R- Package (*inctools*) and Shiny Apps for Incidence Estimation.

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Background

Incidence

- Determining disease incidence, the rate of occurrence of new cases in a population, presents a greater challenge than prevalence. For enduring conditions such as HIV, prevalence is not a good proxy for recent incidence because it depends in detail on historical incidence, demography, and survival.
- Reliable estimates of HIV incidence are critical for epidemiological monitoring, understanding transmission patterns, and in the design and evaluation of intervention programs.

Incidence Estimation

We look at two primary alternative techniques to 'directly observed' incidence estimates from cohort studies:

1. Inferring incidence from cross-sectional surveys using biomarkers to test for 'recent infection' [1]. Kassanjee et al proposed a simple estimator for incidence

$$\hat{I}_T = \frac{P_R - \beta_T P_+}{P_S(\Omega_T - \beta_T T)}$$

where P_R, P_+ and P_S denote proportion of recent infections, proportion of infected individuals and proportion of susceptible individuals respectively. Ω_T denotes the mean duration of recent infection within cutoff time T and β_T is the false-recent rate.

2. Inferring incidence from population renewal equations, given suitable age-stratified prevalence and mortality [2]. According to Mahiane et al, the incidence rate $\lambda(a,t)$ is given by

$$\lambda(a,t) = \frac{1}{1-P(a,t)}\left(\frac{\partial}{\partial t}P(a,t) + \frac{\partial}{\partial a}P(a,t)\right) + \Delta(a,t)P(a,t)$$

where $P(a,t)$ and $\Delta(a,t)$ represent the prevalence and excess mortality rate of infected individuals respectively.

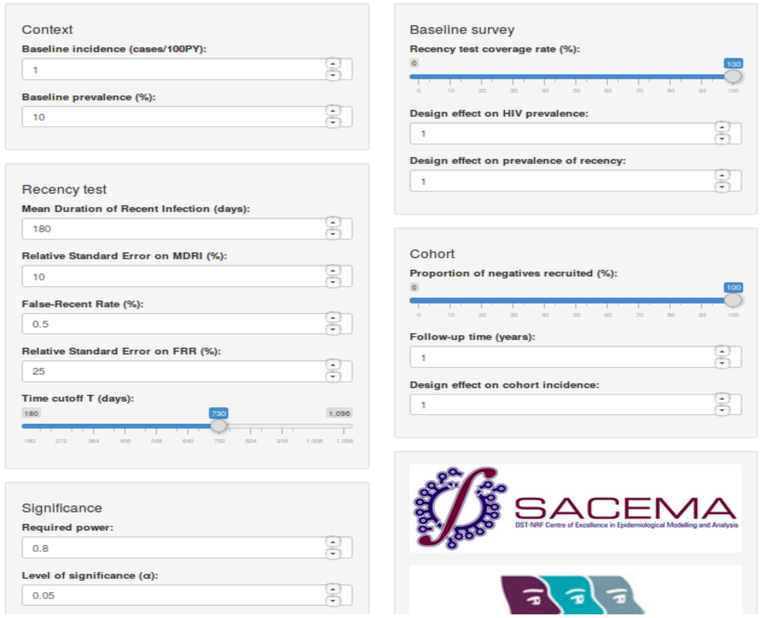
R- Package: *Inctools*

Inctools is a new R-package on CRAN that provides tools for estimating incidence based on Kassanjee et al, and maintained by SACEMA. Functionality can be categorized into three areas:

- **Support of survey design** using the two primary exposed functions *incprecision* and *incpower* which are essential for sample size and power calculations.
- **Analysis of survey data** consisting of subject level records indicating demographic factors and clinical indicators such as HIV and recency status. The primary inctool functions include *inccount*, *prevcount* and *incprop*.
- **Estimation of key performance characteristics of tests for recent infection** using the functions *frrcal* and *mdrical* to estimate false recent-rate and mean duration of recent infection respectively.

Apps for incidence estimation tools:

E.g. Shiny App for **Sample size and power calculations** built based on inctools. Determines the required sample size for power (baseline survey and cohort).



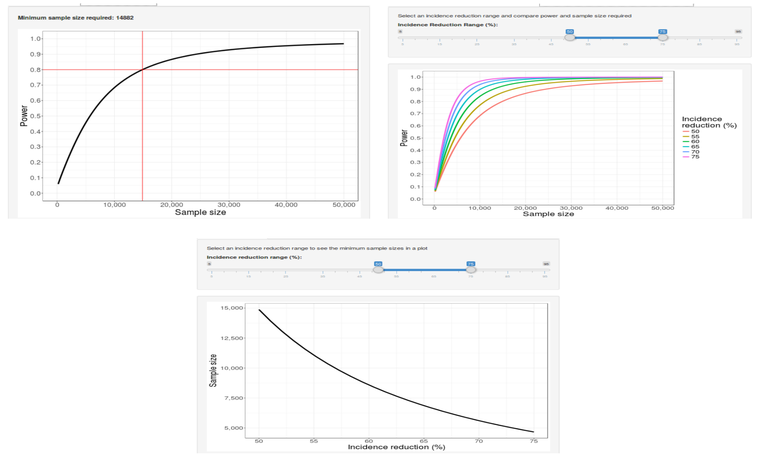


Figure 1: Output– Gives the minimum required sample size to achieve a specified power where respondents are recruited into the cohort to observe an expected decline in incidence. Also evaluates power vs sample size for different values of incidence reduction.

Research Directions

- To extend and recode existing shiny applications using the *inctools* package based on Kassanjee et al.
- Implement key components of Mahiane et al [2] via:
  - A major R-package release for HIV Incidence estimation based on likelihood of individual level data and population renewal equations.
  - Vignettes to demonstrates the use of functions.
  - Shiny Apps for some key components and functionality.

References

[1] Reshma Kassanjee, Thomas A McWalter, Till Bärnighausen, and Alex Welte. A new general biomarker-based incidence estimator. *Epidemiology (Cambridge, Mass.)*, 23(5):721, 2012.

[2] Guy Severin Mahiane, Rachid Ouifki, Hilmarie Brand, Wim Delva, and Alex Welte. A general hiv incidence inference scheme based on likelihood of individual level data and a population renewal equation. *PloS one*, 7(9):e44377, 2012.