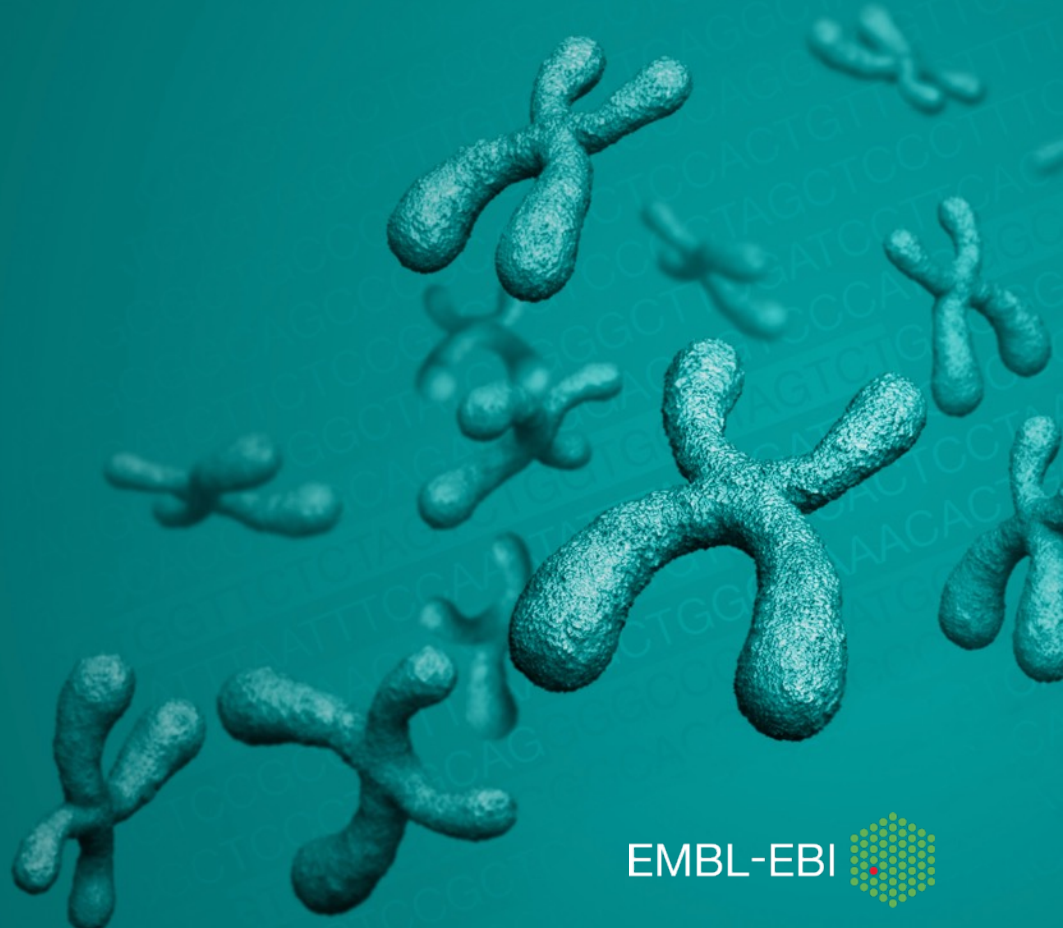
Open access & the International Nucleotide Sequence Database Collaboration

Guy Cochrane



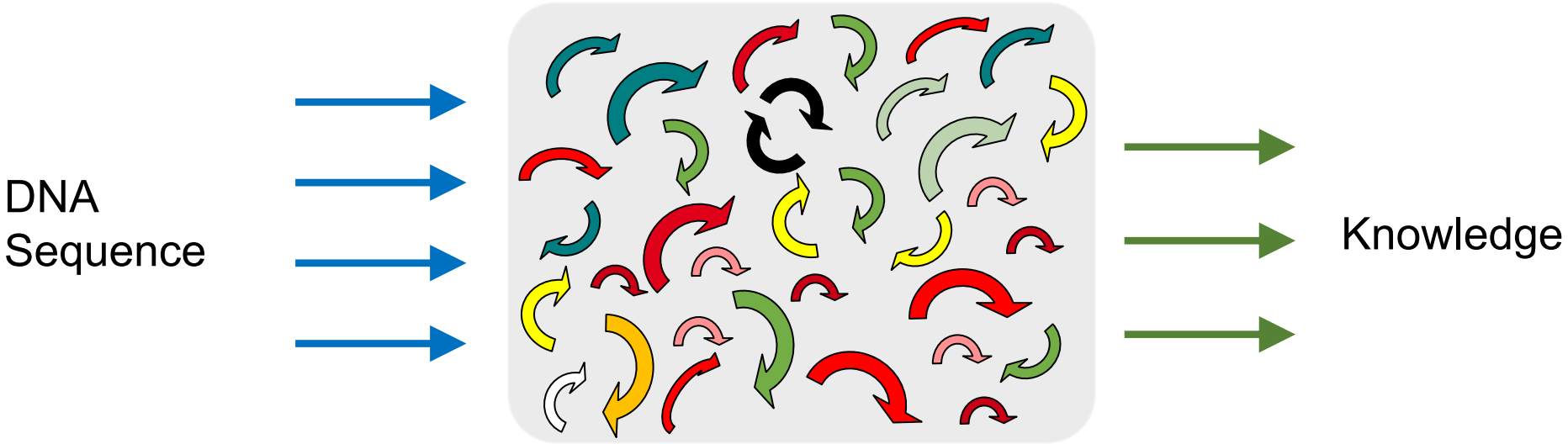
EMBL-EBI

“If I have seen further than others, then it is by standing on the shoulders of giants.”

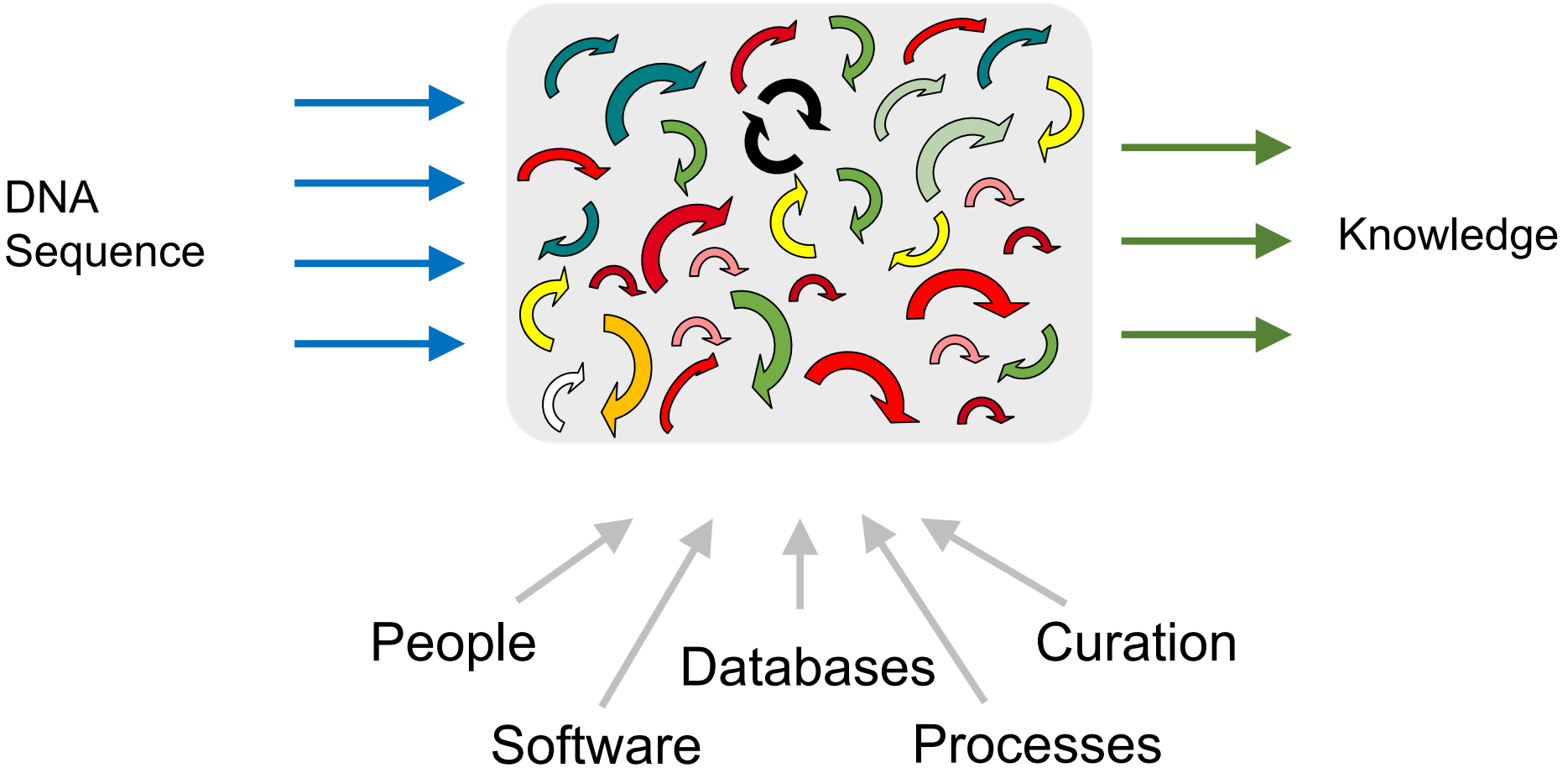
Isaac Newton

EMBL-EBI

The life science “machine”



The life science “machine”

