



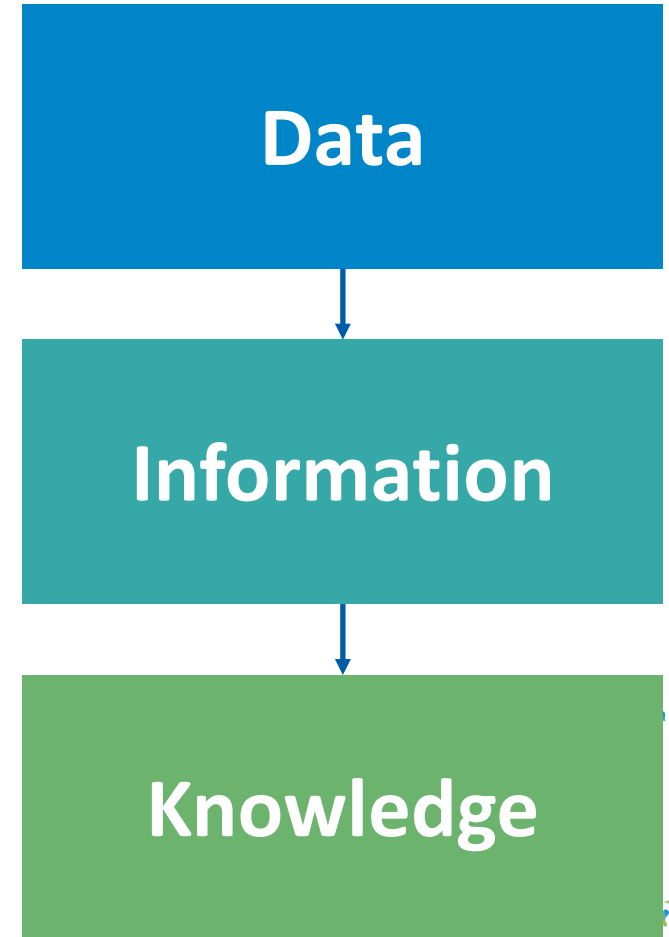
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Alberto Riva, Head of National Facility for
Data Handling and Analysis, Human Technopole

For technical enquiries about the services:
nf.datahandling@fht.org

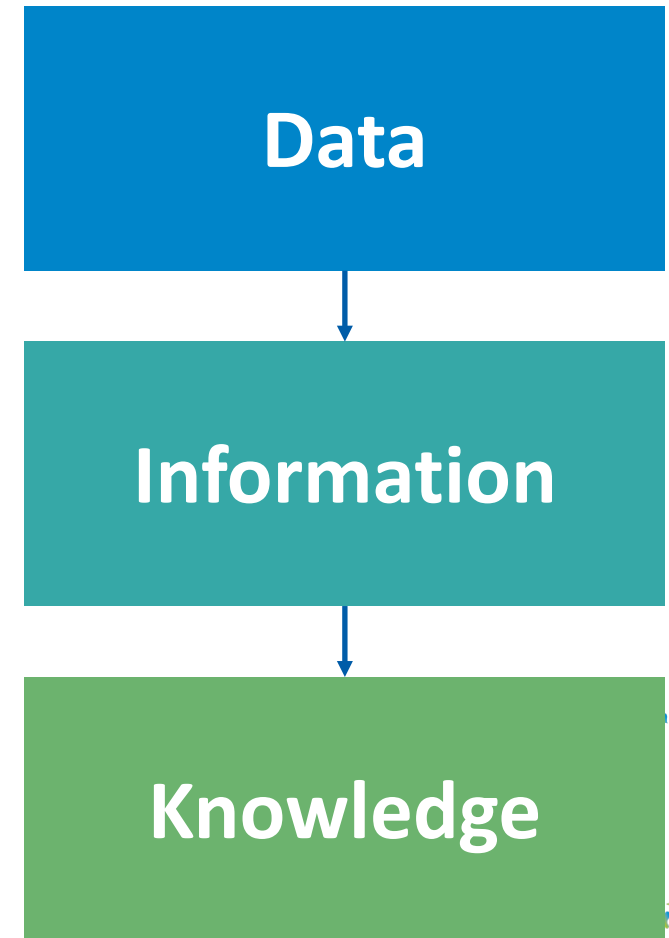
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- NF-DaHa
- **Main focus:** analysis and interpretation of biological data produced by other NFs (or outside sources).
- NF-DaHa is the only NF that does not *produce* data – but can work on data produced by all other NFs.
- What types of data, and what information can we extract from them?



