Automating the Assignment of SF IDs and EO IDs when Preparing a Dataset for Bulk Import

Prior to bulk importing a dataset into Biotics, a new or existing source feature ID and element occurrence ID must be assigned to all records based on species separation distance. When done manually, this process is time-consuming, subjective, and susceptible to human error. In Pennsylvania, we have developed a Python script tool that automates this process by using a series of looped selections and ArcPy cursors to assign an existing EO ID/SF ID or new EO/SF grouping string to all records based on species separation distance. In this webinar, we will explain how the script tool works, demonstrate its use, discuss future improvements, and provide instructions on how to obtain the most current version of the script tool.