Curate, store, analyse, share and publish your bioscience experiment The open source ISA tools and its international community of users and collaborators

The open source ISA metadata tracking tools facilitates standards compliant collection, curation, local management and reuse of datasets in an increasingly diverse set of life-science domains. Built around the 'Investigation' (the project context), 'Study' (a unit of research) and 'Assay' (analytical measurement) metadata categories, the tools are designed to manage studies employing one or a combination of technologies.

Here we show the different components of the ISA software suite and the external tools we plug in to, and how they can help you to: curate, store, analyse, share and publish your research.



ISA software suite Rocca-Serra et al, 2010 Bioinformatics

Towards interoperable bioscience data Sansone et al, 2012, Nature Genetics

The Harvard Stem Cell Discovery Engine Ho Sui et al, 2012, Nucleic Acids Research

Taxonomy-based Glyph Design Maguire et al, 2012, IEEE TVCG

OntoMaton Maguire et al, 2013, Bioinformatics

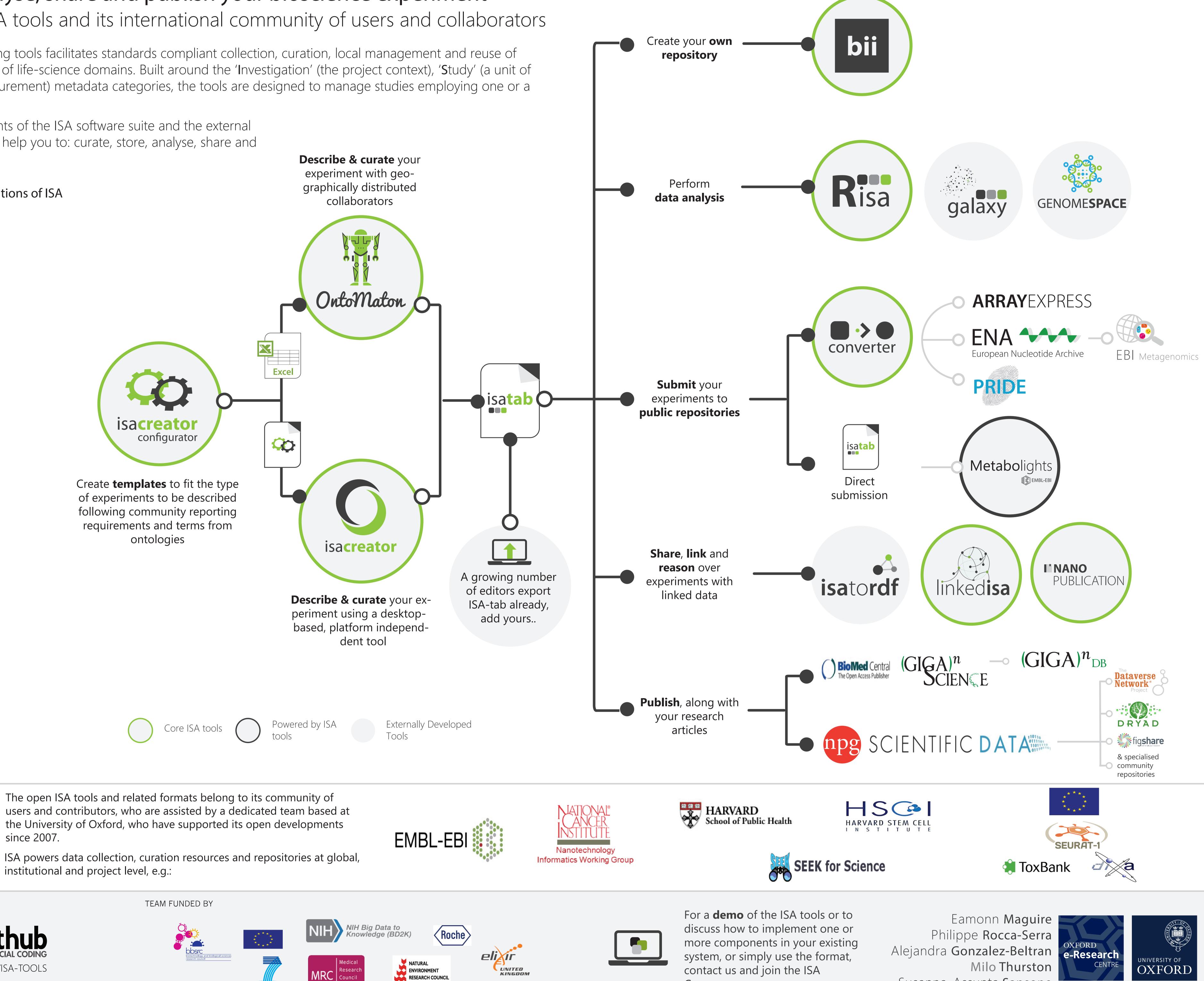
The ToxBank Data Warehouse Kohonen et al, 2013, Molecular Informatics

MetaboLights Haug et al, 2013, Nucleic Acids Research

Standardizing data: ISA-Tab-Nano Baker et al, 2013, Nature Nanotechnology

The Risa R/Bioconductor package Gonzalez-Beltran et al, 2014, BMC Bionformatics

linkedISA Gonzalez-Beltran et al, 2014, BMC Bionformatics







since 2007.

institutional and project level, e.g.:





SEVENTH FRAMEWOR

Commons.

Susanna-Assunta Sansone