CTN-0094 Demographics Analysis

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Quarto

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Running Code

When you click the **Render** button a document will be generated that includes both content and the output of embedded code. You can embed code like this:

```
1 + 1
```

```
[1] 2
```

You can add options to executable code like this

```
[1] 4
```

The `echo: false` option disables the printing of code (only output is displayed).

Introduction

- Illicit opioid use is a major public health crisis associated with high overdose mortality (OpenAI, 2025).
- Medications for opioid use disorder (MOUD) improve retention and reduce mortality.
- The NIDA Clinical Trials Network (CTN) runs large, real-world clinical trials evaluating MOUD effectiveness.
- CTN project **CTN-0094** harmonizes data from projects **CTN-0027**, **CTN-0030**, and **CTN-0051** (public.ctn0094data, 2025).

- This report summarizes baseline demographics across the three randomized CTN studies.

Methods

Software versions

- **R version:** R version 4.5.2 (2025-10-31)
- **public.ctn0094data:** 1.0.6
- **tidyverse:** 2.0.0
- **gtsummary:** 2.4.0

Load & prepare data

"'{r} library(tidyverse) library(public.ctn0094data) library(gtsummary) library(labelled) library(glue) library(scales)

Load datasets

demographics <- public.ctn0094data::demographics randomization <- public.ctn0094data::randomization

Track raw size

n_demo_raw <- nrow(demographics)

Identify FIRST randomization only

first_rand <- randomization |> arrange(who, randomization) |> filter(randomization == 1) |> distinct(who, .keep_all = TRUE)

randomized_ids <- first_rand |> select(who)

Missing data before filtering

n_no_age <- demographics |> filter(is.na(age)) |> nrow() n_no_sex <- demographics |> filter(is.na(is_male)) |> nrow()

Create analysis dataset

analysis <- demographics |> semi_join(randomized_ids, by = "who") |> filter(!is.na(age), !is.na(is_male)) |> mutate(project = case_when(project == 27 ~ "CTN-0027", project == 30 ~ "CTN-0030", project == 51 ~ "CTN-0051", TRUE ~ as.character(project)), project = factor(project, levels = c("CTN-0027","CTN-0030","CTN-0051")), is_male_factor = factor(if_else(is_male == 1, "Male", "Not Male"))) |> labelled::set_variable_labels(who = "Participant ID", age = "Age at Intake", is_male_factor = "Assigned Male Sex at Birth")

n_analysis <- nrow(analysis) n_excluded <- n_demo_raw - n_analysis

Theme

ctn_theme <- theme_minimal(base_size = 14) + theme(plot.title = element_text(face = "bold"), axis.title = element_text(face = "bold"))

Sex proportion differences

sex_by_project <- analysis |> group_by(project) |> summarise(prop_male = mean(is_male_factor == "Male"))

max_diff_male <- max(sex_by_project$prop_male) $-$ $min(sex_by_project$prop_male)$ max_diff_male_fmt <- percent(max_diff_male, accuracy = 0.1)

clinically_meaningful <- 0.05 is_meaningful <- max_diff_male >= clinically_meaningful

Chi-square test (no rstatix)

chi_data <- table(analysis$project, analysis$is_male_factor) chi_test <- chisq.test(chi_data) p_chi <- chi_test$p.value p_chi_fmt <- scales::pvalue(p_chi)