Biological Systematics

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Biological systematics encompasses three distinct activities: taxonomy, classification (which may or may not be a reasonable reflection of phylogeny) and nomenclature (Fig. 1). Although systematists rigorously and distinctly practice these three components, they are often amalgamated under the term "taxonomy." While the breadth of "taxonomy" is clearly understood among most practitioners, it can obscure the methodology and practices of modern systematics to others. On the other hand, not all systematists work across the full breadth of systematics. For example, they can be engaged in the study of molecular phylogenies without applying the results of their studies to the nomenclature of the group. Similarly, the resolution of nomenclatural issues can be carried out without a phylogenetic study of the species or the generation of a new classification, but usually not without extensive library resources.
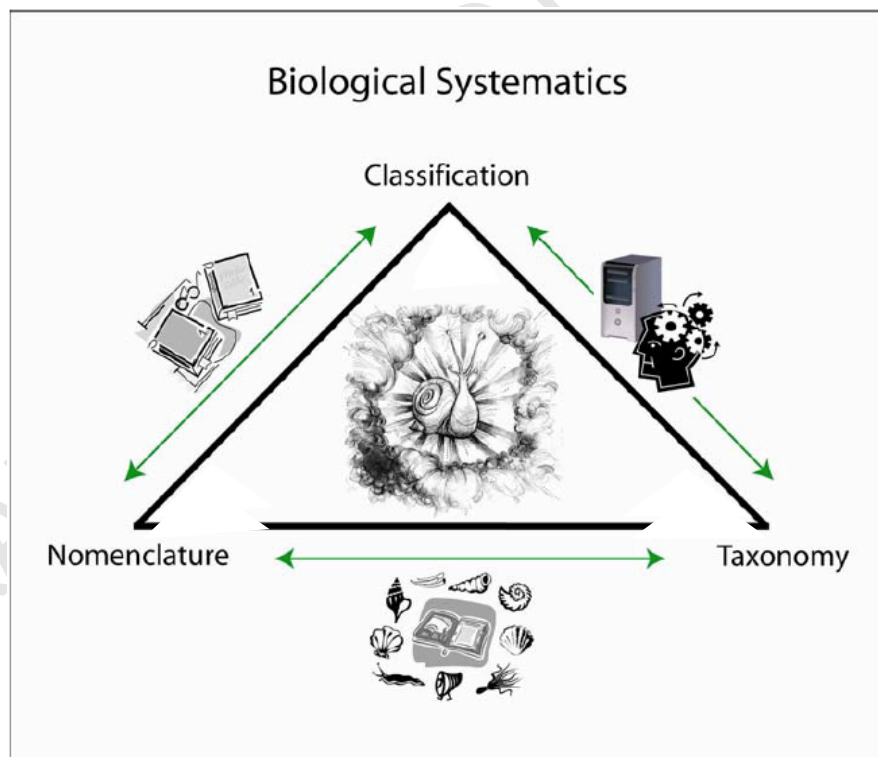

Figure 1. Biological Systematics - a summary showing the relationship between taxonomy, classification, and nomenclature.

The three components of systematics can be described as follows:

Taxonomy

Taxonomy is a process. In this process, a classification (see below) can be referred to but its focus is on the study and description of the objects being classified. It includes the examination of individual organisms and the description, analysis and quantification of taxa by way of the characters they possess. Characters can be taken from morphology (gross morphology to cellular ultrastructure) and at different life history stages (cell division cycles to adults with indeterminate growth). Molecular characters underlie this morphology and scale from base pair to genome. Because of this complexity, character analysis of semaphoronts is critical for the accurate scoring of character states whether it is the homology of morphological structures or the alignment of gene fragments.

The practice of taxonomy requires an extraordinary understanding of a taxon and the ability to rigorously extract and evaluate the necessary character information. To do this systematists may require access to microscopy, imaging, histological and molecular facilities, or some subset of them. For extinct taxa, access to isotopic, thin-section and 3D reconstruction technologies may also be necessary. Unfortunately, and often not from necessity, the taxonomy of many groups is based on little more than a handful of traditional characters.

Taxonomy interacts with both nomenclature and classification (Fig. 1). The taxonomic study describes the characters, and their states, of a taxon or taxa. Through interaction with nomenclature a name can be attached to specimens (grouped as taxa) with unique sets of character states.

The interaction of taxonomy with classification requires an additional step – an analysis of the character states, preferably an algorithmic one. There are three major kinds of analysis: evolutionary systematics, phenetic and cladistic. In evolutionary systematics the analysis is largely dependent on the systematist's intimate knowledge of the group to produce an evolutionary scenario. Similarly, cladistic techniques can be applied without using computers but modern phenetic and cladistic analysis use numerical algorithms and are more computational. Phenetics uses clustering techniques based on overall similarity of the data (*e.g.*, UPGMA and neighbor joining) while cladistic and other phylogenetic reconstruction methods use special similarity (*e.g.*, parsimony) or require an evolutionary model and parameters (e.g., maximum likelihood or Bayesian analysis). Regardless of the method of analysis of the taxonomic data, the process produces a classification.

