Parameter gide

Parameter Descriptions

Group Characteristics

- **Mean (diseased, μ_1):**
  Expected mean value of the diagnostic marker in the *diseased population*.
- **SD (diseased, σ_1):**
  Standard deviation of the diagnostic marker in the *diseased population*.
- **Mean (healthy, μ_2):**
  Expected mean value of the diagnostic marker in the *healthy population*.
- **SD (healthy, σ_2):**
  Standard deviation of the diagnostic marker in the *healthy population*.

Study Design

- **Reference AUC (AUC_0):**
  The null hypothesis AUC value (e.g., 0.5 for random chance). Tests whether the observed AUC exceeds this threshold.
- **Ratio (k):**
  Ratio of healthy to diseased subjects in the study (e.g., *k=1* for balanced groups). If the ratio does not correspond to the prevalence of the disease, the results will be incorrect.
- **Disease prevalence:**
  Expected proportion of diseased subjects in the target population.

Statistical Settings

- **Type I error (α):**
  Significance level (default: 0.05). Probability of falsely rejecting the null hypothesis.
- **Desired power (1−β):**
  Target probability to detect a true effect (default: 0.8 or 80%).
- **Two-sided test:**
  If `TRUE`, tests for AUC ≠ AUC_0; if `FALSE`, tests for AUC > AUC_0 (one-sided).

Simulation Controls

- **Max n (neg group):**
  Maximum allowable sample size for the *healthy (negative) group*.
- **Min n (neg group):**
  Minimum allowable sample size for the *healthy (negative) group*. (the simulation starts with this number)
- **Number of replications:**
  Simulation runs (higher values improve precision but increase computation time).
- **Number of tests planned:**
  Total hypothesis tests planned (for multiplicity adjustment, e.g., Bonferroni).
- **Random seed:**
  Integer to fix simulation results (ensures reproducibility despite stochastic variability).