COPO

COLLABORATIVE OPEN PLANT OMICS

FELIX SHAW & TONI ETUK

BOTTOM LINE

- COPO is for plant scientists to:
  - Easily share research objects
  - Get credit for doing so

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MOTIVATION

- Funding bodies require data sharing
- Improved availability of data
- Citation for all your outputs

. . .AVERAGE TIME FOR A NOVICE TO GET DATA INTO ENA?. . . .3 WEEKS!

Kenneth Haug – EBI

METADATA EXAMPLES


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METADATA EXAMPLES


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METADATA EXAMPLES


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METADATA EXAMPLES


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ALTERNATIVES

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Study Factor Type»"dose"» "chemical compound"»"time"¬
Study Factor Type Term Accession Number»""» ""» ""¬
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Study Assay Technology Platform»"454 Genome Sequencer FLX"» "454 Genome Sequencer FS"¬
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Study Protocol Type Term Source REF»""» ""» ""» ""» ""» ""» ""¬
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frozen in liquid nitrogen until nucelic acid extraction. CO2 bubbled through 11000 L mesocosm to simulate ocean acidification predicted conditions. Then phosphate and nitrate were added to induce a phytoplankton
bloom."»"Total nucleic acid extraction was done as quickly as possible using the method of Neufeld et al, 2007."» "RNA MinElute + substrative Hybridization + MEGAclear For transcriptomics, total RNA was separated
from the columns using the RNA MinElute clean-up kit (Qiagen) and checked for integrity of rRNA using an Agilent bioanalyser (RNA nano6000 chip). High integrity rRNA is essential for subtractive hybridization.
Samples were treated with Turbo DNA-free enzyme (Ambion) to remove contaminating DNA. The rRNA was removed from mRNA by subtractive hybridization (Microbe Express Kit, Ambion), and absence of rRNA and DNA
contamination was confirmed using the Agilent bioanalyser. The mRNA was further purified with the MEGAclearTM kit (Ambion). Reverse transcription of mRNA was performed using the SuperScript III enzyme (Invitrogen)
with random hexamer primers (Promega). The cDNA was treated with RiboShredderTM RNase Blend (Epicentre) to remove trace RNA contaminants. To improve the yield of cDNA, samples were subjected to random amplification
using the GenomiPhi V2 method (GE Healthcare). GenomiPhi technology produces branched DNA molecules that are recalcitrant to the pyrosequencing methodology. Therefore amplified samples were treated with S1 nuclease
using the method of Zhang et al.2006."» ""» "superscript+random hexamer primer"»"1. Sample Input and Fragmentation: The Genome Sequencer FLX System supports the sequencing of samples from a wide variety of starting
materials including genomic DNA, PCR products, BACs, and cDNA. Samples such as genomic DNA and BACs are fractionated into small, 300- to 800-base pair fragments. For smaller samples, such as small non-coding RNA or
PCR amplicons, fragmentation is not required. Instead, short PCR products amplified using Genome Sequencer fusion primers can be used for immobilization onto DNA capture beads as shown below."» ""¬
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Study Person First Name»"Jack"» "Dawn"» "Ying"» "Rob"»"Weizhong"» "Paul"» "Ian"¬
Study Person Mid Initials»"A"»""» ""» ""» ""» ""» ""¬
Study Person Email» "jagi@pml.ac.uk"» ""» ""» ""» ""» ""» ""¬
Study Person Phone» ""» ""» ""» ""» ""» ""» ""¬
Study Person Fax» ""» ""» ""» ""» ""» ""» ""¬
Study Person Address» "Prospect Place, Plymouth, United Kingdom"» "CEH Oxford, Oxford, United Kingdom"» "San Diego State University, San Diego, California, United States of America"»"Argonne National Laboratory,
Argonne, Illinois, United States of America"» "San Diego State University, San Diego, California, United States of America"»"San Diego State University, San Diego, California, United States of America"»"Prospect
Place, Plymouth, United Kingdom"¬
Study Person Affiliation» "Plymouth Marine Laboratory"» "NERC Centre for Ecology and Hydrology"»"California Institute for Telecommunications and Information Technology"» "Department of Computer Science, Mathematics
and Computer Science Division,"» "California Institute for Telecommunications and Information Technology"» "California Institute for Telecommunications and Information Technology"» "Plymouth Marine Laboratory"¬
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ALTERNATIVES