Classification

Like the term taxonomy, classification is commonly used outside the biological systematic community as almost any animate or inanimate object, place, concept or event can be classified according to some criteria or scheme. It is the act of assigning individuals to a class or classes based on some common relations or affinities. Biological classifications, produced by phenetic

and cladistic computations, are trees of hieratical relationships. In evolutionary systematics classifications may be represented by assignment of 'taxonomic' rank (species, genera, families, superfamilies, orders etc.) or by evolutionary scenarios. Classifications may or may not reflect putative evolutionary relationships (phylogenies) and when characters are heavily weighted or the groupings are based on algorithms that feature overall similarity, there is a far greater probably that the classifications will not reflect evolutionary history.

Classification interacts with both taxonomy and nomenclature (Fig. 1). With classifications that provide trees, the tips and nodes can be formally named following nomenclatural practices. Classifications provide predictions that can be tested by examining additional taxa or characters. Previously unstudied taxa can be predicted to have certain character states while the discovery of homoplasy may necessitate reexamination of the study taxa to document putative convergences.

Classification also provides an important interface to other biological enterprises. The benefits of using classifications that reflect the evolutionary history (phylogeny) of a taxon in research, conservation and economic ventures is being increasingly recognized throughout the biological sciences. Unfortunately, the replacement of existing classifications by new classifications that reflect phylogeny often require name changes at various taxon levels that can cause short term angst, but the classification is not the problem. Name changes are nomenclatural (see below). The tips of the trees in classifications may be an individual, a composite taxon (population, species, genus, etc.), or a grade. They do not necessarily have or need formal names and a tree of microcentrifuge tube numbers may be all that is necessary to test competing hypotheses.

Nomenclature
Nomenclature in biological systematics is the assigning of formal names to all or some of the tips and nodes of a hierarchical classification. The International Code of Zoological Nomenclature (ICZN) provides rules on how taxa will be named and how conflicts in nomenclature (not classification) will be resolved. Recently, alternative systems of nomenclature have been proposed [BioCode and Phylocode (http://www.ohiou.edu/phylocode/)], but neither have yet gained general acceptance.

Nomenclature interacts with classification by providing names (and typically ranks[1]) for the different groupings present in the classification and with taxonomy by providing unique names to distinct taxa with certain combinations of character states as discussed above. This latter interaction is well illustrated by the common association of character states and nomenclature in classic dichotomous keys.

Nomenclature provides a relatively stable name governed by a set of rules (unlike the adoption of so called "common names") which allows non-specialists (e.g., conservation and economic communities) and specialists to communicate. Stable or trackable nomenclature is critical to both communities. For example, listing of species for environmental protection requires a 'scientific name' and the units used to estimate biodiversity are almost always formal scientific names

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[1] Under ICZN rules ranks do not need to be assigned for taxa above the family-group. Under Phylocode, ranks are not assigned except at the species level.

parsed by rank (*e.g.*, species, generic, familial diversity). Names of invasive species must be globally understood to be effective in restricting movement. Likewise for the recognition of parasite vectors and patents for natural compounds and the regulation of commercial and sport fisheries.

Summary
Today the practice of systematics is very different than it was for the previous two centuries. Today's classifications are clearly hypotheses, subject to recurrent testing on a scale never imagined or experienced by the monographers of the 19th and 20th centuries. In the past, type material and allocated specimens might be examined once every 50 to 100 years thereby testing the previous systematic monograph or classification of the taxon. Classifications are now based on phylogeny and sometimes tested yearly. The rate of addition of new character sets, especially molecular ones, as well as new taxa, continues to increase every year. Today's classifications are also valued for their predictive value with disciplines as disparate as ecology, physiology, biogeography, medicine or conservation biology benefiting when evolutionary relationships are reflected in the classification.

In addition, the research breadth of many of today's systematists has broaden and deepened. Not only is the extraordinary knowledge of a specific taxon still required, additional knowledge of anatomy, developmental biology, molecular biology and paleontology, *etc.* (all at multiple scales) is vital as well as a working understanding of the methodological literature of character analysis and phylogenetic hypothesis testing. Today's systematists are (or should be) capable of solving primer problems, understanding the implications of various gap coding schemes and appreciating the *in situ* staining patterns of HOX genes in addition to understanding anatomy and histology, providing identifications, author and dates and associated geographical distributions for a taxon.

To refer to this complex systematics research program as 'taxonomy' masks the demanding and rigorous scientific enterprise that modern systematics has become. The recognition of the three distinct components making up systematics provides a framework in which to assess the distinct components of systematics and provides user communities with a better understanding of where different products come from and how they are related to one another. The restriction of the terms taxonomy and classification to specific components rather than as synonyms of biological systematics further aids in understanding the processes of organizational systematics at broader and less parochial levels.