

# **Demographics: qualitative responses**

## **Qualitative responses: subfields**

For Q18, after asking respondents for their broad domain of study, we asked them this free-response question:

What is your primary field? (e.g. astrophysics, neuroscience)

One response is preferred, but if multiple are needed, please separate with commas.

I plan to “classify” these free responses into standardized categories. The taxonomy of academic disciplines that I’ll be using is here:

[https://digitalcommons.elsevier.com/en\\_US/dc-disciplines-taxonomy](https://digitalcommons.elsevier.com/en_US/dc-disciplines-taxonomy)

I downloaded the PDF and did a very tiny amount of curation to make this list of academic fields and subfields machine-readable. (I left a txt file with my curation notes in the `curation_of_disciplines/` folder in the Dryad data deposit.)

This script expects that your data folder contains a folder called `curation_of_disciplines` that in turn contains the lightly curated taxonomy of disciplines (`digital_commons_disciplines.txt`).

I’ll use a fuzzy string matching algorithm to classify the responses—essentially, looking for which item in the taxonomy most closely matches the user’s entry. Hopefully, there will be very few entries that aren’t a good match for anything in the taxonomy, and I can deal with these stragglers manually.

Note that while I am performing classification, there’s no “real” machine learning here.

Note from the future: this code ended up being pretty ugly, with a lot of nested loops. Maybe I could have written less code if I’d used the `fuzzyjoin` package. Oh well. I went for a rudimentary solution, and it worked well enough.

## Import packages and utilities

```
project_root <- here::here() # requires that you be somewhere in the
# project directory (not above it)
# packages
suppressMessages(source(file.path(project_root, "scripts/packages.R")))
# functions and objects used across scripts
suppressMessages(source(file.path(project_root, "scripts/utils.R")))
```

## Define funtions

### get\_all\_hits

- Arguments:
  - `query`: A survey response, e.g. “neuroscience” or “AI”.
  - `tax_df`: The taxonomy, as a data frame with columns `Level1`, `Level2`, and `Level3`. It wasn’t really necessary to include this as an argument since it doesn’t change, but I like to be explicit about what goes into the function.
- Details:
  - For a given query (survey response), return a data frame with the similarity scores between that query and all strings in the DC taxonomy. Each row in the taxonomy gets a row score, which is the minimum distance between the query and any of the three strings in that row. Row score was computed with `get_row_results()`.
- Outputs:
  - A data frame with columns `min_dist`, `level`, and `index`. `index` is just row number for that row in the taxonomy/in this data frame (they have the same number of rows). `level` indicates which level the winning string came from. `index` will be useful later. In the for loop at the end of this script, this df is called `q_scores`.

```
get_all_hits <- function(query, tax_df) {
  n_tax <- nrow(tax_df)

  # Pre-allocate data frame rows for computational efficiency
  query_scores <- data.frame(
    min_dist = rep(NA_real_, n_tax),
    level = rep(NA_character_, n_tax),
    index = seq_len(n_tax),
```

```

    stringsAsFactors = FALSE
  )

# Get metadata for all hits with the minimum distance score
for (i in seq_len(n_tax)) {
  results <- get_row_results(query, tax_df, i)
  query_scores$min_dist[i] <- as.numeric(results[[1]])
  query_scores$level[i] <- results[[2]]
}

return(query_scores)
}

```

### get\_row\_results

- Arguments:
  - **query**: A survey response, e.g. “neuroscience” or “AI”.
  - **tax\_df**: see `get_all_hits`
  - **row\_num**: Row number of the row in `tax_df` you want to analyze.
- Details:
  - For a given query (survey response), and a given row in the taxonomy, record which column’s entry had the lowest distance score. Breaks ties by just choosing the first occurrence of a minimum value. So it prefers Level1 over Level2, and Level2 over Level3. I’m betting that 99% of ties are basically just noise, and not real matches.
- Outputs:
  - A vector with two elements: first, the lowest distance score between the query and any string in that row of the taxonomy, and second, the name of the column that the winning string came from (e.g. `Level1`).

```

get_row_results <- function(query, tax_df, row_num) {

  strL1 <- tax_df[row_num, "Level1"]
  strL2 <- tax_df[row_num, "Level2"]
  strL3 <- tax_df[row_num, "Level3"]

  # compute Levenshtein distances for each level
  dist1 <- as.numeric(
    adist(query, strL1)
  )

