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The dopamine hypothesis is outdated: A meta-analysis of the complexities in the biochemistry of schizophrenia

R Script Instructions

Go to <https://github.com/domicowe/BIO247> -> BIO247Project -> BIO247ProjectSubmissions and download zip file “DomicoProjectZip.zip”

Open “DomicoProjectScript.R” in R software environment and set working directory to DomicoProjectZip.zip

Run code through line 667. Here is what you should expect it to do:

* Import data from PMC articles (which are provided in zip file)
  + The data was pulled from the following articles
    - [PMC3077530](http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3077530)
    - [PMC2775422](http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2775422)
    - [PMC3912837](http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3912837)
    - [PMC2890845](http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2890845)
    - [PMC4724864](http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4724864)
    - [PMC6927206](http://www.ncbi.nlm.nih.gov/pmc/articles/PMC6927206)
    - [PMC3872086](http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3872086)
    - [PMC3827979](http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3827979)
    - [PMC4059435](http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4059435)
    - [PMC3905728](http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3905728)
* Clean and transform data into a singular data frame (“MainData” df in environment”)
* Create scatterplot and bar graph of relative frequency of SNPs per chromosome
  + *Note:* *Chrs 6, 11, and 22 are >2 SDs above mean.*
* Import and clean NCBI data for Chr 6 (“Chr6DataNCBI” df in environment) which includes genes with their positions along the chromosome.
* Create histogram of significant groupings of SNPs on Chr 6. Use these to compare against NCBI data and find genes where these SNPs overlap.
* Repeat last two steps with Chrs 11 and 22.
* Combine data from Chrs 6 and 11 (the data found no significant genes for Chr 22 so its data was dropped).
* Clean data (“genedata” df in environment) and import and clean NDEx pathway data.
* Create excel file (“diseasesdf.xlsx”) of common disorders associated with these pathways.

You should now have a file “diseasesdf.xlsx” saved to the DomicoProjectZip folder. Open this and define new column “Immune.” If the disease in the previous column is autoimmune, put a “1” in the “Immune” column. If not, put a “0.” Rename the file as “diseasesdfrevised.xlsx” and save into DomicoProjectZip.zip. The “answers” are provided below if you don’t want to look it up.

|  |  |  |
| --- | --- | --- |
| **Var1** | **Freq** | **Immune** |
| addison disease | 1 | 1 |
| adrenal gland pheochromocytoma | 1 | 0 |
| alopecia | 1 | 1 |
| arbd | 1 | 0 |
| bladder papillary urothelial neoplasm | 1 | 0 |
| blepharocheilodontic syndrome 2 | 1 | 0 |
| breast cancer | 1 | 0 |
| cardiomyopathy | 1 | 1 |
| crohn disease | 1 | 1 |
| deafness | 1 | 0 |
| entropion | 1 | 0 |
| fanconi renotubular syndrome 2 | 1 | 0 |
| gout | 2 | 0 |
| graves disease | 1 | 1 |
| hashimoto thyroiditis | 1 | 1 |
| hydrolethalus syndrome | 1 | 0 |
| hyperuricemia | 1 | 0 |
| idiopathic pulmonary fibrosis | 1 | 1 |
| joubert syndrome 39 | 1 | 0 |
| juvenile idiopathic arthritis | 1 | 0 |
| leprosy 4 | 1 | 0 |
| lyme disease | 1 | 1 |
| lysosomal storage disease | 1 | 0 |
| mechel syndrome | 1 | 0 |
| multiple sclerosis | 2 | 1 |
| myocardial infarction | 1 | 1 |
| narcolepsy | 1 | 0 |
| nephrolithiasis | 1 | 1 |
| neuromyelitis optica spectrum disorder | 1 | 1 |
| olecranon bursitis | 1 | 0 |
| psoriatic arthritis | 2 | 1 |
| rheumatoid arthritis | 2 | 1 |
| rosacea | 1 | 0 |
| tonsilitis | 1 | 0 |
| toxic shock syndrome | 1 | 0 |
| type 1 diabetes | 2 | 1 |

Run code lines 668-944. Here’s what you should expect it to do:

* Calculate percentage of disorders that are autoimmune.
* Import gene data about Chr 6 and compare known SNPs against genes for the histocompatibility complex.
* Calculate percentage of SNPs that overlap with histocompatibility genes.
* Calculate percentage of each pathway in implicated genes.
* Find common words in pathway titles (“finaldata” df in environment) and cut to only include statistically significant ones (>2 SDs).
* Save excel file “finaldata.xlsx.”

Open file “finaldata.xlsx.” Define new column “kept.” If you decide that the word given is relevant, put a “1” in kept column. If not, put a “0.” The words that I decided were important for my purposes are provided below, but it could be argued that these are not important or that others are important. Save edited file as “finaldatarevised.xlsx” and save in DomicoProjectZip folder.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Var1** | **Freq** | **relfreq** | **numforgraph** | **kept** |
| rna | 164 | 1 | 1 | 0 |
| human | 159 | 0.969512 | 2 | 0 |
| protein | 117 | 0.713415 | 3 | 0 |
| mirna | 107 | 0.652439 | 4 | 0 |
| interactions | 104 | 0.634146 | 5 | 0 |
| network | 101 | 0.615854 | 6 | 0 |
| atlas | 99 | 0.603659 | 7 | 0 |
| blood | 96 | 0.585366 | 8 | 0 |
| cell | 92 | 0.560976 | 9 | 0 |
| expression | 78 | 0.47561 | 10 | 0 |
| brain | 58 | 0.353659 | 11 | 1 |
| hpa | 58 | 0.353659 | 12 | 1 |
| v21.0 | 57 | 0.347561 | 13 | 0 |
| regulatory | 56 | 0.341463 | 14 | 0 |
| types | 54 | 0.329268 | 15 | 0 |
| gene | 53 | 0.323171 | 16 | 0 |
| immune | 51 | 0.310976 | 17 | 1 |
| response | 51 | 0.310976 | 18 | 0 |
| tissue | 50 | 0.304878 | 19 | 0 |
| sapiens | 48 | 0.292683 | 20 | 0 |
| full | 46 | 0.280488 | 21 | 0 |
| string | 46 | 0.280488 | 22 | 0 |
| associations | 41 | 0.25 | 23 | 0 |
| only | 40 | 0.243902 | 24 | 0 |
| consensome | 36 | 0.219512 | 25 | 1 |
| transcriptomic | 36 | 0.219512 | 26 | 1 |
| bioplex | 32 | 0.195122 | 27 | 0 |
| humannet | 32 | 0.195122 | 28 | 0 |
| proteinprotein | 30 | 0.182927 | 29 | 0 |
| from | 28 | 0.170732 | 30 | 0 |
| biogrid: | 27 | 0.164634 | 31 | 0 |
| composite | 26 | 0.158537 | 32 | 0 |
| normal | 26 | 0.158537 | 33 | 0 |
| high | 25 | 0.152439 | 34 | 0 |
| scored | 25 | 0.152439 | 35 | 0 |
| disgenet | 24 | 0.146341 | 36 | 0 |
| links | 24 | 0.146341 | 37 | 0 |
| lines | 22 | 0.134146 | 38 | 0 |
| pathway | 21 | 0.128049 | 39 | 0 |

Run code lines 944-end. Here’s what you should expect it to do:

* Create bar plot of all significant words
* Cut user-cited unimportant words.
* Create second bar plot of only user-cited important words.