**Taxon sources** can represent "complete" taxonomic hierarchies (e.g. ITIS) or specialize (e.g. Howard & Moore). Import re-uses **taxon ids** between sources, but otherwise each source is completely represented in **taxon details**. It would be possible to browse ITIS or browse Howard & Moore, true to their taxonomies.

**How this is supposed to work.** When a new or updated taxon source is imported (e.g. Howard & Moore, or the upcoming Mammals of the World revision), they're assigned a new **source id** and the citation data about that source is added to **taxon sources**. The taxonomy is imported with that **source id** into **taxon details**, connecting to existing **taxon nodes** and adding when necessary.

**Common names** can be linked back to their source, and can be tagged assigned a **sig** that determines which site the common name "belongs" to (e.g. ADW common names vs. BioKIDS "preferred" names).

**How this is supposed to work.** Each **walk id** represents a particular taxonomy, and lets us blend taxon details from multiple sources without pulling our hair out. The details of a particular source can either **replace** the sources in the walk or **augment** them with new data. EMBL may **augment** ITIS, while Howard & Moore would **replace** any other avian data.