```

```

dist2 <- as.numeric(
  ifelse(
    !is.na(strL2),
    adist(query, strL2),
    Inf
  )
)
dist3 <- as.numeric(
  ifelse(
    !is.na(strL3),
    adist(query, strL3),
    Inf
  )
)

dists <- c(dist1, dist2, dist3)
min_dist <- min(dists, na.rm = TRUE)

# which.min gets the index of the lowest element.
# In the event of a tie, it chooses the first one.
# So it will choose level1 over level2, and level2 over level3.
level <- c("Level1", "Level2", "Level3")[
  which.min(dists)
]

# This was a little test I ran to see how common ties are.
# Turns out ties are extremely common. They are all, or nearly
# all, cases where all 3 levels are really different from the query.
# I'm willing to assume that a tie means the taxonomy strings are all
# really different from the query, and I'm not going to fret over the
# fact that this function is practically breaking the tie at random,
# just choosing the first minimum in the list.
# has_tied_min <- function(x, na.rm = FALSE) {
#   m <- min(x, na.rm = na.rm)
#   sum(x == m, na.rm = na.rm) > 1L
# }
#if (has_tied_min(dists)) {message(query, " | ", tax_df[row_num,], " | ", dists)}

return(
  c(min_dist, level)
)
}

```

## **get\_candidates**

- Arguments:
  - `q_scores`: A data frame with columns `min_dist`, `level`, and `index`, produced by `get_all_hits()`.
- Details:
  - Given the minimum distance scores for every row/query pair, find the global minimum across all rows. Handles ties by reporting multiple candidates.
- Outputs:
  - A data frame with the same columns as the input data frame. It has been merely been subsetted so the only rows remaining are those with the minimum distance.

```
get_candidates <- function(q_scores) {  
  
  best_dist <- min(q_scores$min_dist)  
  cands <- q_scores %>% filter(min_dist == best_dist)  
  return(cands)  
}
```

## **get\_winner\_df**

- Arguments:
  - `cands_df`: A data frame with columns `min_dist`, `level`, and `index`, produced by `get_candidates()`.
  - `tax_df`: see `get_all_hits()`.
- Details:
  - Given a set of candidate rows, choose a smaller number of rows to keep. Chooses final picks by preferring Level 3 matches over Level 2 matches, and preferring Level 2 over Level 1. Returns a subset of the taxonomy, not just a bunch of indices and distance scores.
- Outputs:
  - A subset of the taxonomy; the final rows for manual inspection (as a data frame).

```

get_winner_df <- function(cands_df, tax_df) {
  winners <- ""
  lvl3_cands <- subset(cands_df, level == "Level3")
  lvl2_cands <- subset(cands_df, level == "Level2")
  lvl1_cands <- subset(cands_df, level == "Level1")

  if (nrow(lvl3_cands) > 0) {
    winners <- tax_df[lvl3_cands$index, ]
  } else if (nrow(lvl2_cands) > 0) {
    keep_idx <- lvl2_cands$index[is.na(tax_df$Level3[lvl2_cands$index])]
    winners <- tax_df[keep_idx, , drop = FALSE]
  } else {
    keep_idx <- lvl1_cands$index[
      is.na(tax_df$Level2[lvl1_cands$index]) &
      is.na(tax_df$Level3[lvl1_cands$index])
    ]
    winners <- tax_df[keep_idx, , drop = FALSE]
  }
  return(winners)
}

```

## Load data

```

other_quant <- load_qualtrics_data("clean_data/other_quant.tsv")
status <- load_qualtrics_data("clean_data/contributor_status_Q3.tsv")
qual <- load_qualtrics_data("qual_responses.tsv")

# do not read with my load_qualtrics_data function bc it has header = TRUE
tax <- read.csv(
  file = file.path(DATA_PATH, "curation_of_disciplines/digital_commons_disciplines.txt"),
  header = FALSE,
  sep = "\t",
  check.names = FALSE,
  stringsAsFactors = FALSE
)

data <- cbind(status, other_quant)
nrow(data)