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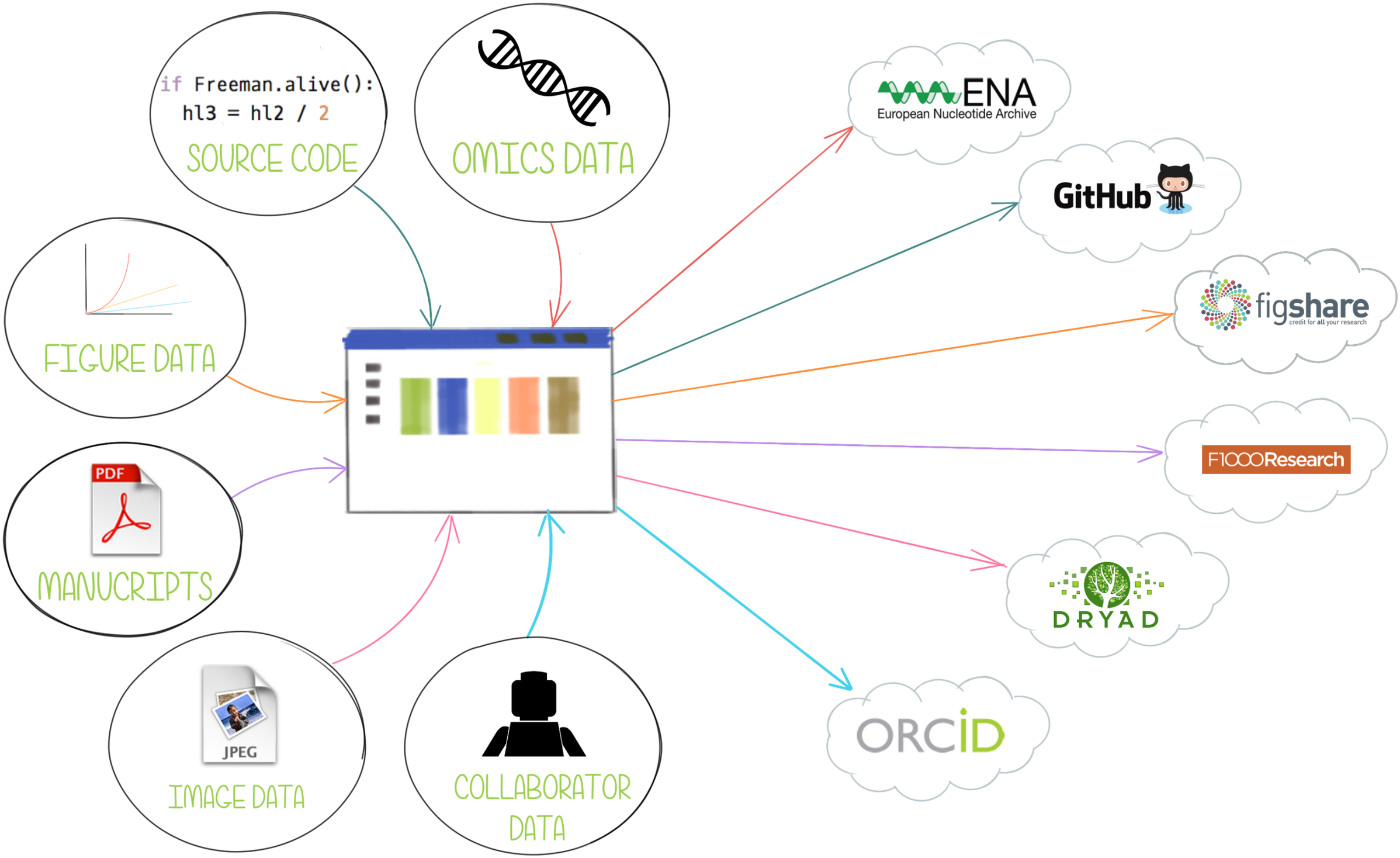
