Data Encoding:

1. An excel spread sheet was set up with the following Column headings:

Site code (PIL code), CAS code, Date, Sample type (rotenone, roving survey, market), Country, Province, Municipality, Barangay, Site, Family, Genus, space (actual space), species, spname (concatenate Genus, space, species), n, notes.

1. Species were then entered into the spreadsheet with one species per row.
2. All unknown species without descriptive notes were designated as sp.1, if specimens had specific designations such as sp. 2 these were used in the spread sheet. If an unknown species had a description this was added to the name and was treated as a separate species (i.e. sp. 2 orange spots on head). If individuals were called sp.2 in multiple sites they were considered the same species.
3. After all data was encoded a pivot table with all species was created to allow for spell checking. Any misspelled names were corrected in the original spreadsheet.

Pivot Tables:

Individual-based

1. For individual-based analyses a pivot table with province (for all three locations) or each municipality (for separate locations) in the Column Labels while spname was placed in the Row Labels. Within in the Values field abundances (n) were entered. This need to be changed from the default which is counts.
2. This table was then copied to a separate excel file as **values only**.
3. Column A (species names) and Row 1 were then deleted. Thus leaving just abundances per site.
4. Two rows were then inserted at the top (1 & 2).
5. In cell A1 the name of the file was entered, in cell B1 *\*Indivudals\** was entered exactly like that with asterisks and in italics. In cell A2 fill in the total number of species and in B2 fill in the number of samples (this should be 1 for individual-based analyses). Thus in the example bellow the file name is Mabini and there were a total of 204 species recorded at this location.

|  |  |
| --- | --- |
| Mabini | *\*Individuals\** |
| 204 | 1 |

1. This file was then saved as a Text file (Tab delimited) such as Mabini\_individuals\_data.txt

Sample-based

1. For sample-based analyses create a pivot table with the CAS\_code or the PIL\_code in the Columns Label and spname in the Row Labels. Within in the Values field abundances (n) were entered. This need to be changed from the default which is counts.
2. This table was then copied to a separate excel file as **values only**.
3. Column A (species names) and Row 1 (sites) were then deleted. Thus leaving just abundances per site.
4. Two rows were then inserted at the top (1 & 2).
5. In cell A1 the name of the file was entered, in cell B1 *\*SampleSet\** was entered exactly like that with asterisks and in italics. In cell A2 fill in the total number of species and in B2 fill in the number of samples (number of sites). Thus in the example bellow the file name is Mabini and there were a total of 204 species recorded in 16 sites.

|  |  |
| --- | --- |
| Mabini | *\*Individuals\** |
| 204 | 16 |

1. This file was then saved as a Text file (Tab delimited) such as Mabini\_samples\_data.txt

EstimateS

Individual-based

1. Under file click Load Data Input File.
2. Select Individual-based abundance data and One individual-based abundance sample
3. Select the individual-based data text file and clik ok
4. For the format type choose Format 1 (sample in columns and species in rows). You do not need to skip rows or columns since you already erased the species names and site names. So keep 0 for both. Click ok then ok again.
5. Under diversity settings.
   1. Randomization and Rarefaction
      1. 100 Runs
      2. Extrapolate rarefaction curves: Extrapolate to a total of x number of individuals (usually 2-3x the sampling effort
      3. Estimation points (default)
   2. Estimators & Indices
      1. Diversity indices (your choice)
      2. Caho1 and Chao2: Use bias-corrected formula
      3. Coverage-based estimators: 10 (default)
      4. Randomization protocol for estimators and indices: Randomization **without** replacement.
   3. Other Options
      1. Export results for each run to text file
      2. Random number generator for randomization: default
      3. Settings usage: default
6. Under the Diversity Tab select: Compute Diversity Stats.
7. Name files appropriately as test files.
8. Export results as a text file and Open it in Excel.

Sample-based

1. Under file click Load Data Input File.
2. Select Sample-based incidence or abundance data and One individual-based abundance sample
3. Select the individual-based data text file and clik ok
4. For the format type choose Format 1 (sample in columns and species in rows). You do not need to skip rows or columns since you already erased the species names and site names. So keep 0 for both. Click ok then ok again.
5. Under diversity settings.
   1. Randomization and Rarefaction
      1. 100 Runs
      2. Extrapolate rarefaction curves: Extrapolate to a total of x number of samples (usually 2-3x the sampling effort
      3. Estimation points (default)
   2. Estimators & Indices
      1. Diversity indices (your choice)
      2. Caho1 and Chao2: Use bias-corrected formula
      3. Coverage-based estimators: 10 (default)
      4. Randomization protocol for estimators and indices: Randomization **without** replacement.
   3. Other Options
      1. Export results for each run to text file
      2. Random number generator for randomization: default
      3. Settings usage: default
6. Under the Diversity Tab select: Compute Diversity Stats.
7. Name files appropriately as test files.
8. Export results as a text file and Open it in Excel.