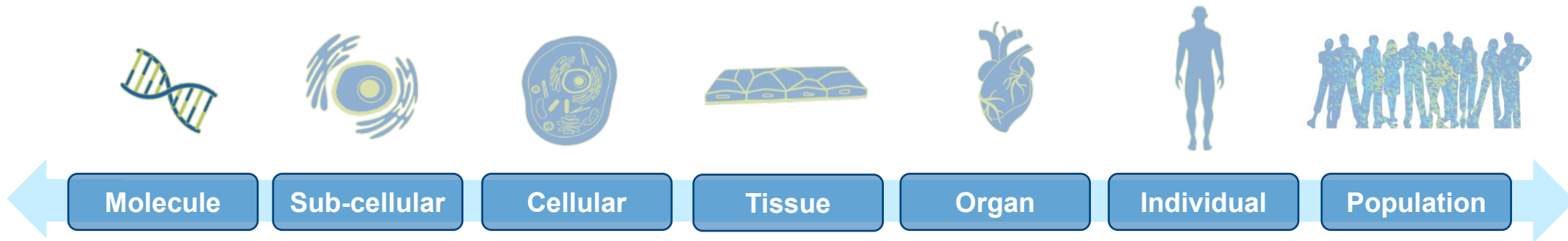
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- Types of data
- **Sequence data:** sequences from DNA or RNA molecules (and possibly proteins).
 - ← Genomics NF
 - ← Structural Biology NF
 - ← External sources
- **Bioimage data:** images produced by microscopy technologies.
 - ← Light Imaging NF
 - ← Genome Engineering and Disease Modeling NF
 - ← External sources



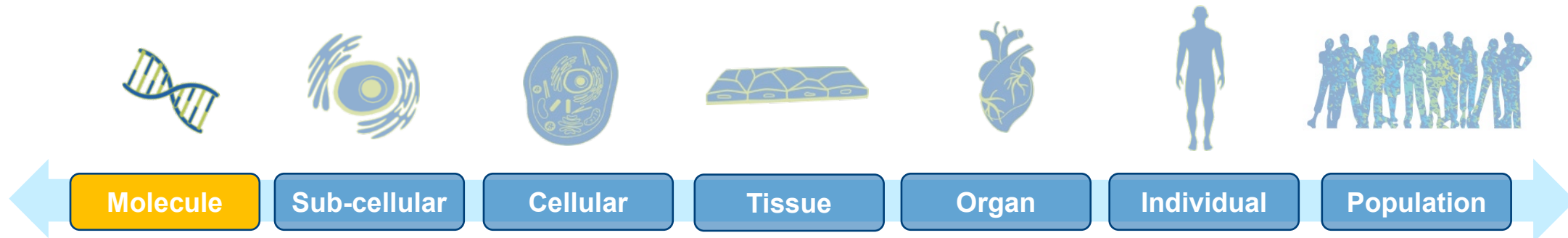
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What can we learn from each data type?



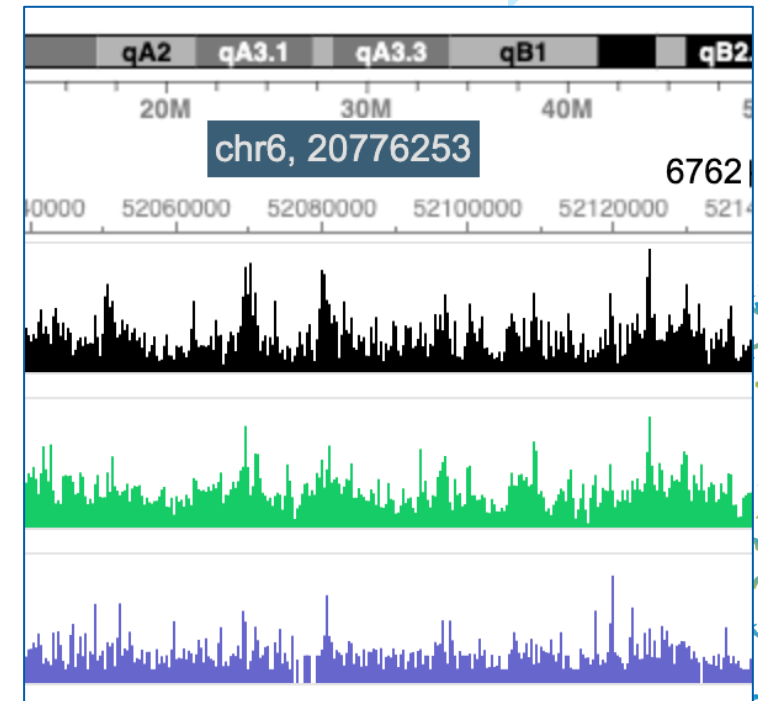
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What can we learn from each data type?