```

[1] 332

```
head(data)
```

	Past	Future	campus	favorite_solution	field_of_study
1	True	True	UC Santa Barbara	Sustainability grants	Math and CS
2	True	True	UC Santa Barbara	Containerization	Life sciences
3	True	True	UC Santa Barbara	Computing environments	Humanities
4	True	True	UC Santa Barbara	Sustainability grants	Math and CS
5	True	True	UC Santa Barbara	Documentation help	Life sciences
6	False	True	UC Santa Barbara		Math and CS

job\_category staff\_categories

1	Faculty
2	Post-Doc
3	Other research staff
4	Faculty
5	Faculty
6	Other research staff

```
tmp <- data$job_category[nzchar(data$job_category)]
job_count <- data.frame(table(tmp))
names(job_count) <- c("Job", "Count")

academics <- sum(subset(job_count, Job != "Non-research Staff")[, "Count"])
```

```
qual_fields <- qual$subfield[nzchar(qual$subfield)]
length(qual_fields)
```

```
[1] 174
```

```
academics
```

```
[1] 188
```

This question was not mandatory, but 174/188 academics answered it.

```
head(qual_fields)
```

[1] "AI and neuroscience"	"Plant Biology / Ecology"
[3] "Digital humanities, History"	"Computer science, neuroscience"
[5] "Evolutionary Genomics"	"Medical Imaging, Vision Science"

Let's standardize the capitalization in this vector. The capitalization will now match my taxonomy, which is important since the fuzzy string matching algorithm I'll be using is case-sensitive.

```
qual_fields <- unname(  
  sapply(  
    qual_fields,  
    function(x) tools::toTitleCase(tolower(x)) )  
)  
  
head(qual_fields)  
  
[1] "Ai and Neuroscience"           "Plant Biology / Ecology"  
[3] "Digital Humanities, History"   "Computer Science, Neuroscience"  
[5] "Evolutionary Genomics"         "Medical Imaging, Vision Science"
```

Hmm. The correction of “AI” to “Ai” is unfortunate, but let’s see how it goes.

Here’s our taxonomy:

```
head(tax)  
  
V1  
1 Architecture  
2 Architecture: Architectural Engineering  
3 Architecture: Architectural History and Criticism  
4 Architecture: Architectural Technology  
5 Architecture: Construction Engineering  
6 Architecture: Cultural Resource Management and Policy Analysis
```

Let’s tidy this data frame.

```
tax <- tax %>%  
  separate(  
    col = names(tax)[1],  
    into = c("Level1", "Level2", "Level3"),  
    sep = ": ",  
    fill = "right",    # any missing pieces become NA  
    extra = "merge"    # if there were >2 colons, they'd all merge into Level3  
)  
  
head(tax)
```

	Level1	Level2	Level3
1 Architecture		<NA>	<NA>
2 Architecture		Architectural Engineering	<NA>
3 Architecture		Architectural History and Criticism	<NA>
4 Architecture		Architectural Technology	<NA>
5 Architecture		Construction Engineering	<NA>
6 Architecture	Cultural Resource Management and Policy Analysis		<NA>

You can take my word for it that I looked back and forth between the data frame and the data file, and made sure that the data frame looks good. (Correct # of rows, row numbers match line numbers, etc.)

Cool! Now we are ready for fuzzy string matching. Let's start with a very rudimentary method, and we can do something fancier if this appears insufficient.

We are just using the adist() function in base R to calculate the Levenshtein distance between pairs of strings—the minimum number of substitutions needed to turn ‘string a’ into ‘string b’.