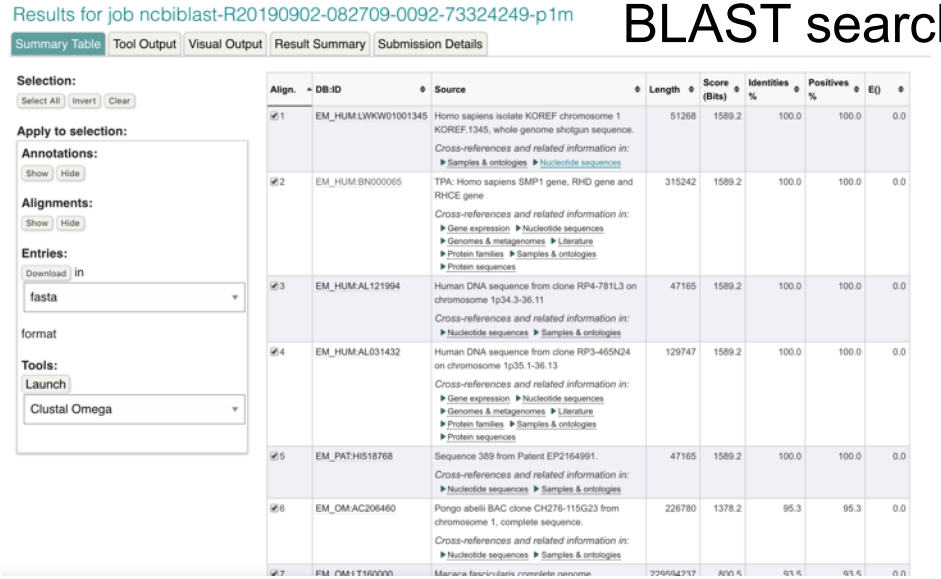


Open data are essential

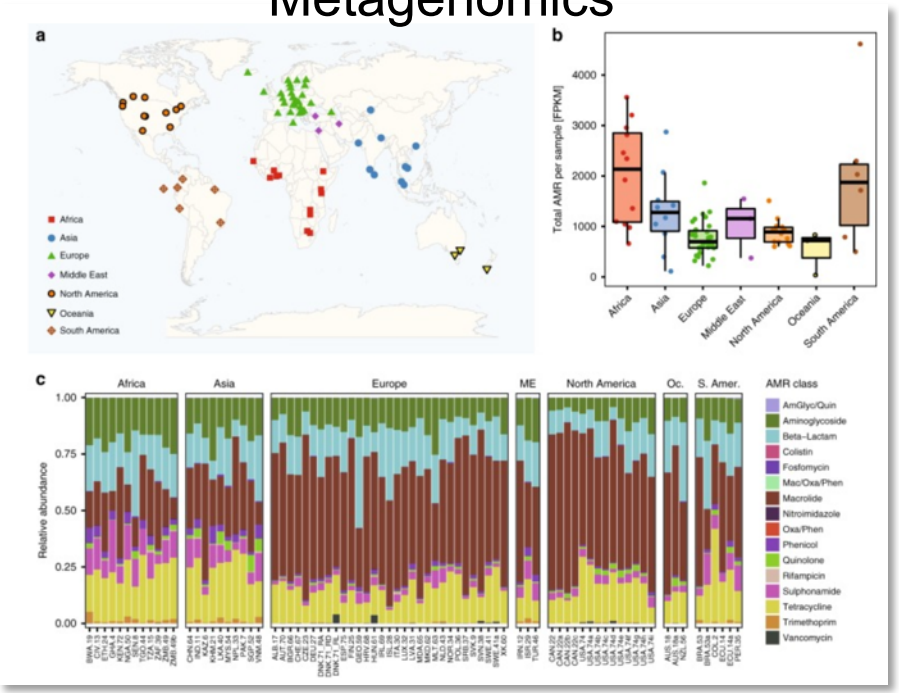
Tree building

Pimlapas Leekitcharoenphon *et al.* Appl. Environ. Microbiol. 2016; doi:10.1128/AEM.03821-15

BLAST search

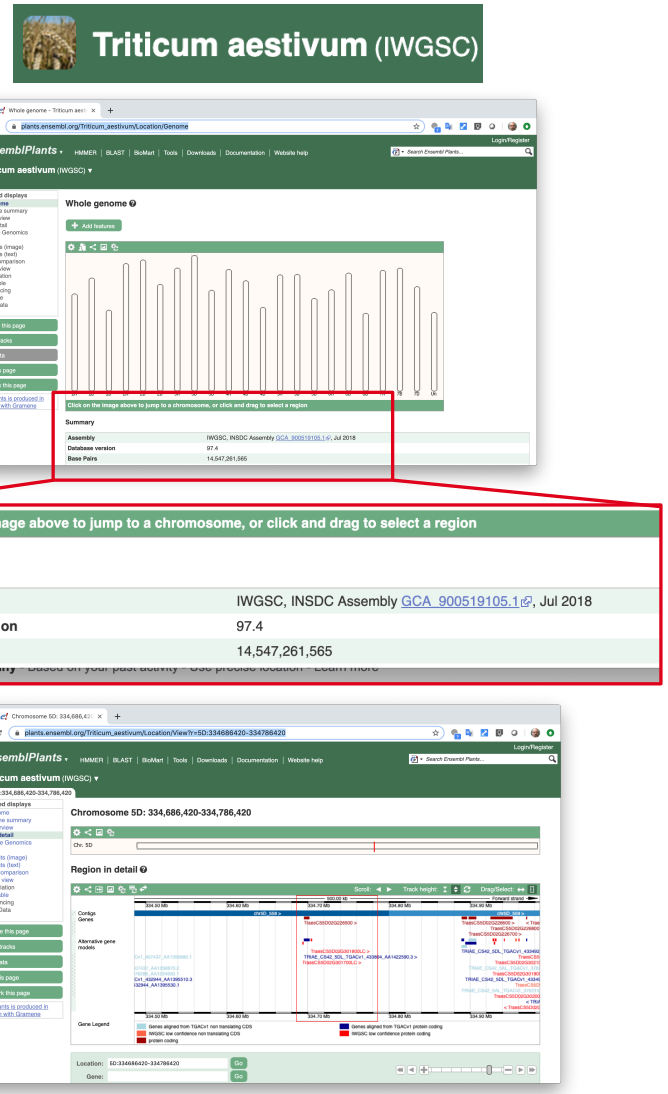


Metagenomics



Hendriksen RS, *et al*. Nat Commun. 2019; 10: 1124.

Annotation by reference



https://plants.ensembl.org/Triticum_aestivum/Info/Index?db=core

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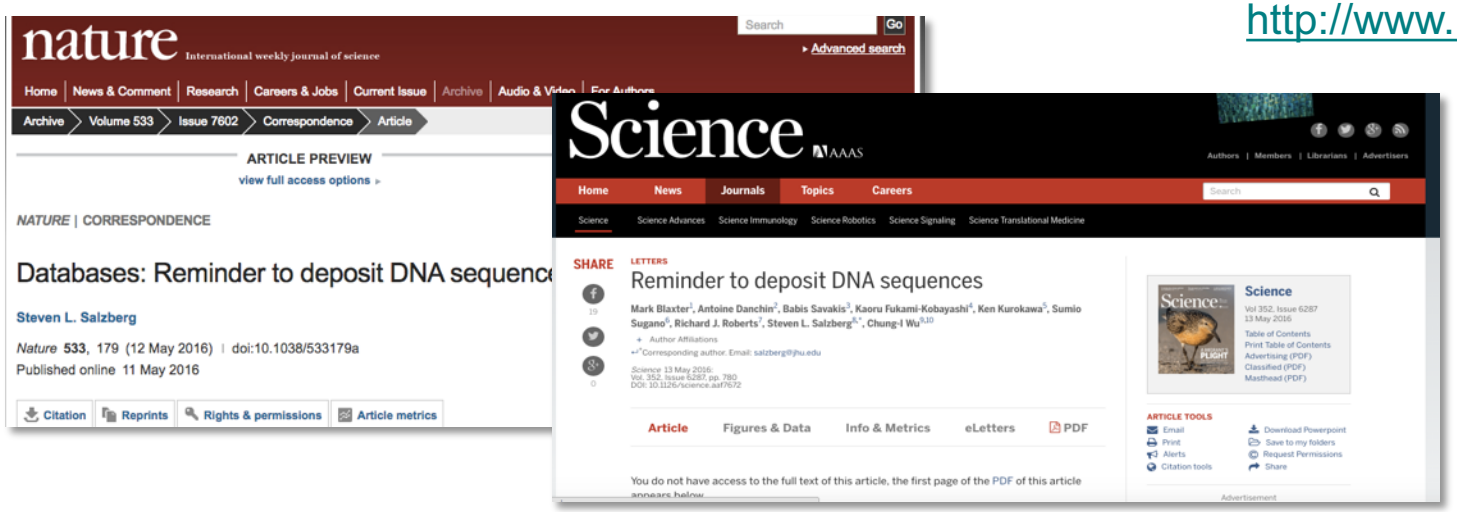
International Nucleotide Sequence Database Collaboration (INSDC)

Values

- open access for all
- globally comprehensive
- spanning life science domains
- permanent database of record
- public forum for the scientific process

Organisation

- established early 1980s
- major ongoing investment
- structure and governance
- model for scientific collaboration



http://www.insdc.org/

Instruments

- regular data exchange
- accession scheme
- data standards
- mandatory submission agreement
- services and software (node-level)

