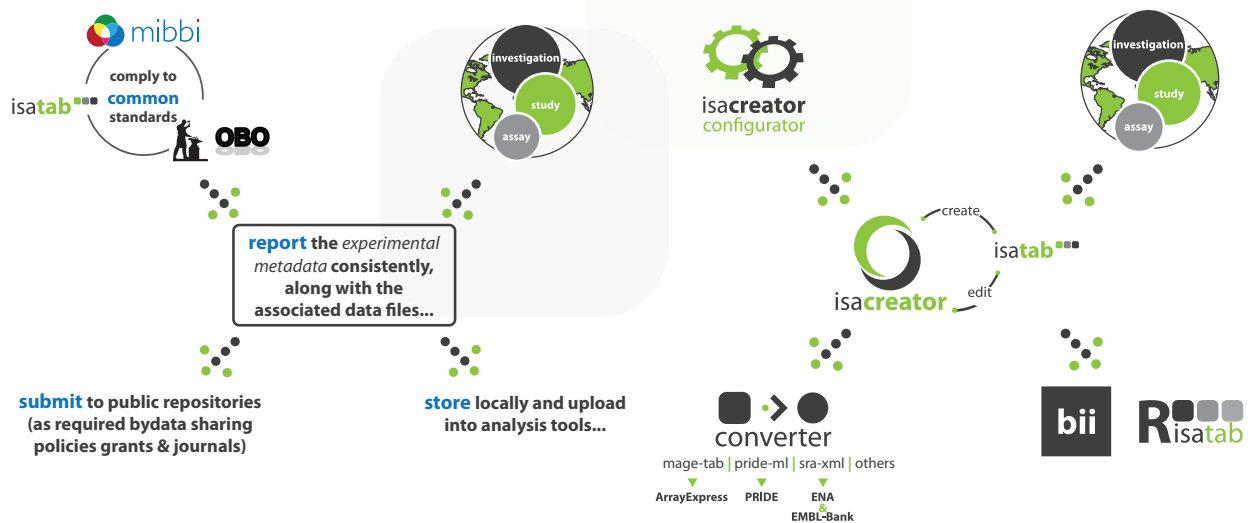


The **ISA Infrastructure** is the first freely available resource that empowers communities to aggregate their own sets of multi-assay bio-investigations, comply with relevant reporting standards, store metadata locally and/or submit to international repositories such as **ArrayExpress** (transcriptomics), **PRIDE** (proteomics) and the **European Nucleotide Archive** (DNA studies).



Nowadays, researchers increasingly perform multi-assay studies where the same sample is run through two or more analytical technologies (omics or conventional) in combination. There is a pressing need to make provisions for reporting and sharing these complex bio-investigations that, crucially, must allow for robust and regularized management of metadata (such as descriptions of the experimental design, samples and their preparation, analytical protocols and instrumentation, sample / data file relations and related publications).

**Furthermore, the trend is now for funders and journals to require both that researchers make more of their data public, for example submitting it to public repositories, and that they begin to utilise community-defined minimum information checklists, ontologies and formats to produce richly annotated bio- investigations .**

Currently, more than thirty community checklists are registered with the Minimum Information about a Biological or Biomedical Investigation initiative (MIBBI) . More than eighty ontologies sit under the Open Biomedical Ontologies Foundry umbrella (OBO) . A growing number of communities work collaboratively on a common tabular framework for presenting the Investigation, Study and Assay metadata (ISA-Tab)<sup>4</sup>. The ISA Infrastructure enables, and thereby promotes the uptake of community-defined standards through the provision of a set of freely available tools and a database, facilitating and assisting in the reporting process.



