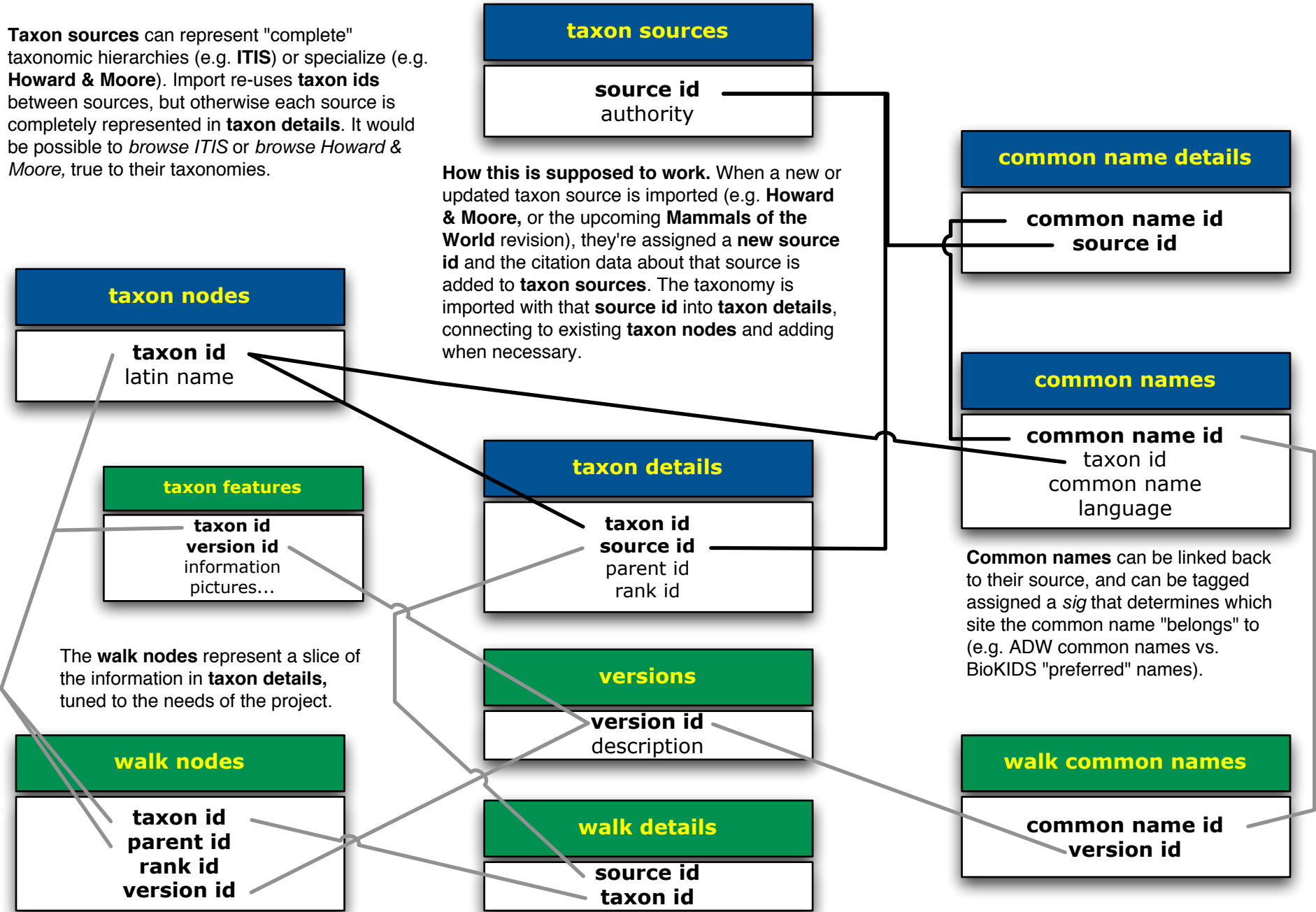**Taxon sources** can represent "complete" taxonomic hierarchies (e.g. **ITIS**) or specialize (e.g. **Howard & Moore**). Import re-uses **taxon ids** between sources, but otherwise each source is completely represented in **taxon details**. It would be possible to *browse ITIS* or *browse Howard & Moore,*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

taxon sources

source id
authority

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 name details

common name id
source id

taxon nodes

taxon id
latin name

common names

common name id
taxon id
common name
language

taxon features

taxon id
version id
information
pictures…

taxon details

taxon id
source id
parent id
rank id

The **walk nodes** represent a slice of the information in **taxon details,** tuned to the needs of the project.

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).

versions

version id
description

walk nodes

taxon id
parent id
rank id
version id

walk common names

common name id
version id

walk details

source id
taxon id

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.