USCC RCN 2018 Abstract: NamesforLife DOI Services August 21, 2018

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A common problem in the life sciences is understanding the correct application of a name to an organism or higher taxon, especially in microbiology. Names provide a primary means of accessing the scientific, technical and medical (STM) literature, databases and other resources ranging from analytical platforms to culture collections. Names also serve as a concise way to summarize all that is known about a particular strain, a species or a higher taxon at a specific point in time, including revisions and emendations of prior taxonomies and names. Historically, taxonomists were affiliated with biological collections or other centers of excellence, but over the last 25 years, sequenced based methodologies significantly changed the way the science is practiced. Today, taxonomic revisions occur on a near daily basis and have outstripped the ability of end users, information and service providers and device manufacturers to keep pace. This has prompted calls from the end user communities to provide support for curation of taxonomic databases to ensure reproducibility to ensure reproducibility and replicability of results. But those calls fail to recognize the much larger need that extends across the entire field, from publishers to biological repositories and culture collections. Taxonomy has evolved a highly dynamic field and changes in our understanding must flow back into all of the resources from which our knowledge is derived. This is particularly challenging when much of that knowledge is captured in static form.

NamesforLife is a unique information architecture and a proprietary system and method that was developed to resolve ambiguity in nomenclature that arises as a result of taxonomic revisions. This information architecture provides way to continuously monitor and track changes in a taxonomy and nomenclature to ensure that all of the underlying data are properly annotated and are persistently accessible, whether the current name or an earlier synonym is used in queries. NamesforLife services provide a means of continuously and effortlessly refreshing the published literature, databases and other resources via Digital Object Identifiers (DOIs) as part of a middle layer that correctly links together all of the key information. These services not only help to prevent a loss of knowledge, they also provide a way of reducing duplicated curatorial costs while improving overall information quality.

In this presentation, I will discuss the NamesforLife Information Architecture, web services that are built on top of this architecture that were developed for the publishing industry, curated data resources that are now created automatically through our information harvesting efforts, and derivative web services of relevance to culture collections. Those include a strain resolution service and web-analytical that allow monitoring of research artifacts (e.g., strains, sequences, other concrete and abstract research products), by individual and by institution, in real time. These latter services provide a novel and direct means of assessing the impact of research products by individuals and research institutions that are used by the community but rarely

cited. NamesforLife provides a way to correct this deficiency and objectively assess the impact of curators and resource providers.