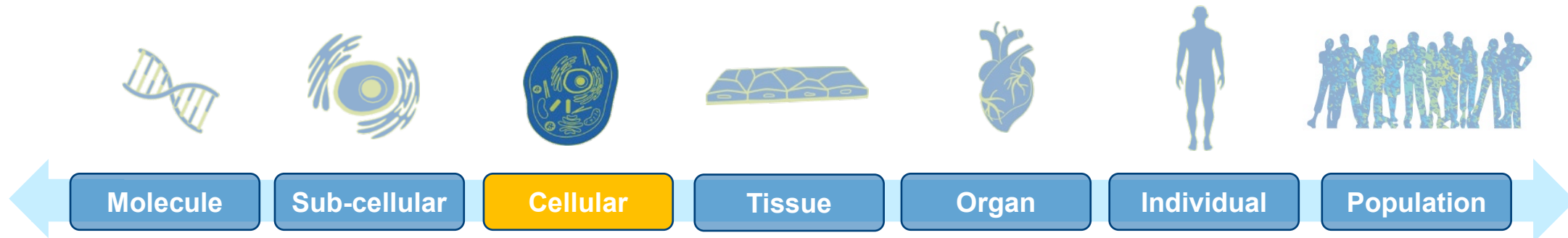
Molecular level: sequence of individual DNA or RNA molecules

- Presence of genetic and structural variants;
- Methylation state;
- DNA-protein binding, chromatin accessibility.



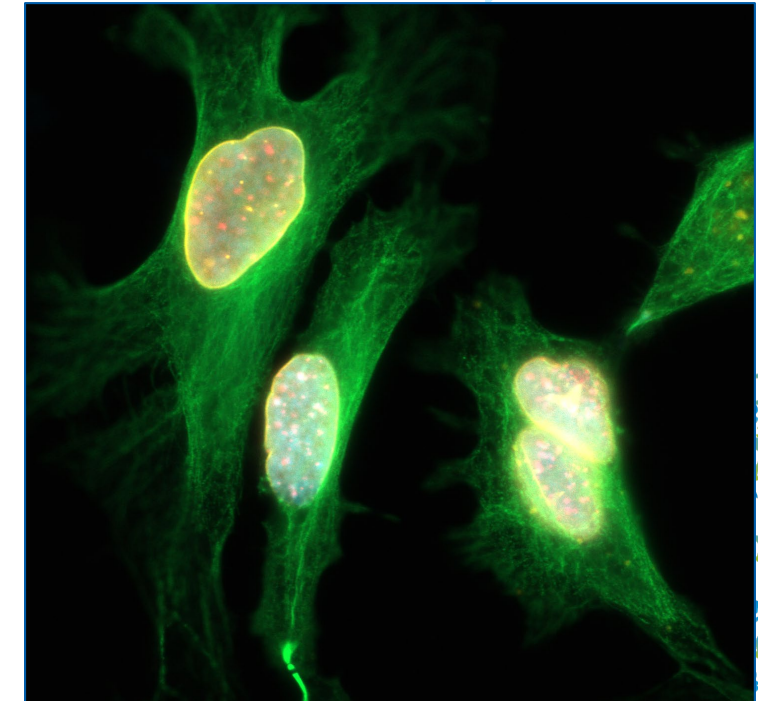
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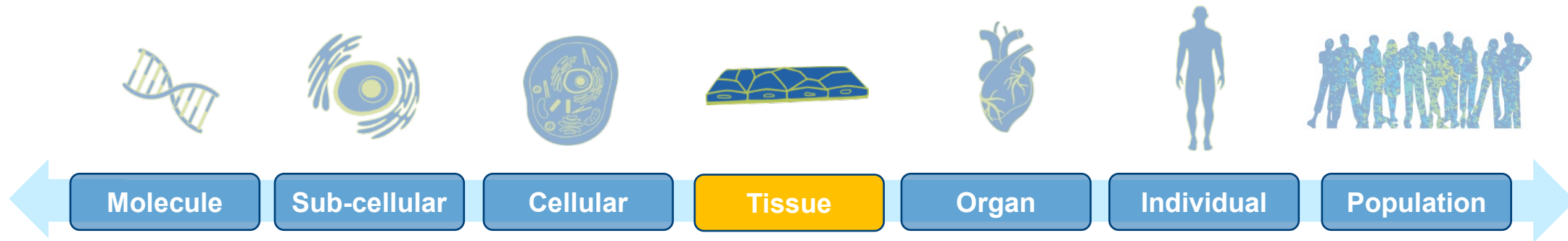
Cellular level: RNA molecules from individual cells; single-cell microscopy images