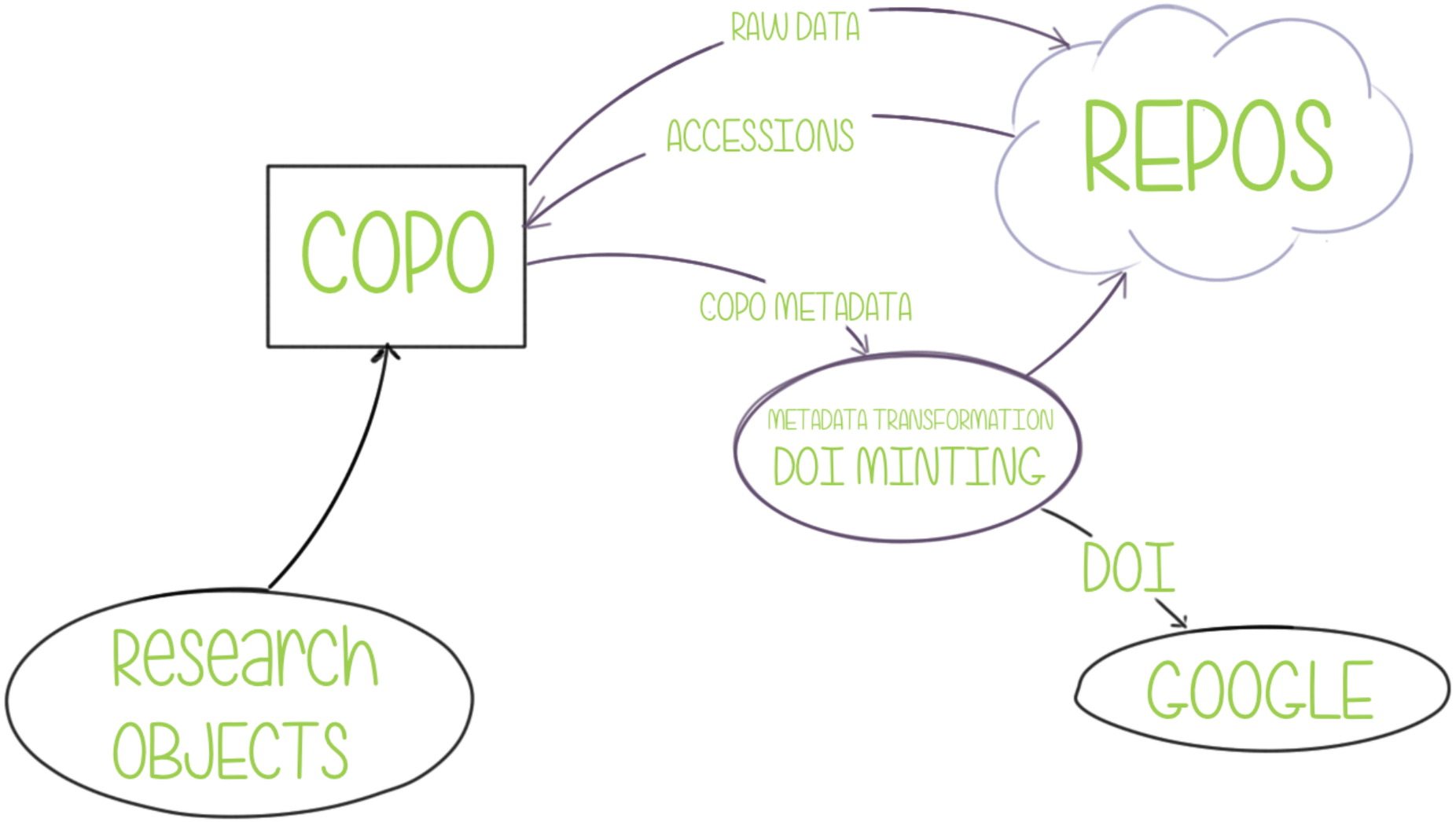
PROFILE OVERVIEW