Since we invited people to separate multiple disciplines with a comma, we'll need to parse those and track participant IDs. Several people used a slash instead of a comma, so we'll use a regex that looks for that, too.

```
# I think the data need to be a tibble for unnest to work

responses_df <- tibble(
  participantID = seq_along(qual_fields),
  response = strsplit(qual_fields, "\\\\s*[,/]\\\\s*", perl = TRUE)
  # \\\\s* matches zero or more whitespace (first backslash is an escape)
  # [,/] will match either a comma or a slash
  # With base R strsplit(), \\\s only works if you set perl = TRUE
) %>%
  unnest_longer(response) %>% # takes a column of type list, where the entries
  # are themselves vectors, and turns each element of those vectors
  # into its own row, duplicating the other fields appropriately.
  mutate(response = trimws(response)) %>%      # strip whitespace around each field
  filter(response != "")                      # drop empty entries (from e.g. A,,B)

responses_df

# A tibble: 192 x 2
  participantID response
        <int>   <chr>
1             1
2             2
3             3
4             4
5             5
6             6
7             7
8             8
9             9
10            10
11            11
12            12
13            13
14            14
15            15
16            16
17            17
18            18
19            19
20            20
21            21
22            22
23            23
24            24
25            25
26            26
27            27
28            28
29            29
30            30
31            31
32            32
33            33
34            34
35            35
36            36
37            37
38            38
39            39
40            40
41            41
42            42
43            43
44            44
45            45
46            46
47            47
48            48
49            49
50            50
51            51
52            52
53            53
54            54
55            55
56            56
57            57
58            58
59            59
60            60
61            61
62            62
63            63
64            64
65            65
66            66
67            67
68            68
69            69
70            70
71            71
72            72
73            73
74            74
75            75
76            76
77            77
78            78
79            79
80            80
81            81
82            82
83            83
84            84
85            85
86            86
87            87
88            88
89            89
90            90
91            91
92            92
93            93
94            94
95            95
96            96
97            97
98            98
99            99
100           100
101           101
102           102
103           103
104           104
105           105
106           106
107           107
108           108
109           109
110           110
111           111
112           112
113           113
114           114
115           115
116           116
117           117
118           118
119           119
120           120
121           121
122           122
123           123
124           124
125           125
126           126
127           127
128           128
129           129
130           130
131           131
132           132
133           133
134           134
135           135
136           136
137           137
138           138
139           139
140           140
141           141
142           142
143           143
144           144
145           145
146           146
147           147
148           148
149           149
150           150
151           151
152           152
153           153
154           154
155           155
156           156
157           157
158           158
159           159
160           160
161           161
162           162
163           163
164           164
165           165
166           166
167           167
168           168
169           169
170           170
171           171
172           172
173           173
174           174
175           175
176           176
177           177
178           178
179           179
180           180
181           181
182           182
183           183
184           184
185           185
186           186
187           187
188           188
189           189
190           190
191           191
192           192
```

```

1      1 Ai and Neuroscience
2      2 Plant Biology
3      2 Ecology
4      3 Digital Humanities
5      3 History
6      4 Computer Science
7      4 Neuroscience
8      5 Evolutionary Genomics
9      6 Medical Imaging
10     6 Vision Science
# i 182 more rows

```

Again, you can take my word for it that I visually compared this df to the raw survey data and it looks good. Now let's get to the meat of the script: for each discipline entered by a survey participant, get rows that contain the best possible fuzzy match (allowing multiple rows for ties).

This code takes a minute to run.

```

results <- vector("list", nrow(responses_df))

for (i in seq_len(nrow(responses_df))) {
  current_query <- responses_df$response[i]
  current_participantID <- responses_df$participantID[i]

  q_scores <- get_all_hits(current_query, tax)
  candidates <- get_candidates(q_scores)
  winnerdf <- get_winner_df(candidates, tax)

  # add participant info
  winnerdf$participantID <- current_participantID
  winnerdf$response <- current_query
  results[[i]] <- winnerdf
}

final_results <- dplyr::bind_rows(results) %>%
  # move participantID to be the first column
  dplyr::relocate(participantID, response)

head(final_results, n=50)

```

participantID	response	Level1
---------------	----------	--------

1	1	Ai and Neuroscience	Life Sciences
2	2	Plant Biology	Life Sciences
3	2	Ecology	Life Sciences
4	2	Ecology	Medicine and Health Sciences
5	2	Ecology	Medicine and Health Sciences
6	2	Ecology	Physical Sciences and Mathematics
7	3	Digital Humanities	Arts and Humanities
8	3	History	Arts and Humanities
9	4	Computer Science	Physical Sciences and Mathematics
10	4	Neuroscience	Medicine and Health Sciences
11	5	Evolutionary Genomics	Education
12	5	Evolutionary Genomics	Life Sciences
13	6	Medical Imaging	Medicine and Health Sciences
14	6	Vision Science	Engineering
15	7	Physics	Physical Sciences and Mathematics
16	8	Linguistics	Social and Behavioral Sciences
17	9	Information Science	Physical Sciences and Mathematics
18	9	Information Science	Social and Behavioral Sciences
19	10	Geography	Social and Behavioral Sciences
20	11	Physics	Physical Sciences and Mathematics
21	12	Ai	Law
22	13	Marine Conservation	Social and Behavioral Sciences
23	13	Marine Conservation	Social and Behavioral Sciences
24	14	Neuroscience	Medicine and Health Sciences
25	15	Physical Oceanography	Medicine and Health Sciences
26	16	Environmental Data Science	Physical Sciences and Mathematics
27	17	Computer Science	Physical Sciences and Mathematics
28	18	Environmental Sciences	Physical Sciences and Mathematics
29	19	Mathematics	Physical Sciences and Mathematics
30	20	Ecology	Life Sciences
31	20	Ecology	Medicine and Health Sciences
32	20	Ecology	Medicine and Health Sciences
33	20	Ecology	Physical Sciences and Mathematics
34	21	Biomedical Physics	Physical Sciences and Mathematics
35	22	Political Science	Social and Behavioral Sciences
36	23	Health Policy	Social and Behavioral Sciences
37	24	Cfd Engineering	Engineering
38	25	High Energy Physics	Physical Sciences and Mathematics
39	26	Oral History	Arts and Humanities
40	27	Neuroscience	Medicine and Health Sciences
41	28	Psychology	Social and Behavioral Sciences
42	29	Computer Science	Physical Sciences and Mathematics
43	30	Computer Science	Physical Sciences and Mathematics

44	31	Radiology	Medicine and Health Sciences
45	32	Urban Planning	Social and Behavioral Sciences
46	33	Ecology	Life Sciences
47	33	Ecology	Medicine and Health Sciences
48	33	Ecology	Medicine and Health Sciences
49	33	Ecology	Physical Sciences and Mathematics
50	34	Astrophysics	Arts and Humanities
			Level2
1		Neuroscience and Neurobiology	Neuroscience
2		Plant Sciences	Plant Biology
3		Animal Sciences	Zoology
4		Medical Specialties	Oncology
5		Medical Specialties	Urology
6		Earth Sciences	Geology
7		Digital Humanities	<NA>
8		History	<NA>
9		Computer Sciences	<NA>
10		Medical Sciences	Neurosciences
11		Education Economics	<NA>
12		Genetics and Genomics	<NA>
13		Medical Sciences	Medical Anatomy
14		Biomedical Engineering and Bioengineering	Vision Science
15		Physics	<NA>
16		Linguistics	<NA>
17		Computer Sciences	Information Security
18		Library and Information Science	Information Literacy
19		Geography	<NA>
20		Physics	<NA>
21		<NA>	<NA>
22		Communication	Mass Communication
23		Public Affairs, Public Policy and Public Administration	Transportation
24		Medical Sciences	Neurosciences
25		Rehabilitation and Therapy	Physical Therapy
26		Environmental Sciences	<NA>
27		Computer Sciences	<NA>
28		Environmental Sciences	<NA>
29		Mathematics	<NA>
30		Animal Sciences	Zoology
31		Medical Specialties	Oncology
32		Medical Specialties	Urology
33		Earth Sciences	Geology
34		Earth Sciences	Mineral Physics
35		Political Science	<NA>

36	Public Affairs, Public Policy and Public Administration	Health Policy
37	<NA>	<NA>
38	Earth Sciences	Mineral Physics
39	History	Oral History
40	Medical Sciences	Neurosciences
41	Psychology	<NA>
42	Computer Sciences	<NA>
43	Computer Sciences	<NA>
44	Medical Specialties	Radiology
45	Public Affairs, Public Policy and Public Administration	Urban Studies
46	Animal Sciences	Zoology
47	Medical Specialties	Oncology
48	Medical Specialties	Urology
49	Earth Sciences	Geology
50	Philosophy	Metaphysics

