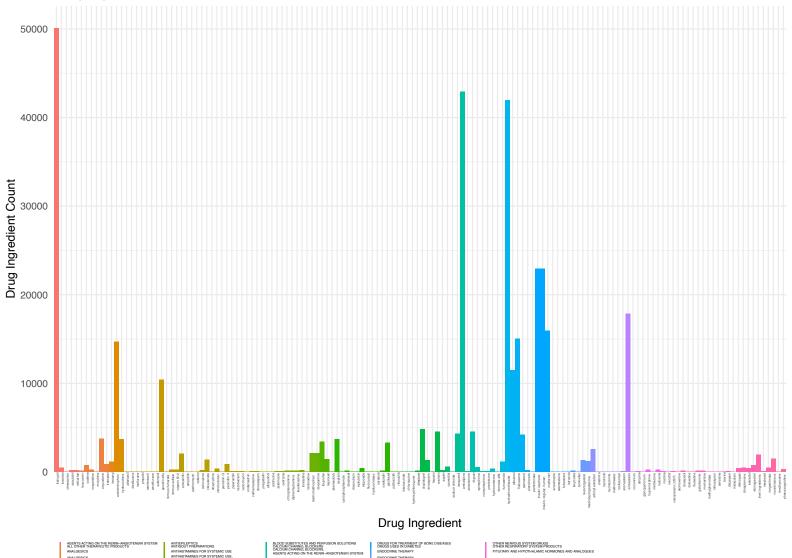
Drug Exposure Concept Distribution

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```
library(polyesterData)
library(ggplot2)
library(pg13)
This vignette is profiling the frequency of drugs in the Drug Exposures Table based on RxNorm Ingredient
and ATC Class. The Drug Exposures table is joined to the Concept Ancestor and Concept tables to derive
the RxNorm Ingredients as well as the ATC 2nd Concept Class that the drug records belong to.
staging_table <- pg13::write_staging_table(conn = conn, schema = "patelm9", drop_existing = FALSE,</pre>
    drop_on_exit = FALSE, data = DRUG_EXPOSURE)
class_output <- pg13::query(conn = conn, sql_statement = SqlRender::render("</pre>
              SELECT de.drug_concept_id, c2.*
              FROM patelm9.@staging_table de
              LEFT JOIN omop_vocabulary.concept c
              ON de.drug_concept_id = c.concept_id
              INNER JOIN omop_vocabulary.concept_ancestor ca
              ON ca.descendant concept id = c.concept id
              INNER JOIN omop_vocabulary.concept c2
              ON c2.concept id = ca.ancestor concept id
              WHERE c2.concept_class_id = 'ATC 2nd'
              ;",
    staging table = staging table))
ingredient_output <- pg13::query(conn = conn, sql_statement = SqlRender::render("</pre>
              SELECT DISTINCT de.drug_concept_id, c2.concept_name AS ingredient
              FROM patelm9.@staging_table de
              LEFT JOIN omop_vocabulary.concept c
              ON de.drug_concept_id = c.concept_id
              INNER JOIN omop_vocabulary.concept_ancestor ca
              ON ca.descendant_concept_id = c.concept_id
              INNER JOIN omop_vocabulary.concept c2
              ON c2.concept_id = ca.ancestor_concept_id
              WHERE c2.concept class id = 'Ingredient'
    staging_table = staging_table))
output <- class_output %>% dplyr::left_join(ingredient_output)
pg13::drop_all_staging_tables(conn = conn, schema = "patelm9")
```

Drug Ingredient Record Frequencies by Class



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