International Nucleotide Sequence Database Collaboration (INSDC)

```
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Sequence

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DT   04-NOV-2019 (Rel. 142, Last updated, Version 1)
XX
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DE   gene, partial cds; mitochondrial.
XX
KW   .
XX
OS   Narcine maculata
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Batoidea; Torpediniformes; Narcinidae; Narcine.
OG   Mitochondrion
XX
RN   [1]
RP   1-679
RA   Arulmoorthy M.P., Sureandiran B.;
RT   ;
RL   Submitted (13-APR-2019) to the INSDC.
RL   Cas in Marine Biology, Annamalai University, Anna Kovil, Parangipettai,
RL   Tamil Nadu 608502, India
XX
DR   MD5; f83e14e5913fb53c7d28dc9e9960a043.
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FT                   PEV"
XX
SQ   Sequence 679 BP; 197 A; 166 C; 109 G; 207 T; 0 other;
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     tgactgctca tgcattcgtt ataatcttct ttatagttat accaattata atcggcgggt       180
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     aataccaaac accacttttt gtgtgatcat tacttatcac tgcaattctt ctacttctat       540
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     ttggccaccc agaagtcta                                                    679
//
```
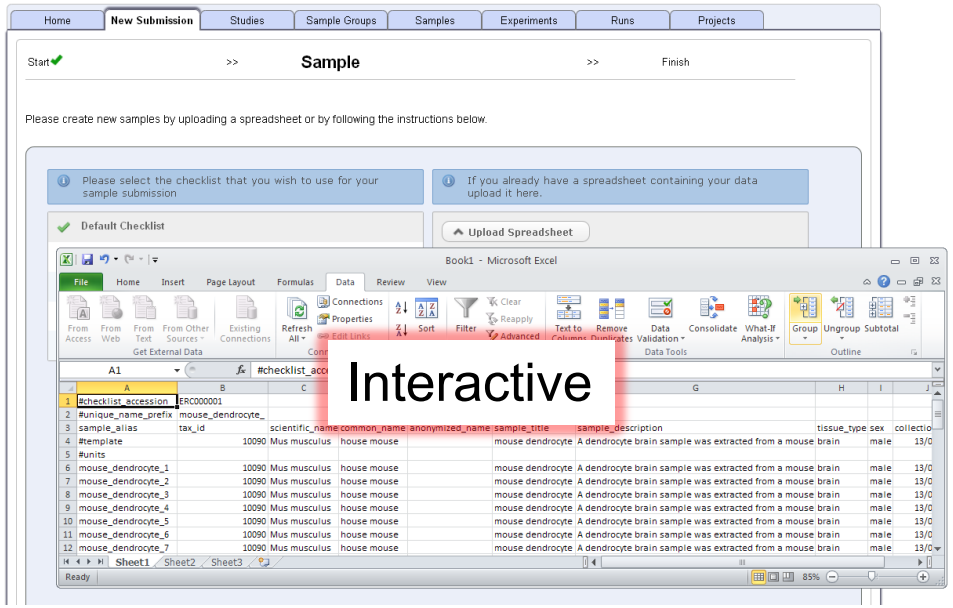
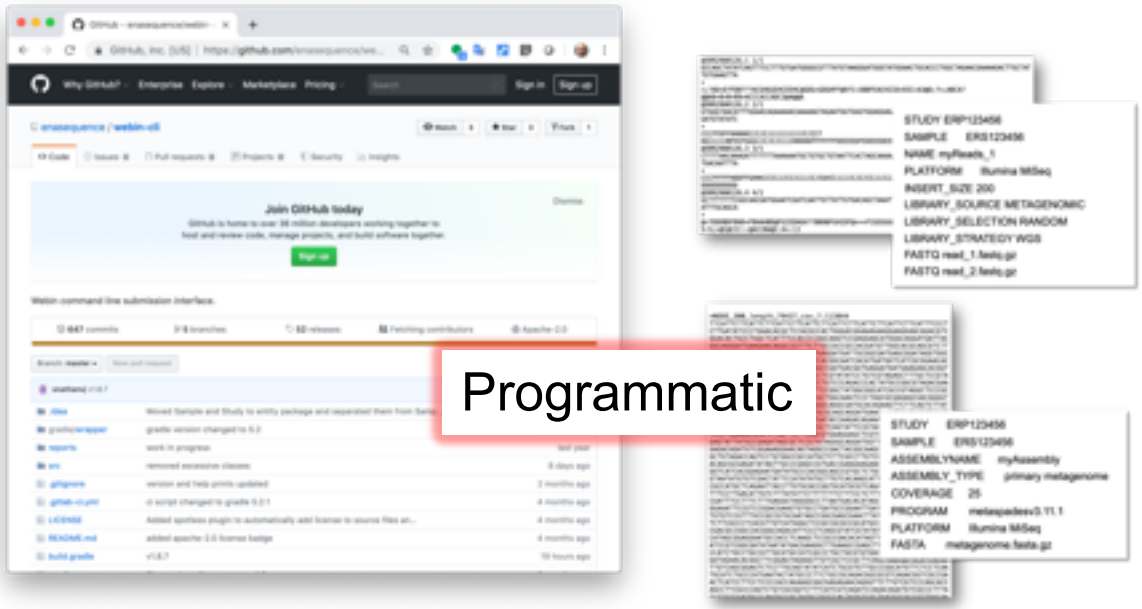

- Clerical information
- Taxonomy
- Literature
- Cross-references
- Source information
- Biological features

http://www.insdc.org/

The data submission process

- Data provider
  - Validation, organization, adding structure and curation
  - Compliance with standards and established conventions
  - Links to external data (e.g. academic publications)
- Database
  - Curation and integration with the overall corpus
  - Indexing for discovery and reuse
  - Open services, freely available to the world





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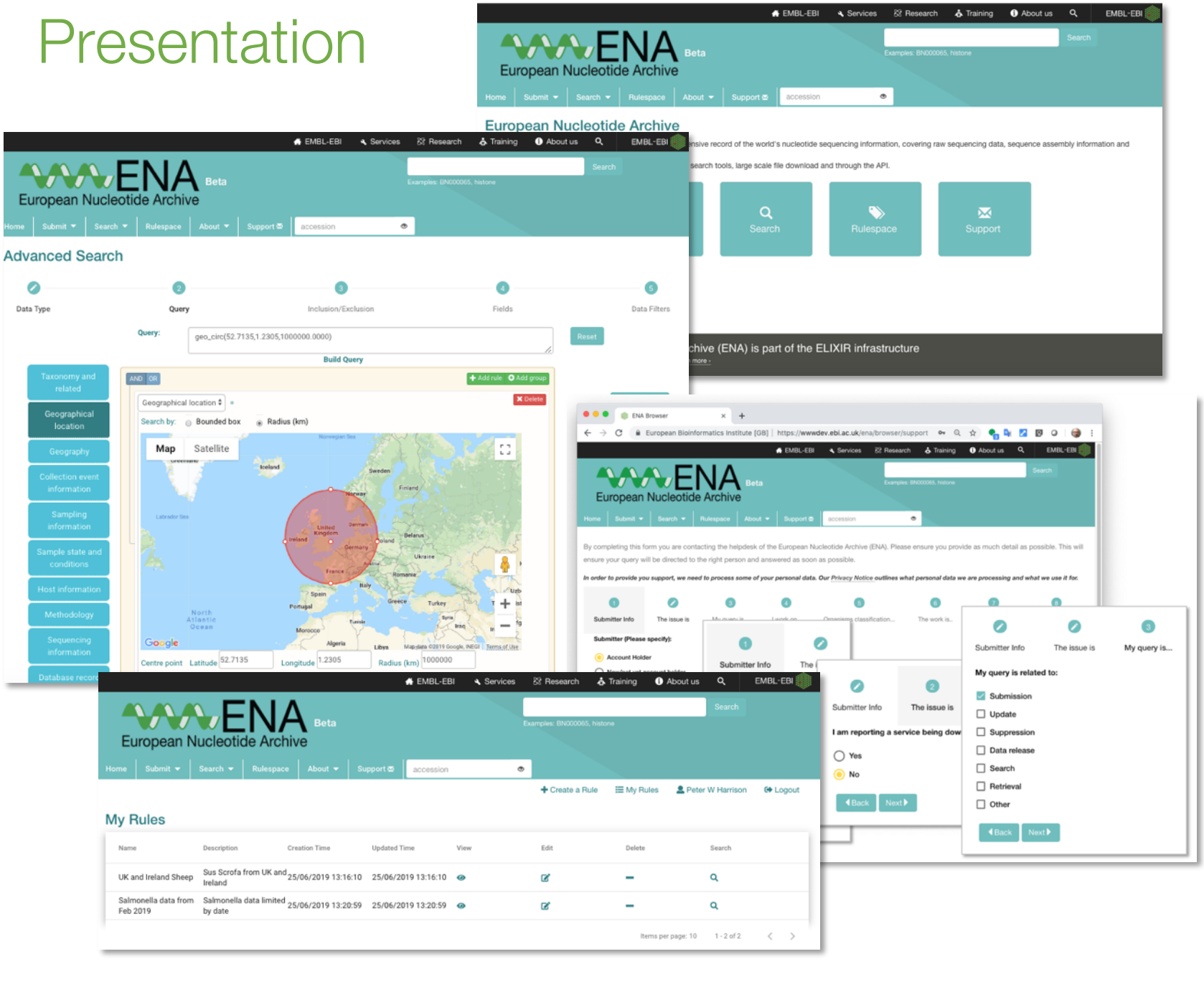
Presentation



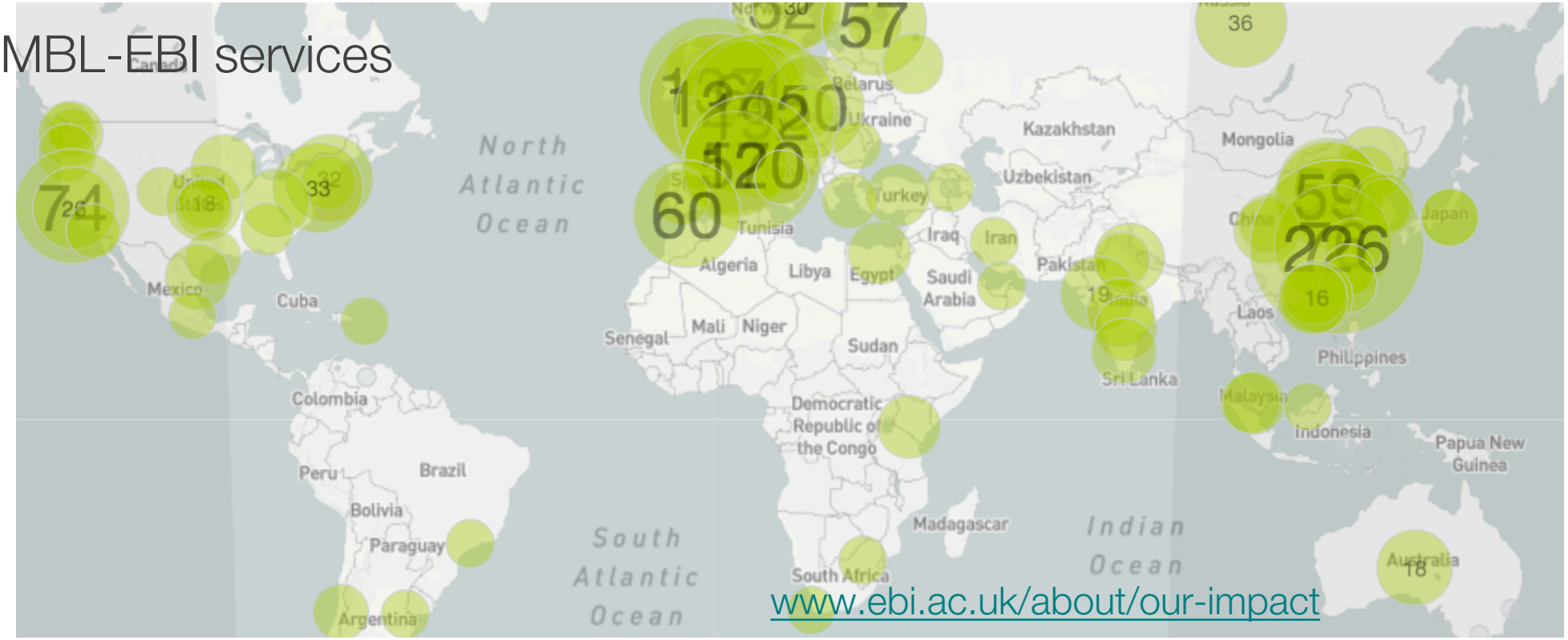
- Search
  - Sample characteristics
  - Function
  - Sequence similarity
- Browse
  - Study
  - Taxonomy
  - Sequencing method
  - Historic versions
- Filter
  - Reusable/shareable rules
  - Synchronisation with latest data
- Retrieve
  - Download tools

