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
     303 GO terms are associated with    169 of    193 study items
  METHOD fdr_bh:
       1 GO terms found significant (< 0.05=alpha) (  1 enriched +   0
purified): statsmodels fdr_bh
     141 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[8] = 0 BP + 1 MF + 7 CC
      8 items WROTE: GO_analysis_module_darkred.xlsx
      8 GOEA results for   150 study items. WROTE:
GO_analysis_module_darkred.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:05.413095 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes

Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association
```

```
Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 700 IDs … 85%    598 of
700 study items found in association
100%    700 of    700 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
   2,482 GO terms are associated with    598 of    700 study items
  METHOD fdr_bh:
       2 GO terms found significant (< 0.05=alpha) (  2 enriched +   0
purified): statsmodels fdr_bh
      15 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 700 IDs … 90%    628 of
700 study items found in association
100%    700 of    700 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
     539 GO terms are associated with    628 of    700 study items
  METHOD fdr_bh:
      28 GO terms found significant (< 0.05=alpha) ( 28 enriched +   0
purified): statsmodels fdr_bh
     589 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 700 IDs … 89%    622 of
700 study items found in association
100%    700 of    700 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
     821 GO terms are associated with    622 of    700 study items
  METHOD fdr_bh:
       4 GO terms found significant (< 0.05=alpha) (  4 enriched +   0
purified): statsmodels fdr_bh
     488 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[34] = 2 BP + 4 MF + 28 CC
      34 items WROTE: GO_analysis_module_pink.xlsx
      34 GOEA results for   629 study items. WROTE: GO_analysis_module_pink.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
```

```
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:05.579850 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes

Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 2211 IDs … 87%  1,915 of
2,211 study items found in association
100%  2,211 of  2,211 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
   4,067 GO terms are associated with  1,915 of  2,211 study items
  METHOD fdr_bh:
     140 GO terms found significant (< 0.05=alpha) (131 enriched +   9
purified): statsmodels fdr_bh
   1,132 study items associated with significant GO IDs (enriched)
      58 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 2211 IDs … 92%  2,035 of
2,211 study items found in association
100%  2,211 of  2,211 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
     861 GO terms are associated with  2,035 of  2,211 study items
  METHOD fdr_bh:
     181 GO terms found significant (< 0.05=alpha) (173 enriched +   8
purified): statsmodels fdr_bh
   1,936 study items associated with significant GO IDs (enriched)
     305 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 2211 IDs … 91%  2,008 of
2,211 study items found in association
100%  2,211 of  2,211 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
```

```
    1,387 GO terms are associated with  2,008 of  2,211 study items
  METHOD fdr_bh:
      95 GO terms found significant (< 0.05=alpha) ( 85 enriched +  10
purified): statsmodels fdr_bh
   1,865 study items associated with significant GO IDs (enriched)
     108 study items associated with significant GO IDs (purified)
Significant results[416] = 140 BP + 95 MF + 181 CC
    416 items WROTE: GO_analysis_module_blue.xlsx
    416 GOEA results for  2074 study items. WROTE: GO_analysis_module_blue.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:06.100211 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes

Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 184 IDs … 78%    144 of
184 study items found in association
100%    184 of    184 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
     871 GO terms are associated with    144 of    184 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 184 IDs … 82%    150 of
184 study items found in association
100%    184 of    184 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
     214 GO terms are associated with    150 of    184 study items
```

```
  METHOD fdr_bh:
      2 GO terms found significant (< 0.05=alpha) (  2 enriched +   0
purified): statsmodels fdr_bh
     20 study items associated with significant GO IDs (enriched)
      0 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 184 IDs … 74%    136 of
184 study items found in association
100%    184 of    184 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
     254 GO terms are associated with    136 of    184 study items
  METHOD fdr_bh:
      0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
      0 study items associated with significant GO IDs (enriched)
      0 study items associated with significant GO IDs (purified)
Significant results[2] = 0 BP + 0 MF + 2 CC
      2 items WROTE: GO_analysis_module_lightgreen.xlsx
      2 GOEA results for    20 study items. WROTE:
GO_analysis_module_lightgreen.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:06.036047 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes

Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 307 IDs … 89%    272 of
307 study items found in association
100%    307 of    307 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
   1,478 GO terms are associated with    272 of    307 study items
```

```
  METHOD fdr_bh:
      20 GO terms found significant (< 0.05=alpha) ( 20 enriched +   0
purified): statsmodels fdr_bh
      77 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)


Run CC Gene Ontology Analysis: current study set of 307 IDs … 92%    281 of
307 study items found in association
100%    307 of    307 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
     353 GO terms are associated with    281 of    307 study items
  METHOD fdr_bh:
      45 GO terms found significant (< 0.05=alpha) ( 45 enriched +   0
purified): statsmodels fdr_bh
     232 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 307 IDs … 88%    270 of
307 study items found in association
100%    307 of    307 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
     430 GO terms are associated with    270 of    307 study items
  METHOD fdr_bh:
       6 GO terms found significant (< 0.05=alpha) (  6 enriched +   0
purified): statsmodels fdr_bh
     195 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[71] = 20 BP + 6 MF + 45 CC
      71 items WROTE: GO_analysis_module_lightcyan.xlsx
      71 GOEA results for   271 study items. WROTE:
GO_analysis_module_lightcyan.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:05.291330 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes


Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association


Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
```

```
  74% 21,438 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 471 IDs … 92%    431 of
471 study items found in association
100%    471 of    471 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
   2,889 GO terms are associated with    431 of    471 study items
  METHOD fdr_bh:
     232 GO terms found significant (< 0.05=alpha) (231 enriched +   1
purified): statsmodels fdr_bh
     348 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 471 IDs … 95%    449 of
471 study items found in association
100%    471 of    471 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
     422 GO terms are associated with    449 of    471 study items
  METHOD fdr_bh:
      68 GO terms found significant (< 0.05=alpha) ( 68 enriched +   0
purified): statsmodels fdr_bh
     439 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 471 IDs … 93%    440 of
471 study items found in association
100%    471 of    471 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
     705 GO terms are associated with    440 of    471 study items
  METHOD fdr_bh:
      32 GO terms found significant (< 0.05=alpha) ( 32 enriched +   0
purified): statsmodels fdr_bh
     392 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[332] = 232 BP + 32 MF + 68 CC
    332 items WROTE: GO_analysis_module_purple.xlsx
    332 GOEA results for   447 study items. WROTE: GO_analysis_module_purple.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:06.513058 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
```

```
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes

Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 1233 IDs … 91%  1,121 of
1,233 study items found in association
100%  1,233 of  1,233 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
   3,575 GO terms are associated with  1,121 of  1,233 study items
  METHOD fdr_bh:
      61 GO terms found significant (< 0.05=alpha) ( 58 enriched +   3
purified): statsmodels fdr_bh
     607 study items associated with significant GO IDs (enriched)
       5 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 1233 IDs … 95%  1,176 of
1,233 study items found in association
100%  1,233 of  1,233 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
     736 GO terms are associated with  1,176 of  1,233 study items
  METHOD fdr_bh:
     110 GO terms found significant (< 0.05=alpha) (108 enriched +   2
purified): statsmodels fdr_bh
   1,147 study items associated with significant GO IDs (enriched)
      77 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 1233 IDs … 94%  1,159 of
1,233 study items found in association
100%  1,233 of  1,233 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
   1,113 GO terms are associated with  1,159 of  1,233 study items
  METHOD fdr_bh:
```

```
      46 GO terms found significant (< 0.05=alpha) ( 43 enriched +   3
purified): statsmodels fdr_bh
   1,068 study items associated with significant GO IDs (enriched)
       3 study items associated with significant GO IDs (purified)
Significant results[217] = 61 BP + 46 MF + 110 CC
    217 items WROTE: GO_analysis_module_red.xlsx
    217 GOEA results for  1196 study items. WROTE: GO_analysis_module_red.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:06.322407 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes

Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 290 IDs … 90%    261 of
290 study items found in association
100%    290 of    290 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
   1,768 GO terms are associated with    261 of    290 study items
  METHOD fdr_bh:
     251 GO terms found significant (< 0.05=alpha) (251 enriched +   0
purified): statsmodels fdr_bh
     222 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 290 IDs … 96%    277 of
290 study items found in association
100%    290 of    290 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
     269 GO terms are associated with    277 of    290 study items
  METHOD fdr_bh:
      65 GO terms found significant (< 0.05=alpha) ( 65 enriched +   0
```

purified): statsmodels fdr_bh
     265 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 290 IDs … 92%    267 of
290 study items found in association
100%    290 of    290 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
     467 GO terms are associated with    267 of    290 study items
  METHOD fdr_bh:
      35 GO terms found significant (< 0.05=alpha) ( 35 enriched +   0
purified): statsmodels fdr_bh
     231 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[351] = 251 BP + 35 MF + 65 CC
    351 items WROTE: GO_analysis_module_grey60.xlsx
    351 GOEA results for   275 study items. WROTE: GO_analysis_module_grey60.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:06.066688 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes


Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association


Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association


Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,357 of 29,107 population items found in association


Run BP Gene Ontology Analysis: current study set of 234 IDs … 68%    159 of
234 study items found in association
100%    234 of    234 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
     635 GO terms are associated with    159 of    234 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh

```
        0 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)


Run CC Gene Ontology Analysis: current study set of 234 IDs … 71%    167 of
234 study items found in association
100%    234 of    234 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
     167 GO terms are associated with    167 of    234 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 234 IDs … 65%    152 of
234 study items found in association
100%    234 of    234 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
     280 GO terms are associated with    152 of    234 study items
  METHOD fdr_bh:
       1 GO terms found significant (< 0.05=alpha) (  1 enriched +   0
purified): statsmodels fdr_bh
      41 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[1] = 0 BP + 1 MF + 0 CC
      1 items WROTE: GO_analysis_module_salmon.xlsx
      1 GOEA results for    41 study items. WROTE: GO_analysis_module_salmon.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-09-01) 47,191 GO Terms
HMS:0:00:05.791595 330,404 annotations, 20,688 genes, 18,642 GOs, 1 taxids READ:
gene2go
CC 19,433 annotated human genes
BP 18,501 annotated human genes
MF 18,194 annotated human genes

Load BP Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 70% 20,231 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
 74% 21,438 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
fisher module not installed.  Falling back on scipy.stats.fisher_exact
```

```
  70% 20,357 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 417 IDs … 88%    369 of
417 study items found in association
100%    417 of    417 study items found in population(29107)
Calculating 12,416 uncorrected p-values using fisher_scipy_stats
  12,416 GO terms are associated with 17,843 of 29,107 population items
   1,923 GO terms are associated with    369 of    417 study items
  METHOD fdr_bh:
     10 GO terms found significant (< 0.05=alpha) ( 10 enriched +   0
purified): statsmodels fdr_bh
     118 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 417 IDs … 93%    387 of
417 study items found in association
100%    417 of    417 study items found in population(29107)
Calculating 1,752 uncorrected p-values using fisher_scipy_stats
   1,752 GO terms are associated with 18,721 of 29,107 population items
     350 GO terms are associated with    387 of    417 study items
  METHOD fdr_bh:
     18 GO terms found significant (< 0.05=alpha) ( 18 enriched +   0
purified): statsmodels fdr_bh
     323 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 417 IDs … 92%    382 of
417 study items found in association
100%    417 of    417 study items found in population(29107)
Calculating 4,418 uncorrected p-values using fisher_scipy_stats
   4,418 GO terms are associated with 17,841 of 29,107 population items
     610 GO terms are associated with    382 of    417 study items
  METHOD fdr_bh:
     12 GO terms found significant (< 0.05=alpha) ( 12 enriched +   0
purified): statsmodels fdr_bh
     314 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[40] = 10 BP + 12 MF + 18 CC
     40 items WROTE: GO_analysis_module_greenyellow.xlsx
     40 GOEA results for   367 study items. WROTE:
GO_analysis_module_greenyellow.txt
```

[ ]: