FAIR GENOMES: community development of guidelines, schema & systems for reuse of NGS data

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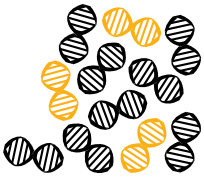
GENOME DATA IS UNFAIR

Next-generation Sequencing (NGS) has revolutionized healthcare and research, but the data is fragmented across providers and institutes. By making NGS data more FAIR (Findable, Accessible, Interoperable, Reusable), we can unlock their full potential for everyone's health benefit.



FINDING COMMON UNDERSTANDING

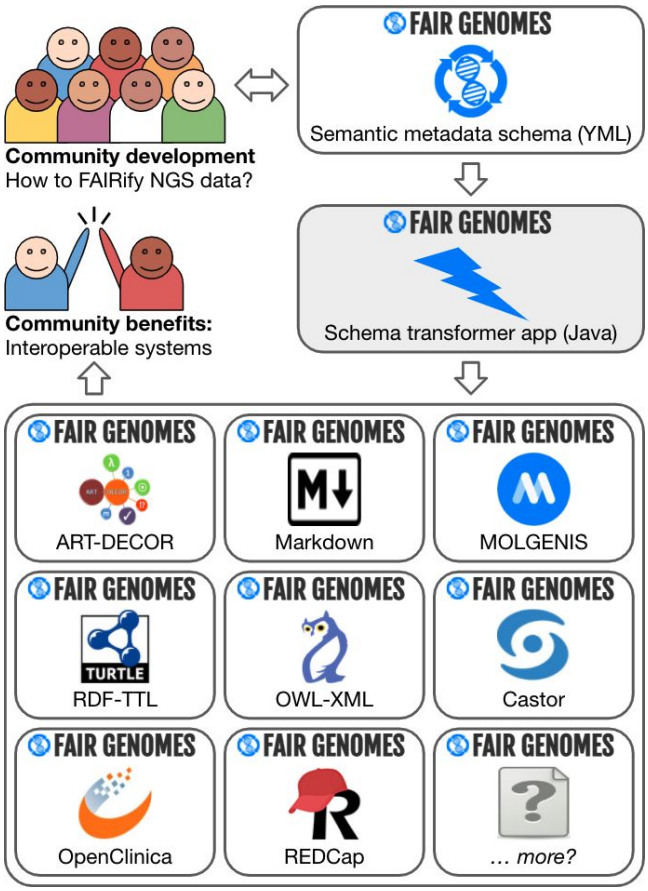
The FAIR Genomes consortium and friends (X-omics, EJP-RD, JRC CDE, 1+MG, SolveRD, GA4GH, MIABIS, ...) are creating a guideline and are defining data elements essential for sharing NGS data in a semantic schema. v0.2 has 107 elements in 9 modules, linked to common ontologies.

TRY IT YOURSELF AND JOIN US

Open source development:
https://github.com/fairgenomes
Public demo available:
https://fairgenomes-acc.gcc.rug.nl

SEAMLESS EDC INTEROPERABILITY

The schema is transformed into all formats for e.g. MOLGENIS. We plan to use iCRF Generator to also support Castor, OpenClinica and REDCap.



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ZonMw