EMBL-EBI

Scale

- **Rate**: 1 new dataset every 6 minutes
- **Data**: $2x10^9$ sequences and $1x10^{16}$ base pairs of read data across $2x10^6$ taxa
- **Usage**: 2,000 submitters; 10x thousands monthly consumers; 10x millions of monthly hits, many times this globally
- **Support**: 46 tickets per day and in-person training delivered to more than 350 users per annum
- **Adoption**: *the sequence database of record for the broadest scientific community*

EMBL-EBI services



www.ebi.ac.uk/about/our-impact

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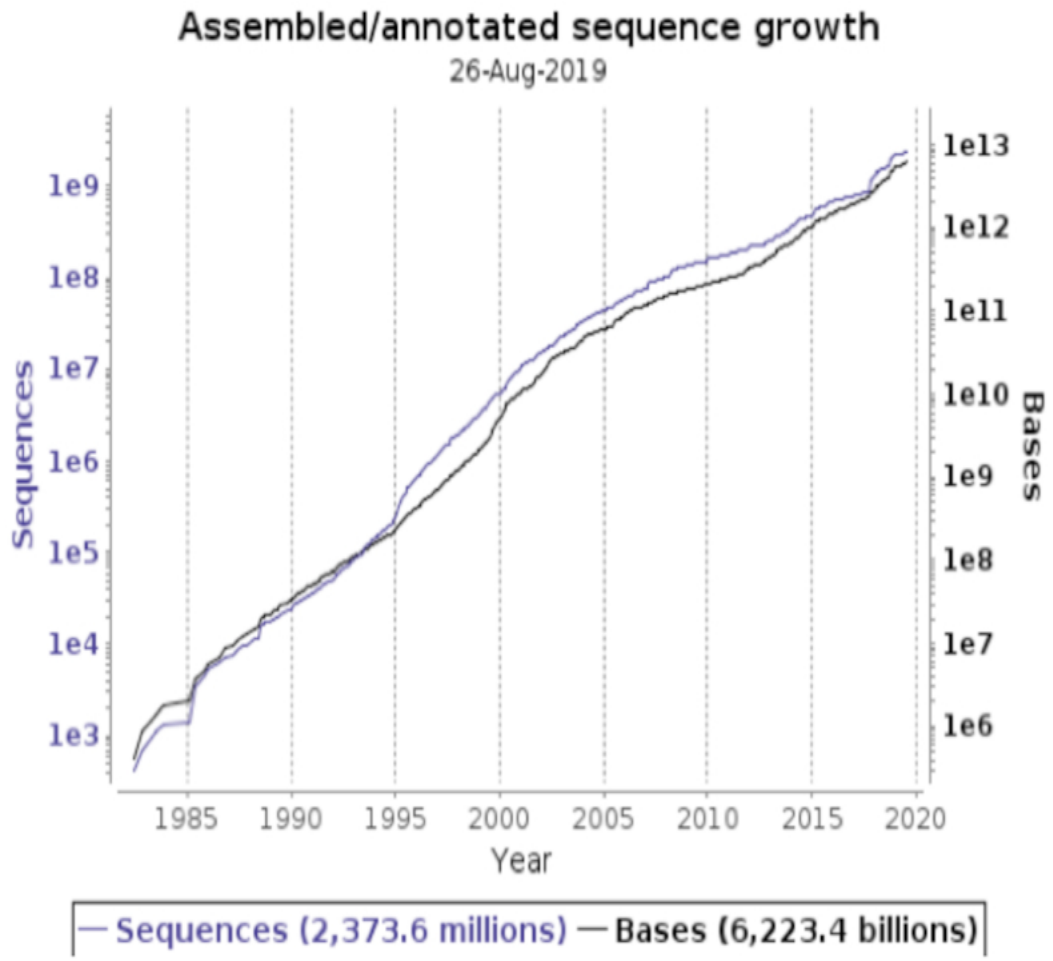
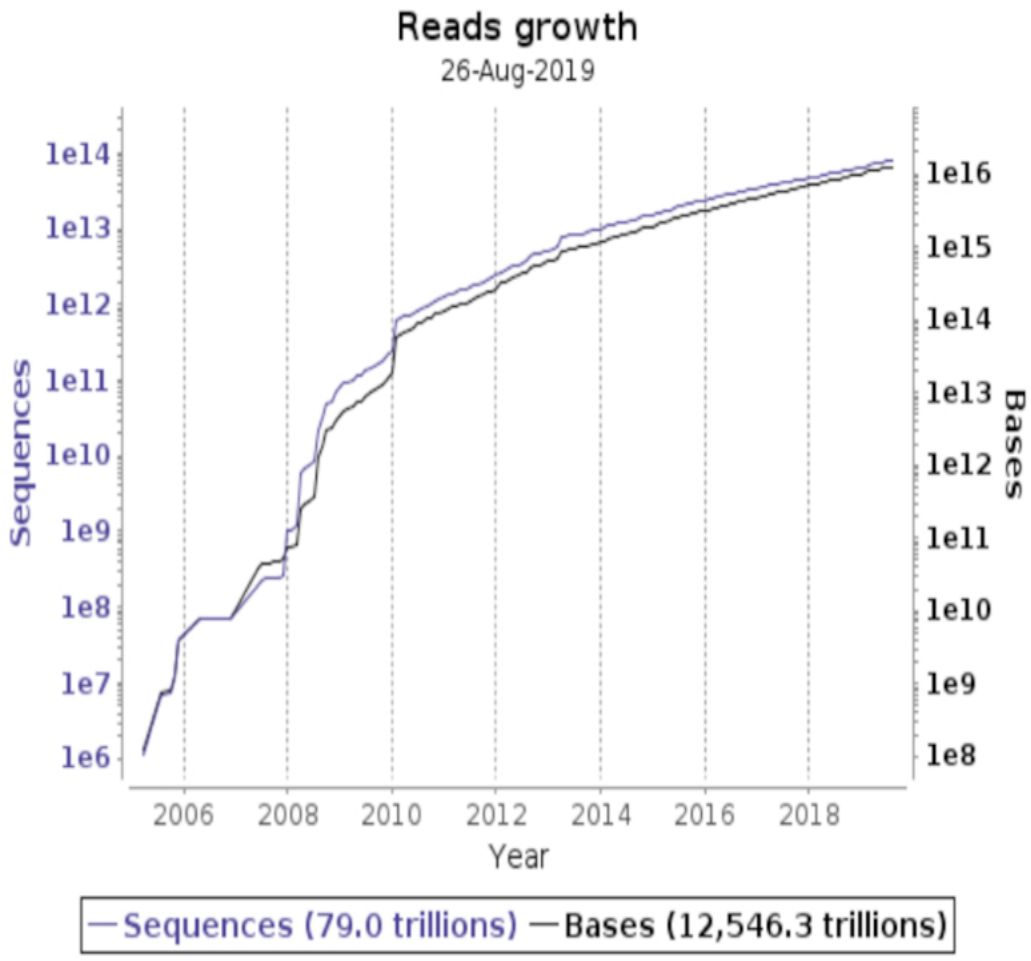
Data growth



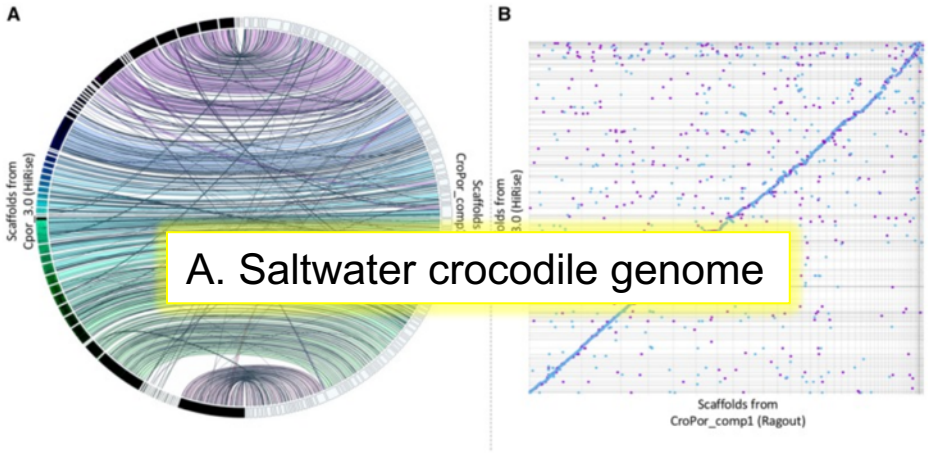


Nucleic Acids Research, Volume 48, Issue D1, 08 January 2020, Pages D70–D76, https://doi.org/10.1093/nar/gkz1063

