

progenetix oncogenomic resource

Qingyao Huang^{1,2}, Paula Carrio-Cordo^{1,2}, Bo Gao^{1,2}, Rahel Paloots^{1,2}, Ziyang Yang^{1,2}, Michael Baudis^{1,2}

¹ Swiss Institute of Bioinformatics, 8057 Zurich ² University of Zurich, Winterthurerstrasse 190, 8057 Zurich

01

Introduction

Progenetix resource

The Progenetix oncogenomics resource provides sample-specific cancer genome profiling data and biomedical annotations as well as provenance data for cancer studies. Especially through more than 100k genomic copy number number (CNV) profiles from over 500 cancer types, Progenetix is the most comprehensive reference resources for copy number aberration in cancer, empowers comparative analyses vastly exceeding individual studies and diagnostic concepts as well as supports development of data standards and exchange protocols through Global Alliance for Genomics and Health (GA4GH). Database URL: progenetix.org

02

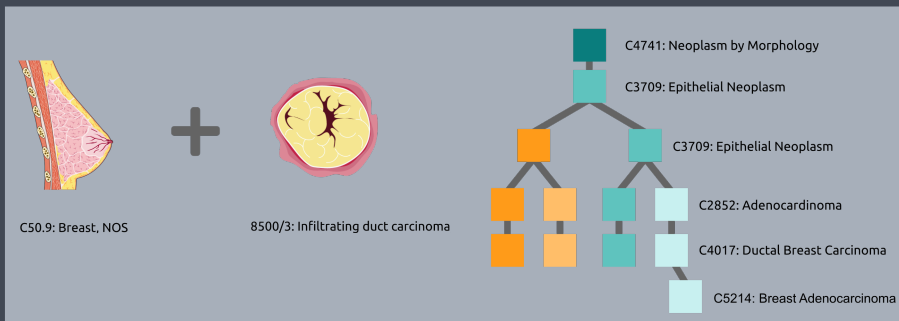
New meta-data

Domain-specific mapping

ICD-O system

v.s.

NCI thesaurus



ICD topography

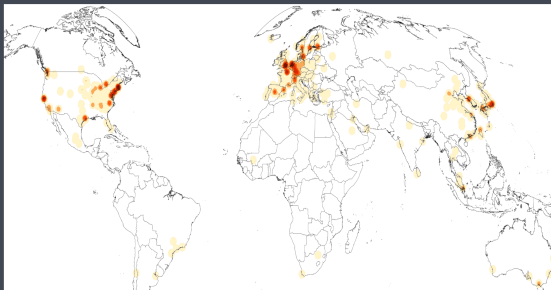
Geographic provenance

Clinical and diagnostic aspects



Uberon

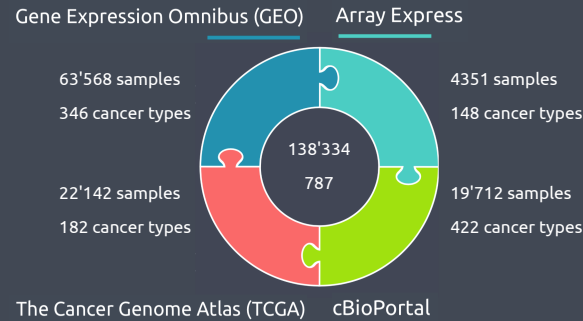
Cross-species anatomy
Developmental lineages
Cross-database reference
Spatial relations



03

New data sources

Sample expansion



04

Data standards

CURIE, GA4GH, Phenopackets schema

Findability

Accessibility

Interoperability

Reusability

FAIR

- Compact URI (CURIE) syntax, e.g. [pgx:pgxbbs-kftvgk8h](http://pgx.pgxbbs-kftvgk8h)
- GA4GH specification for variation data, i.e. individual -> biosample -> callset -> variant
- Phenopackets for phenotype data, i.e. id, phenotypes, EHR, provenance, biosample, biosample...

05

Beacon protocol

Features and prospects



- A Beacon answers a query for a specific variant against an individual or aggregated collection
- Support single or range query
- Filter by disease, phenotype, ...
- Authentication (to come...)



06

New web interface

Many features...

Just scan and visit...