consensus\_tax\_bestRez:

Overview:

This function merges multiple taxonomy arrays into a single taxonomy array incorporating information from all input taxonomy arrays. It does this by following a series of rules, outlined below.

Inputs:

1. *…* = an arbitrary number of taxonomy tables (dataframes). They should be identical dimensions with OTUs/ASVs as rows and taxonomic ranks as columns. The order of ASVs should be the same across all tables
2. *tablenames* = a character vector including the names of each taxonomy dataframe supplied in *…*
3. *ranknamez* = the names of each rank (column) of the input dataframes. The output consensus taxonomy will have these as column names.
4. *tiebreakz* = a 1x1 character vector or a list of 1x2 character vectors. If a 1x1 character vector, it must be either “none” or “LCAlike”. If a list of 1x2 character vectors, *tiebreakz*[[X]][1] should match one the entries in tablenames, and *tiebreakz*[[X]][2] should be NA or should match any taxonomic name in *tiebreakz*[[X]][1]. These values indicate the taxonomy table to prioritize for all remaining tiebreakers (if *tiebreakz*[[X]][2] is NA) or for a particular taxonomic group (if *tiebreakz*[[X]][2] is a taxonomic name). The list should be in order of the priority in which you want the rules applied. By supplying a series of taxonomy table names alongside taxonomic names, you can thus prioritize a series of names before prioritizing a single taxonomy table for the remaining names.

Outputs:

A list including the following:

* [[1]] = dataframe containing the consensus taxonomy table
* [[2]] = a list with each of the original taxonomy dataframes
* [[3]] = a vector containing the row indices of the taxonomy tables that require further tie-breaking. If there were none given the input rules, this is an empty array.

Taxonomy merging rules:

1. For each ASV, the most resolved taxonomy (lowest number of NA ranks) is prescribed to the output.
2. If multiple input taxonomy arrays have identical resolution and taxonomic name assignments, the common taxonomic path is simply prescribed to the output.
3. If ASVs (rows) have equivalent resolution with non-equivalent names across multiple taxonomy arrays, a series of tie-breakers are used to determine the final taxonomic assignment for that ASV. Tiebreakers are user-specified and can include the following:
   1. “none” – no tie-breaking is done, and the output taxonomy array will be entirely unassigned at points where taxonomy tables have equal resolution but non-equal names at any rank
   2. “LCAlike” – a search is conducted to determine the rank (if any) at which the taxonomy arrays with equivalent resolution agree. If one is found, the ranks with names in agreement are used in the final output array, and all further ranks are left unassigned.
      1. “LCAlike” can be included at any position in the list in 3c below and will be prioritized relative to other entries in the list according to it’s position in the list
   3. A list containing specific instructions for prioritizing particular taxonomy arrays (and taxonomic groups within them) to break ties. See input arguments for details.