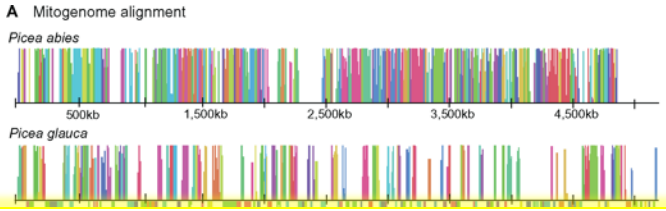
OXFORD
UNIVERSITY PRESS

Direct use

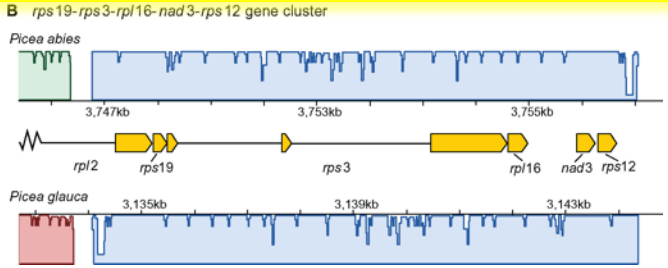
- 1,306 publications citing sequence accessions since the 1st Jan. 2020

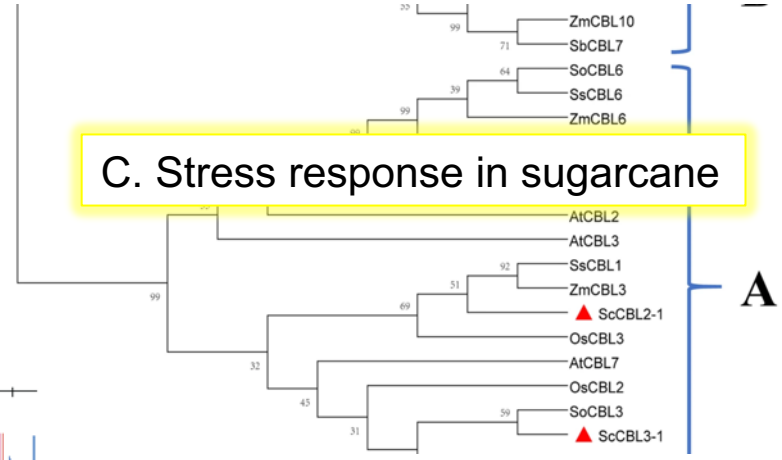


A. Saltwater crocodile genome

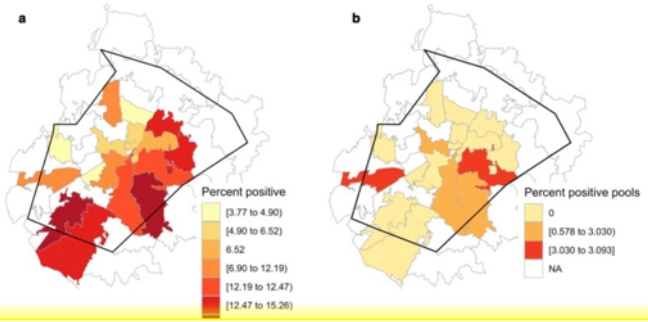


B. Norway spruce evolutionary biology

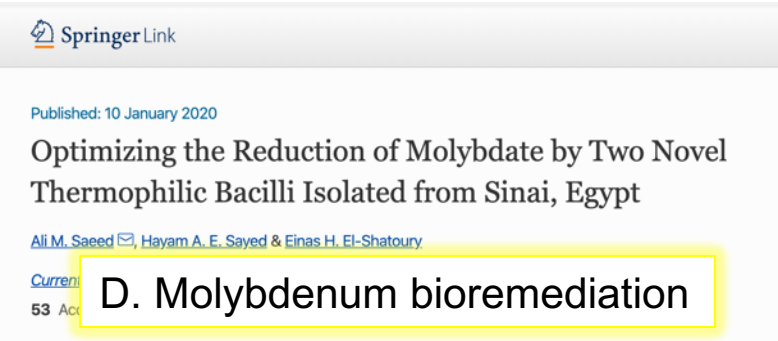




C. Stress response in sugarcane



E. Mosquito-borne heartworm in dogs

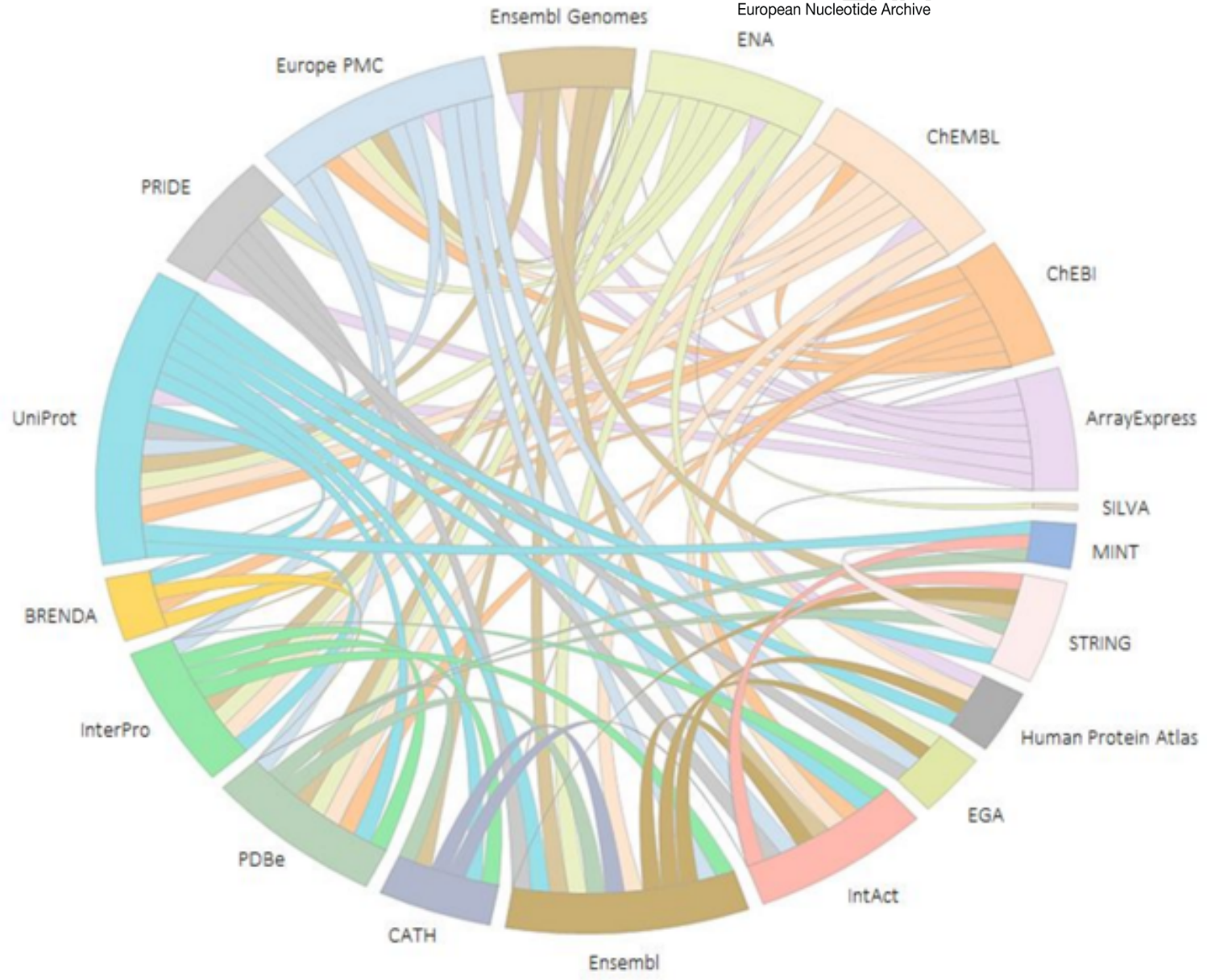


D. Molybdenum bioremediation

A. Ghosh A et al., Genome Biol Evol. 2020 Jan;12(1) 3635-3646. doi:10.1093/gbe/evz269. PMID: 31821505; © The Author(s) 2020; http://creativecommons.org/licenses/by/4.0/
B. Sullivan AR et al., Genome Biol Evol. 2020 Jan;12(1) 3586-3598. doi:10.1093/gbe/evz263. PMID: 31774499; © The Author(s) 2020; http://creativecommons.org/licenses/by-nc/4.0/
C. Su W et al., Sci Rep. 2020 Jan;10(1) 167. doi:10.1038/s41598-019-57058-7. PMID: 31932662; http://creativecommons.org/licenses/by/4.0/
D. Saeed AM et al., Curr Microbiol. 2020 Jan . doi:10.1007/s00284-020-01874-y. PMID: 31925514.
E. Spence Beaulieu MR et al., Parasit Vectors. 2020 Jan;13(1) 12. doi:10.1186/s13071-019-3874-0. PMID: 31924253; PMCID: PMC6953185. http://creativecommons.org/licenses/by/4.0/; http://creativecommons.org/publicdomain/zero/1.0/

Data reach

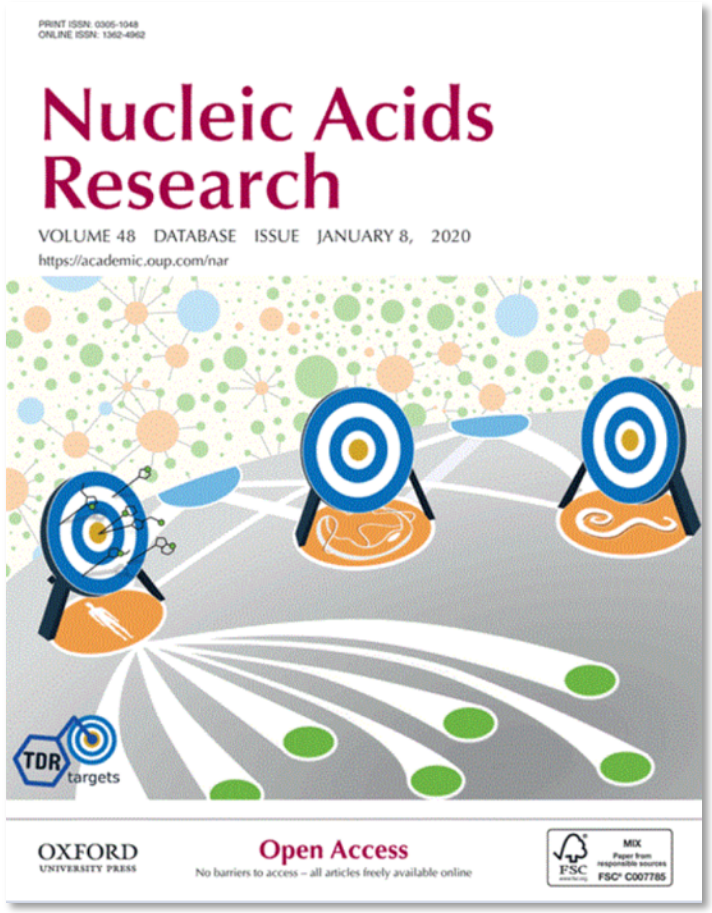
ENA
European Nucleotide Archive



elixir
Core Data Resource

Core resource connectivity figure from Drysdale *et al.*, https://www.biorxiv.org/content/10.1101/598318v1