COPO OVERVIEW



SINGLE SIGN-ON

ORCiD

orcid.org/0000-0001-9649-5906

- One login for multiple services
- De-facto standard for services / repositories
- Provides access to full researcher profile
  - Work history, Publications, Grants etc.
- API provided

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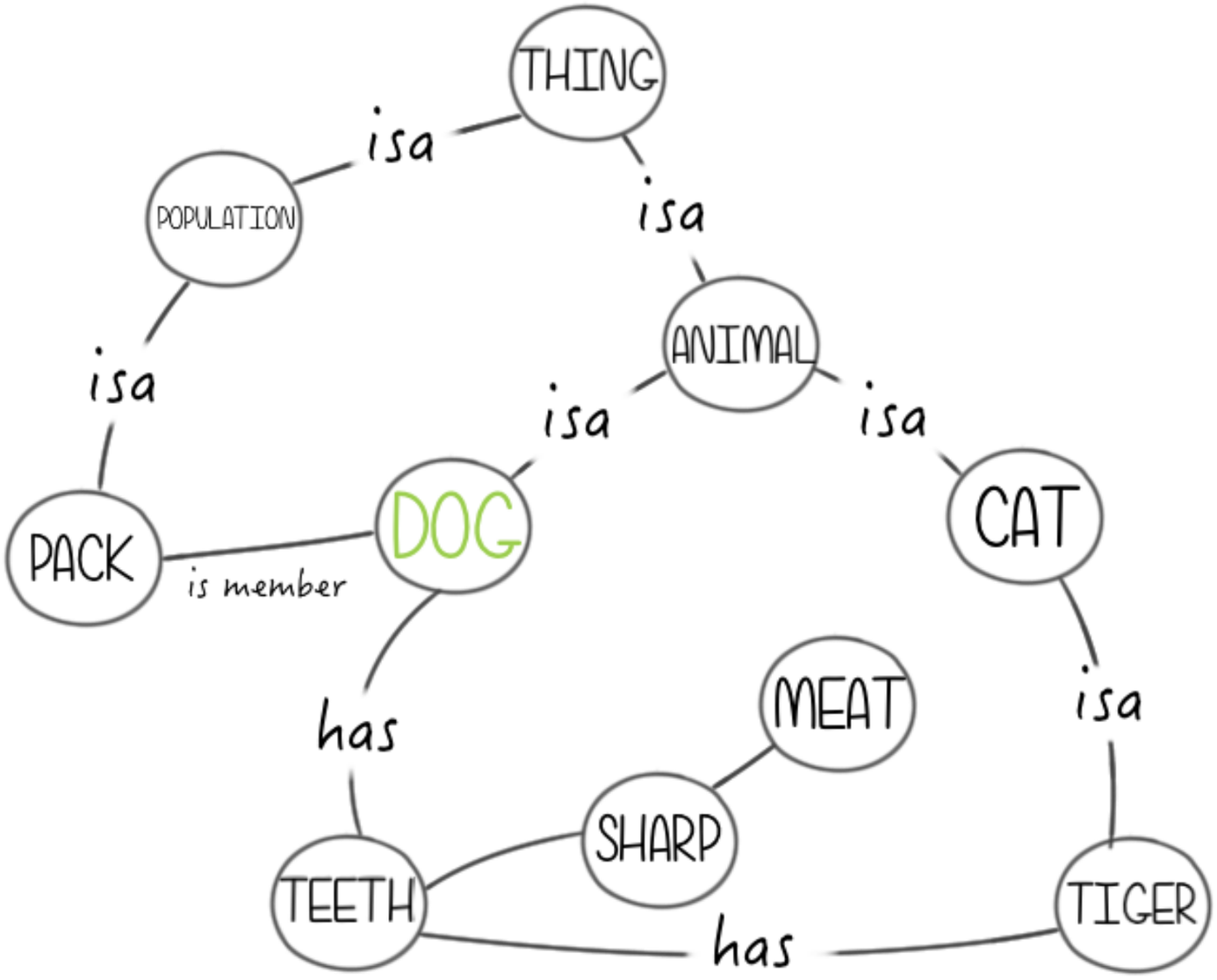
ONTOLOGIES


THING
isa
isa
POPULATION
ANIMAL
isa
isa
isa
PACK
DOG
CAT
is member
MEAT
has
isa
SHARP
TEETH
TIGER
has

SUMMARY

- Aggregation and Deposition Portal
  - Add research objects to profiles
  - Objects efficiently labelled with community standard metadata and ontology terms
  - Profiles deposited to public repositories
  - Identifiers minted for logical groups

SUMMARY

- Current Users
  - Initially test base at Earlham Institute
  - Some users at John Innes Centre
  - Recent interest from CGIAR centers:
    - CIMMYT
    - Africa Rice
    - IRRI
    - Bioversity International

QUESTIONS?

- Questions on this section