NANSH Working Group
Methods Generation
4.01.2014

Generalized Methods:

Basic Premise

3 Species Categories: Criteria:
-   Rare   Ranked in state (S1 and S2)
-   Invasive   Invasive in natural communities
-   Native   Native but neither invasive nor rare

Generation of Species Lists

Four separate lists of ten species: S1, S2, Invasive, and Native

1. Locate an appropriate source list:

    The most desirable source list is one containing the most recent and comprehensive
    coverage of the category (Rare, Invasive, or Native).

    Possible Sources Include:

    o   DNR/DFW, EPPC, or other unbiased organizational lists
    o   State Floras
    o   Peer Reviewed Studies

2. Convert the list into a sortable spreadsheet and order species alphabetically by Latin name.

    If the source list is not digitized or is impractically formatted it may be necessary to use a
    different approach to species selection (See R. McCauley's methods at document bottom).

3. Noting the total number of species in the spreadsheet representing the category, generate a
    random integer set of twenty numbers between one and the total number of species.

    Use www.random.org to generate the number set.

4. Apply the generated number set to the category list to determine ten randomly selected
    species.

    Hold the remaining numbers in reserve in case one or several of the selected species are
    present on another list (for example plants present on the native list may also be rare).

Overarching Organization (projected):

Actively collaborating researchers in seven states used uniform methods to randomly select species
from each state in three different categories: Rare (20 species), Invasive (10 species), and Native (10
species). Herbaria in each state were then categorized into different size classes and investigated to
determine specimen presence/absence for species on the randomly generated lists. The results of these

investigations were charted and compared between size classes in order to determine what each size class contributes to scientific knowledge. Once determined, these contributions were visualized to make them more readily understandable for interested parties.

Current Status of Project:

Researchers in each state have coordinated to make preliminary decisions. Several species lists have been generated.

Next Steps:

- Generate all lists for each state and ensure that common methods have been followed
- Establish definite size classes for herbaria
- Begin collecting data

Background Material:

Ross McCauley's Methods (slightly adapted):

From a printed checklist containing the 3430 unique taxa reported for the state of Colorado:

1) Use random.org to generate a random integer list including the page numbers that contain the printed checklist of species.
2) Select the first complete entry on each randomly selected page. Add the entry to the list of native species if it is not on the state S1 or S2 list and is not listed as invasive by the Colorado Weed Management Association.
3) If it is on one of these lists continue down to the next complete entry on the page.

Travis Marisco's Methodology:

1) Obtain your state's Natural Heritage "tracked species" list.
2) organize list by S ranking, followed by Species Name alphabetically (see attached Excel spreadsheet).
3) Determine the number of taxa (in my case 208) that have the S1 designation.
4) Go to Random.org, and use the random integer set generator (see screen shot document attached). You need one set with 10 unique random integers. I selected integers between (and including) 2 and 209, since line 1 of my spreadsheet was the headings. Also, use the default settings, which provides the numbers in sequential order.
5) Random.org will give 10 unique randomly generated values (see page 2 of attached screen shot document).
6) Highlight the lines in spreadsheet that represent the randomly selected taxa.
7) Make an alphabetical list of the 10 taxa (also attached).

This exercise makes me think about something important (here is where I'm throwing the wrench into the works). S1 taxa are often found from a single location or two. They are rare, and at the state-level exceedingly so. I wonder if we would not be better served by also (or instead) doing the same analysis

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on S2 taxa, which are known from a handful or dozen or two dozen locations within a state. The reason this may be important is that for the ultra-rare taxa, we are biasing our sample such that no herbaria within the state can have unique collections. That is if a plant species is known from a single location within a state, the options are for that taxon to be represented in only one collection in the state or more than one collection in the state. In either case, the vouchers will be from the single location, and if represented in more than one collection, these will represent redundancies without any unique information across collections. If we are arguing that small collections make important back-ups for larger collections, then this will be ok, but if we are interested in what unique vouchers small collections may have, then S2 collections may provide enough site locations in the states that show which collections have redundancies, and which provide unique information. It seems to me that S1 and S2 may tell different stories, which makes me think we should include both in our analysis, but that doubles our numbers from 10 to 20 just for "rare" taxa.

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