Further reach



Public database inventory

NAR database summary	–	**1778** (100%)
DBs focussing on NSD	–	**808** (45%)
Non-Human DBs	–	**743** (42%)
DBs allowing upload	–	**38** (<2.4%)
Operating outside INSDC	–	**0** (0%)

Rohden F, Huang S, Dröge G, Hartman Scholz A, and contributing authors (2019). Combined study in DSI in public and private databases and DSI traceability. https://www.cbd.int/abs/DSI-peer/Study-Traceability-databases.pdf

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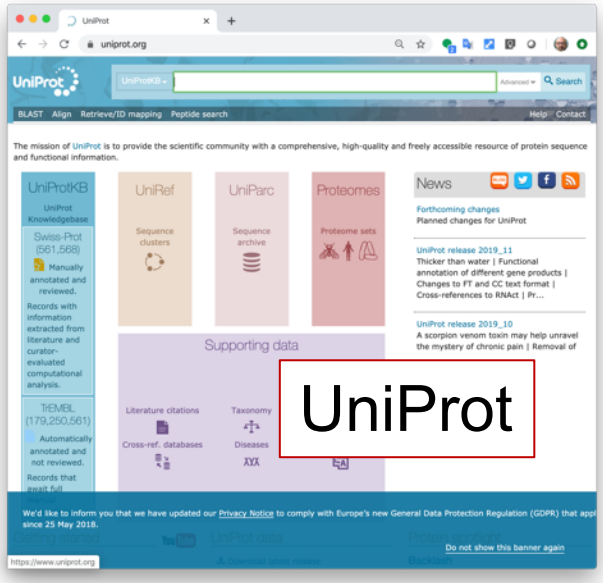
Secondary databases

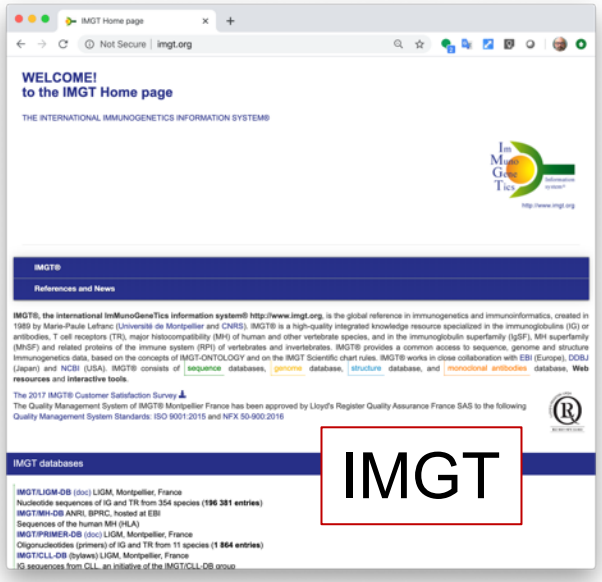
- Connected to INSDC services and content
- More specialist services to user communities



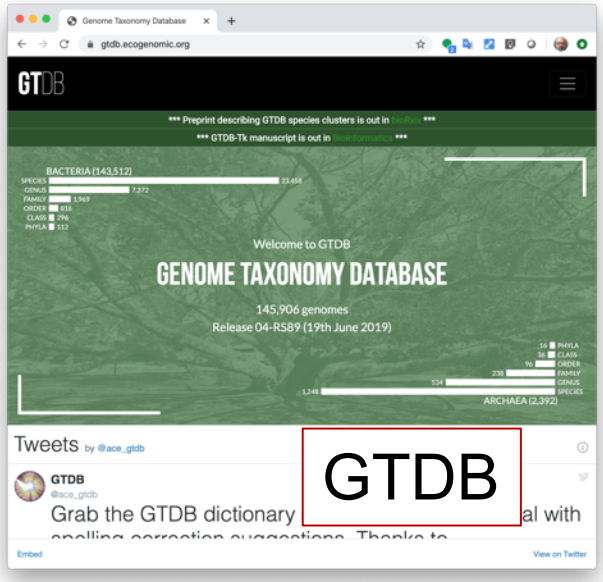
https://www.uniprot.org/

http://www.mirbase.org/

https://www.arb-silva.de/

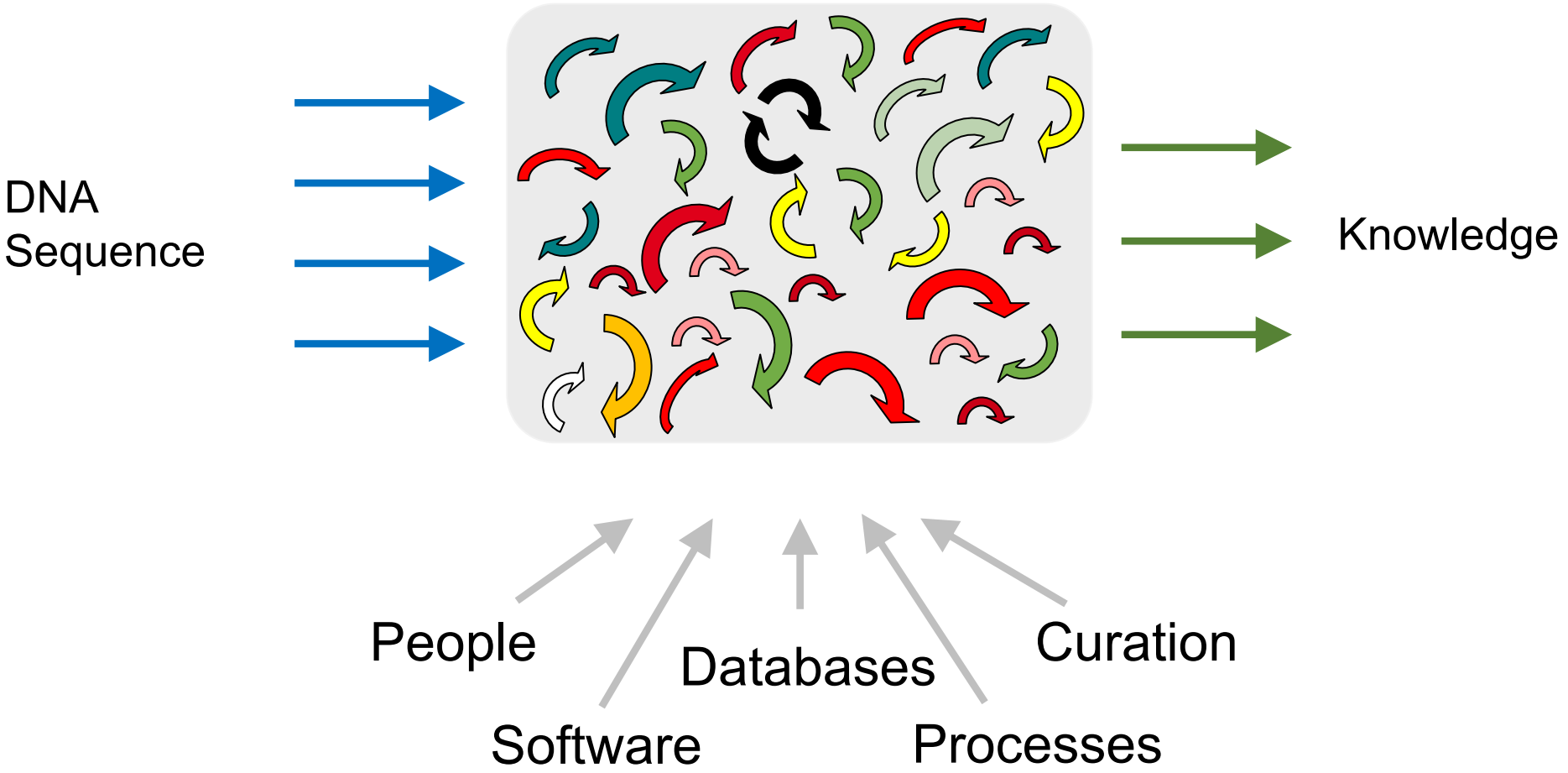


http://www.imgt.org/



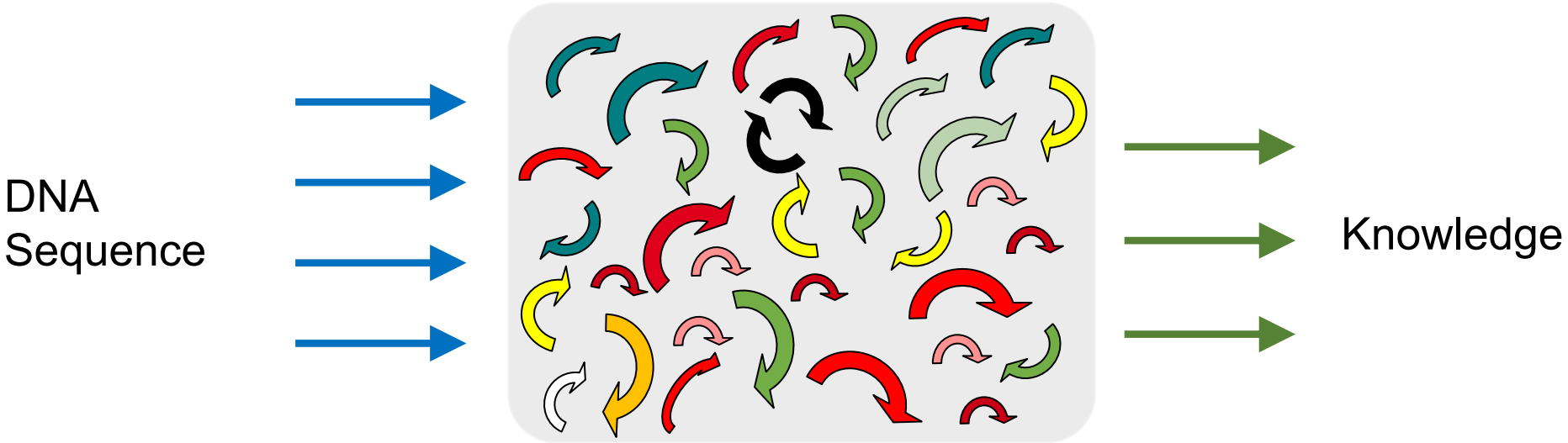
https://gtdb.ecogenomic.org/

The life science “machine”