Okay, well I got results, but there's a pretty high rate of crappy matches. And then there's some that only a sophisticated algorithm would catch, and a couple that I'M not even sure how to classify. I think experimenting with better algorithms, or "real ML" classifiers, would probably take longer than just manually sifting through these. My code is ugly, and I hate that my procedure is not reproducible, but it's fast. So I'm just going to manually review these classifications in Microsoft Excel.

```
write_df_to_file(final_results, "curation_of_disciplines/qual_fields_guesses.tsv")
```

```
sessionInfo()
```

```
R version 4.4.2 (2024-10-31)
Platform: aarch64-apple-darwin20
Running under: macOS 26.1
```

```
Matrix products: default
BLAS:    /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRblas.0.dylib
LAPACK:  /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRlapack.dylib
```

```
locale:
[1] C.UTF-8/C.UTF-8/C.UTF-8/C/C.UTF-8/C.UTF-8
```

```
time zone: America/Los_Angeles
tzcode source: internal
```

```
attached base packages:
```

```

[1] tools      grid       stats      graphics   grDevices datasets  utils
[8] methods    base

other attached packages:
[1] treemapify_2.5.6     tidyverse_1.3.1      svglite_2.2.1
[4] stringr_1.5.1        scales_1.4.0        readr_2.1.5
[7] pwr_1.3-0            patchwork_1.3.2    ordinal_2023.12-4.1
[10] lme4_1.1-37          Matrix_1.7-1       languageserver_0.3.16
[13] here_1.0.1           gtools_3.9.5       ggforce_0.5.0
[16] FSA_0.10.0           fpc_2.2-13       forcats_1.0.0
[19] factoextra_1.0.7    ggplot2_3.5.2      emmeans_1.11.2
[22] dplyr_1.1.4          corrplot_0.95     ComplexHeatmap_2.22.0
[25] cluster_2.1.8.1     BiocManager_1.30.26

loaded via a namespace (and not attached):
[1] Rdpack_2.6.4          rlang_1.1.6        magrittr_2.0.3
[4] clue_0.3-66           GetoptLong_1.0.5   matrixStats_1.5.0
[7] compiler_4.4.2         flexmix_2.3-20    systemfonts_1.2.3
[10] png_0.1-8             callr_3.7.6       vctrs_0.6.5
[13] pkgconfig_2.0.3       shape_1.4.6.1     crayon_1.5.3
[16] fastmap_1.2.0         utf8_1.2.6        rmarkdown_2.29
[19] ggrepittext_0.10.2    tzdb_0.5.0       ps_1.9.1
[22] nloptr_2.2.1          purrr_1.1.0      xfun_0.53
[25] modeltools_0.2-24    jsonlite_2.0.0    tweenr_2.0.3
[28] parallel_4.4.2        prabclus_2.3-4   R6_2.6.1
[31] stringi_1.8.7         RColorBrewer_1.1-3 boot_1.3-31
[34] diptest_0.77-2        numDeriv_2016.8-1.1 estimability_1.5.1
[37] Rcpp_1.1.0              iterators_1.0.14  knitr_1.50
[40] IRanges_2.40.1         splines_4.4.2     nnet_7.3-19
[43] tidyselect_1.2.1       yaml_2.3.10      doParallel_1.0.17
[46] codetools_0.2-20      processx_3.8.6   lattice_0.22-6
[49] tibble_3.3.0           withr_3.0.2      evaluate_1.0.4
[52] polyclip_1.10-7       xml2_1.4.0       circlize_0.4.16
[55] mclust_6.1.1           kernlab_0.9-33   pillar_1.11.0
[58] renv_1.1.5              foreach_1.5.2    stats4_4.4.2
[61] reformulas_0.4.1       generics_0.1.4   rprojroot_2.1.1
[64] S4Vectors_0.44.0       hms_1.1.3        minqa_1.2.8
[67] xtable_1.8-4            class_7.3-22    glue_1.8.0
[70] robustbase_0.99-4-1    mvtnorm_1.3-3    rbibutils_2.3
[73] colorspace_2.1-1       nlme_3.1-166    cli_3.6.5
[76] textshaping_1.0.1       gtable_0.3.6     DEoptimR_1.1-4
[79] digest_0.6.37          BiocGenerics_0.52.0 ucminf_1.2.2
[82] ggrepel_0.9.6          rjson_0.2.23    farver_2.1.2

```

```
[85] htmltools_0.5.8.1    lifecycle_1.0.4      GlobalOptions_0.1.2  
[88] MASS_7.3-61
```