Using *UIDcollision\_Uniform.r*

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1. Description

The file UIDcollision\_Uniform.r contains the primary function UIDerror, as well as supporting function estP2same and ecol. UIDerror simulates the results of a next-generation sequencing run performed with barcoding and processed into consensus sequences by family. estP2same estimates the probability that at least 2 sample molecules have the same UID. ecol calculates the expected number of samples that will have non-unique UIDs.

1. Usage

UIDerror(nsamp, mutFreq, nUID, seed=1, conFrac=0.95, PCRcyc=25, PCRsuc=0.5)

1. Arguments

|  |  |
| --- | --- |
| nsamp | Number of sample molecules, must be a positive integer |
| mutFreq | Actual underlying frequency of mutation in data, note that if the mutFreq x nsamp does not results in an integer number of mutants, then the number of mutant molecules will be rounded according to rules of round() |
| nUID | Number of possible UIDs, can be any positive integer |
| seed | Random generator seed, default 1 |
| conFrac | Fraction of molecules within each UID family that must agree in order for a consensus sequence to be called. Default 0.95 (95%) |
| PCRcyc | Number of PCR cycles, default 25 |
| PCRsuc | Probability of success for each PCR cycle, default 0.5 |

1. Details

UIDerror simulates binding of UID molecules to sample molecules as sampling with replacement. Only 1 locus of mutation is simulated. Please see in-code notes for further details.

1. Value

UIDerror returns a numerical vector with the following components in order:

|  |  |
| --- | --- |
| emutFreq1 | Mutation frequency estimated from the data assuming that families without a consensus call are removed from the denominator. |
| err1 | Error of the emutFreq1 compared to mutFreq |
| emutFreq2 | Mutation frequency estimated from the data assuming that all families, including those without a consensus call, are included in the denominator. |
| err2 | Error of emutFreq2 compared to mutFreq |
| ncfreq | Fraction of UID families that did not produce a consensus sequence |
| uUIDs | Number of unique UIDs used |
| nreads | Number of reads expected for sequencing based on success of PCR amplification |