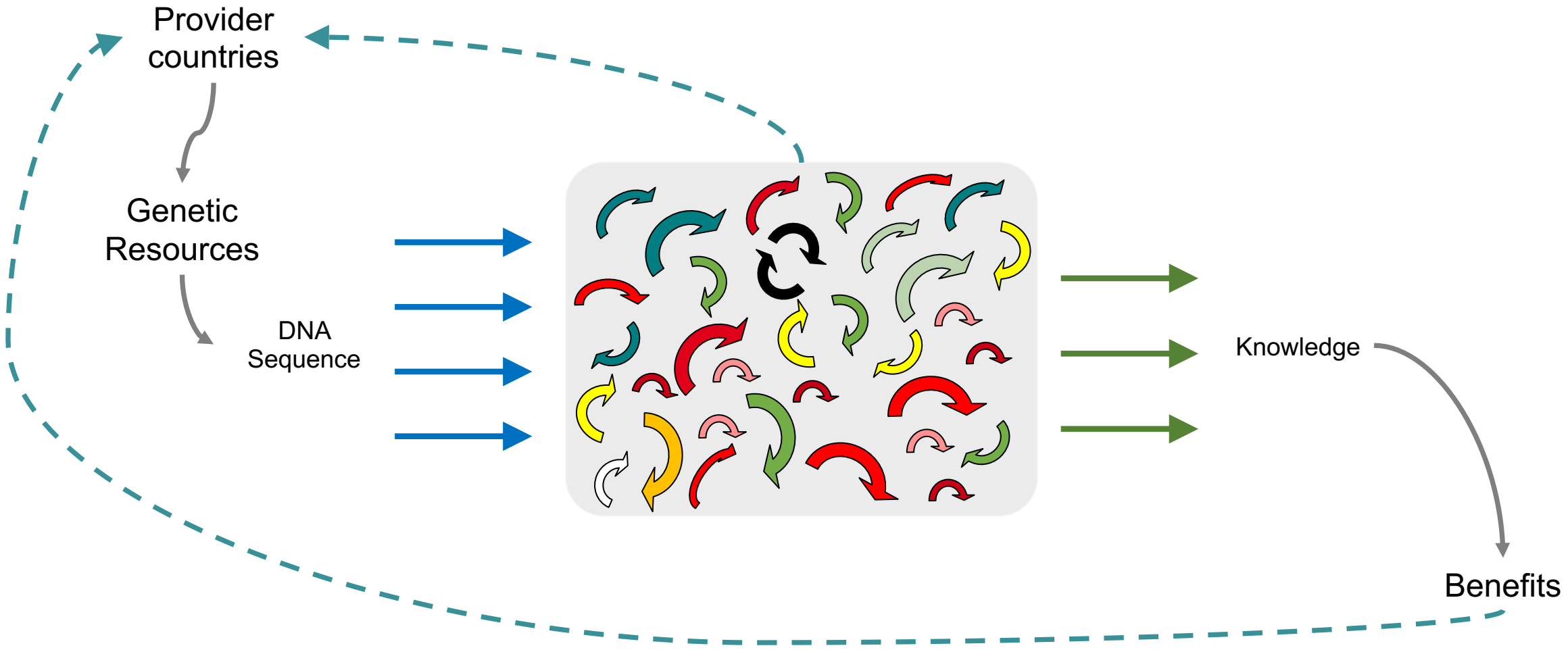
The life science “machine”

- High productivity drives scientific progress



Productivity in the machine

- High productivity drives ABS



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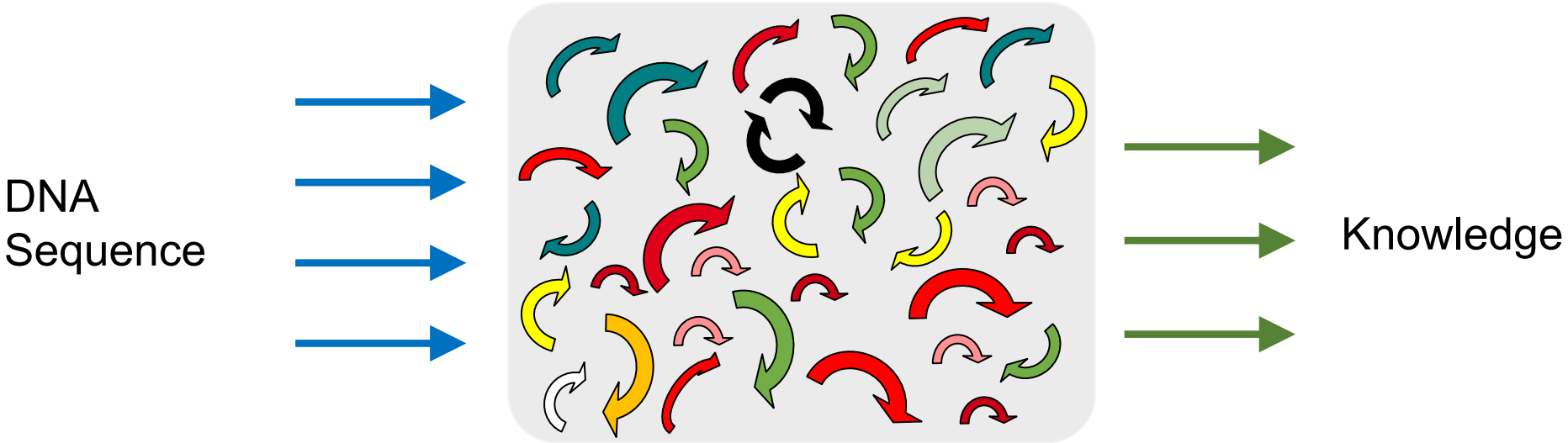
Productivity in the machine

- Understand risks
- Assert core values
- Identify opportunities

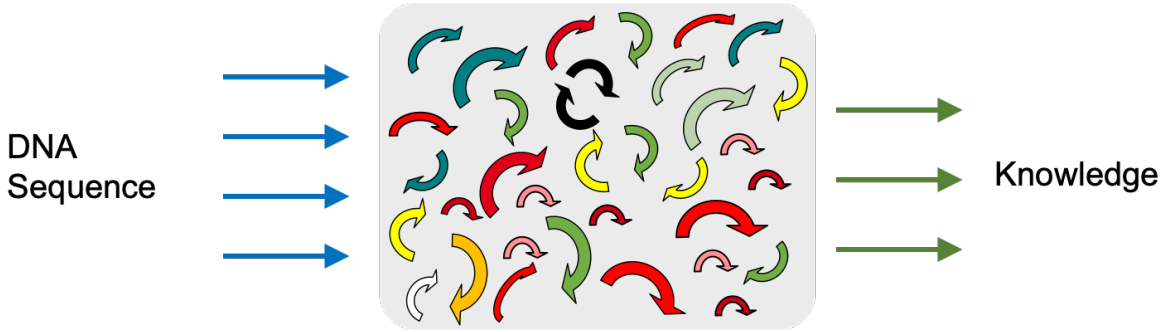


What if.. visibility of sequence were reduced?

- E.G. users had to register and log-in
- Agreement not to redistribute in any form

- Researchers couldn't provide evidence trails for their findings
- Secondary databases wouldn't be able to show data to users

- Productivity drops to near-zero



Critical property of machine:

Data must be visible

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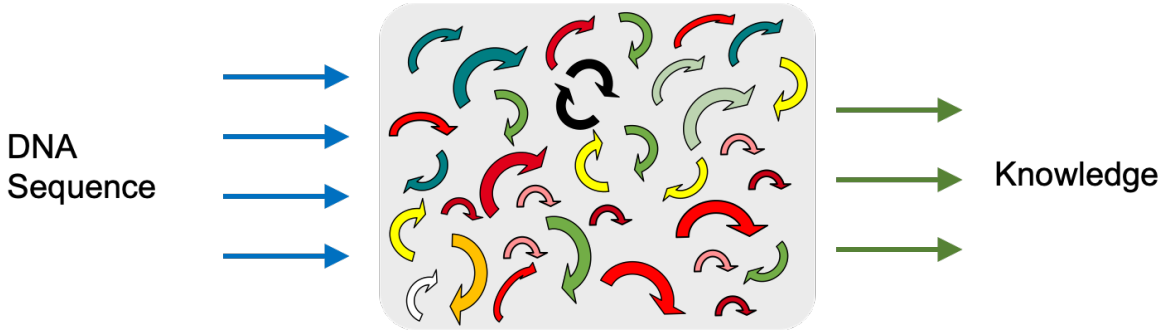
What if.. each sequence travelled with unique terms of use?

- E.G. license connected to each record, many different licenses

- Immediacy of reuse would be lost, researchers would have significant clerical work
- Secondary databases would either propagate license (impractical or impossible) or reject

- Productivity reduced substantially



Critical property of machine:

Terms of use must be uniform across sequences

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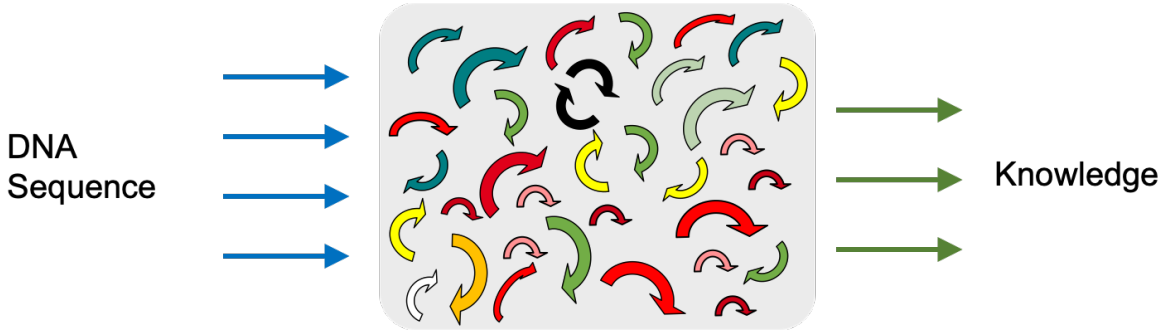
What if.. location of sequenced material was mandatory?

