

# 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,
  drop_on_exit = FALSE, data = DRUG_EXPOSURE)
```

```
class_output <- pg13::query(conn = conn, sql_statement = SqlRender::render("
  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("
  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

