Bench sheet · EnGeL-SAMPL-EFFORT

Measuring sampling effort and completeness: rarefaction, extrapolation and richness estimators (iNEXT, SpadeR) · version 1.1.0 (2026-11-20). Full protocol: EnGeL-SAMPL-EFFORT. Tick each step when done; write deviations in Notes.

Date	
Operator	
Plate ID / samples	
R and package versions	
Input data (file, date, number of sampling units)	

1. Set up

☐	No.	Step
☐	1	Open the project's R project and load the packages:
!		**CRITICAL** The source script loads BiodiversityR, but the functions `ChaoSpecies`, `Diversity`, `ChaoShared` and `SimilarityMult` used below come from SpadeR: load SpadeR.
☐	2	Optional, to learn the functions: run the steps below on the example data supplied with the packages (`data(spider)` in iNEXT, abundance data; `data(ChaoSpeciesData)` and `data(ChaoSharedData)` in SpadeR, incidence data).

2. Rarefaction and extrapolation (iNEXT)

☐	No.	Step
☐	3	Read your data into a named list of incidence matrices (one per site or treatment) and run iNEXT for q = 0, 1 and 2:
☐	4	Plot the curves: sample-size-based curves (`type = 1`), the sample completeness curve (`type = 2`) and coverage-based curves (`type = 3`), with one panel per site:
☐	5	Save the numerical results (`out$DataInfo`, which includes the sample coverage, and `out$AsyEst`, the asymptotic estimates) as tables in `results/`.

3. Richness estimators and shared species (SpadeR)

☐	No.	Step
☐	6	Asymptotic richness estimators and diversity profiles for one site, saving the full output as text:
☐	7	Species shared between two sites (the matrix holds the sampling units of both sites, side by side; `units` gives the number of units of each site):

Notes / deviations