- Submitters would be required to provide source location, such as country name or coordinates

- Submission blocked if this condition is not satisfied
- Data – particularly for biodiversity and ecology applications - are enriched



Opportunity:

Location information is scientifically informative

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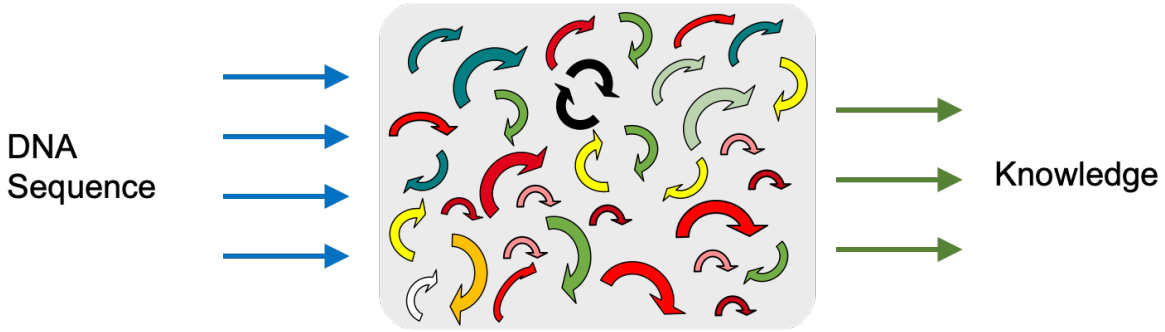
What if.. collaboration networks were tracked?

- E.G. INSDC would provide services to show networks of data owning institutions or networks of co-authors

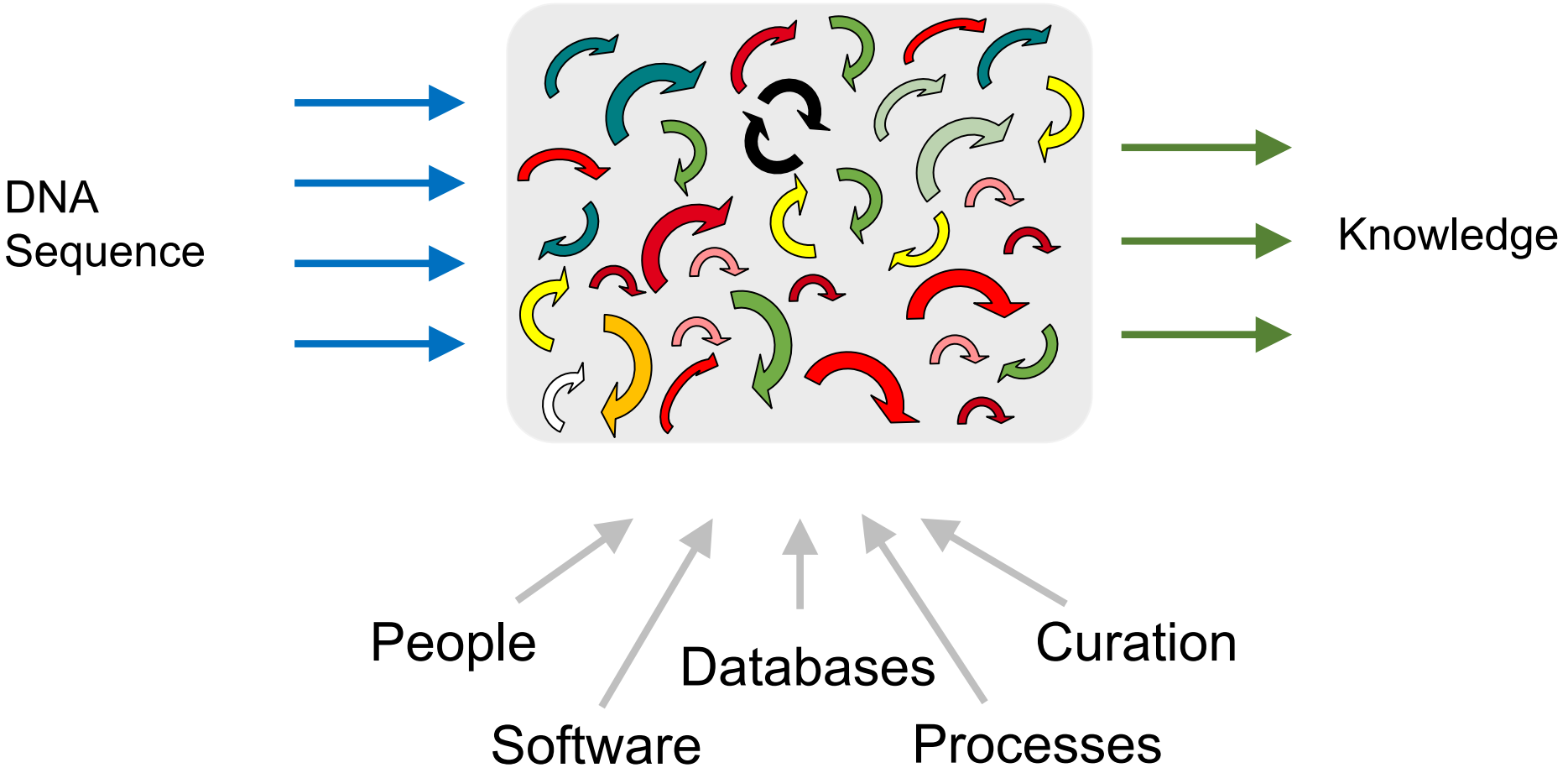
- Scientists would be able to identify potential collaborators
- Co-owned data or co-publishing authors may reveal data links

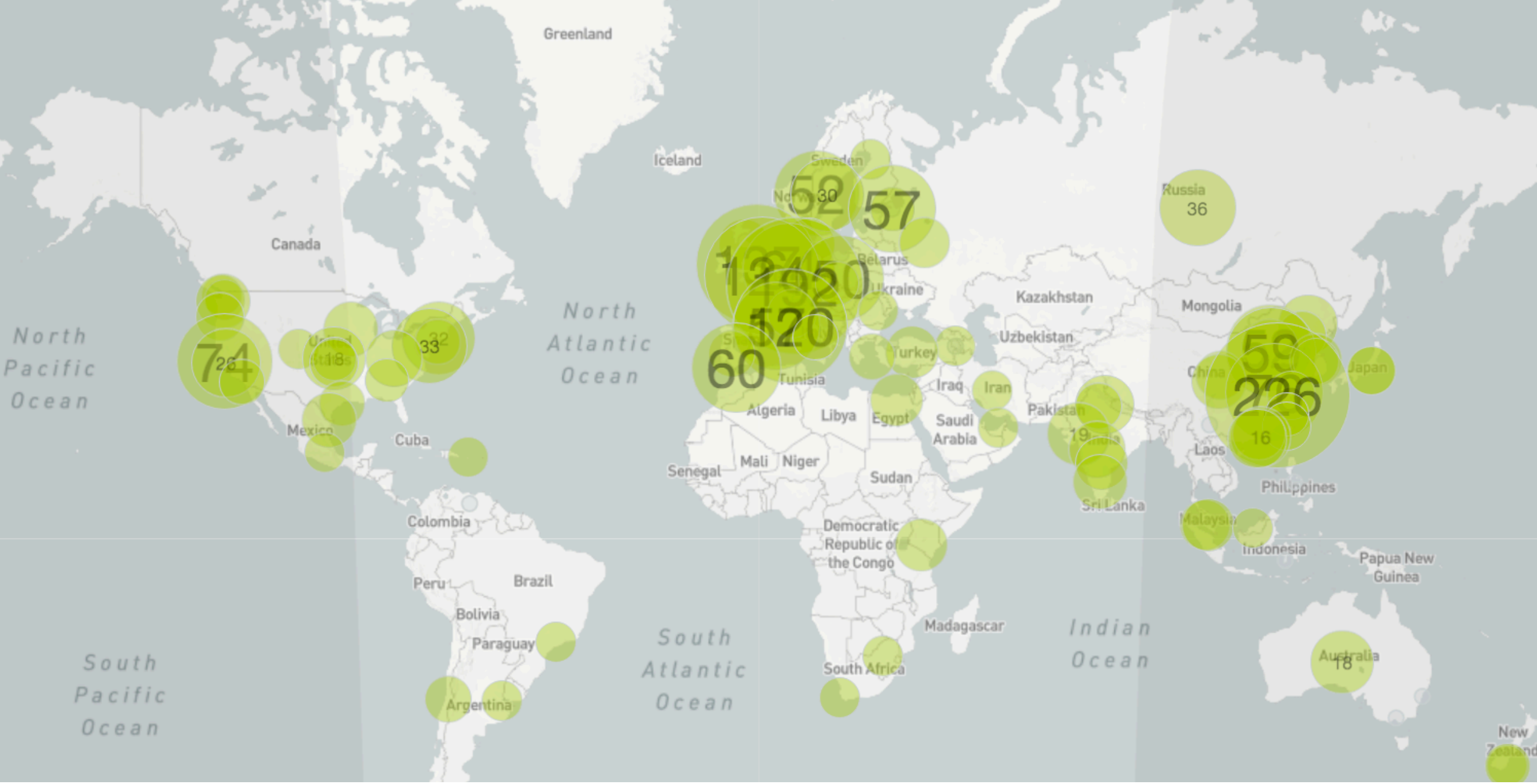


Opportunity:

Ownership of, and interest in, sequence can add productivity

The life science “machine”





https://www.ebi.ac.uk/web/livemap/live-data-map.html