- Cell-specific gene expression patterns;
- Cell type identification;
- Cell differentiation, temporal trajectories;
- Spatial distribution of proteins within cells.



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What can we learn from each data type?



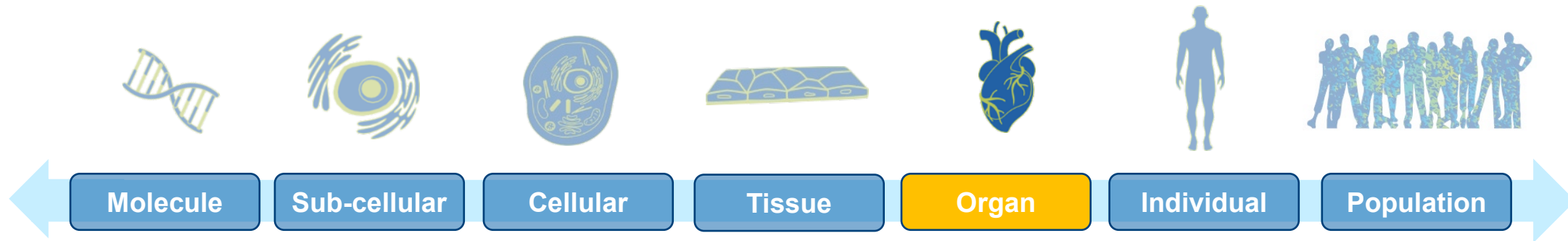
Tissue level: “bulk” gene expression

- Average gene expression values in a cell population;
- Differential gene expression in response to treatments or other stimuli;
- Spatial distribution of cell types in tissue.



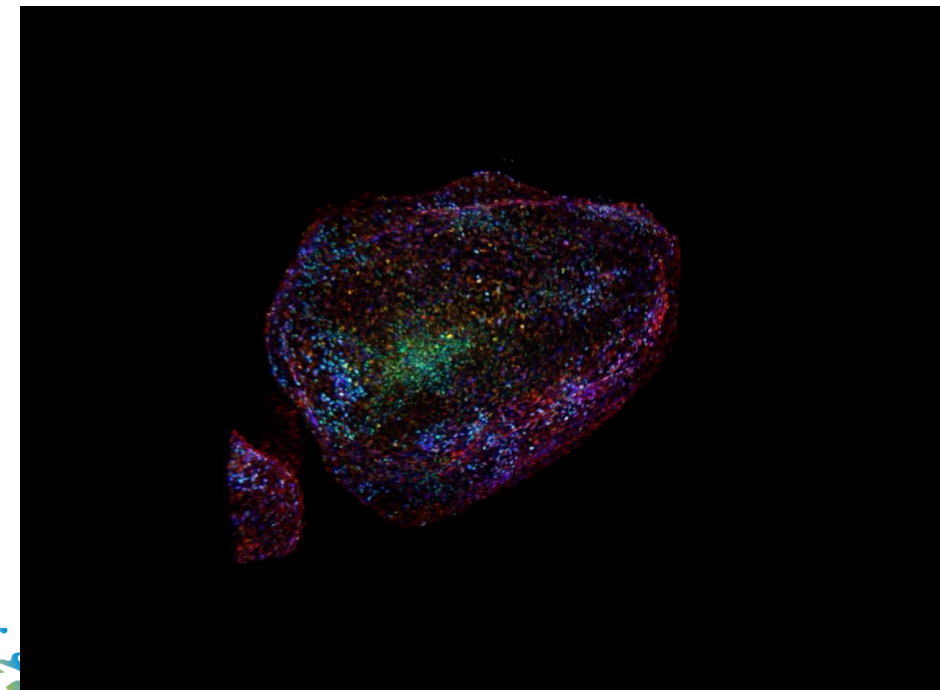
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What can we learn from each data type?



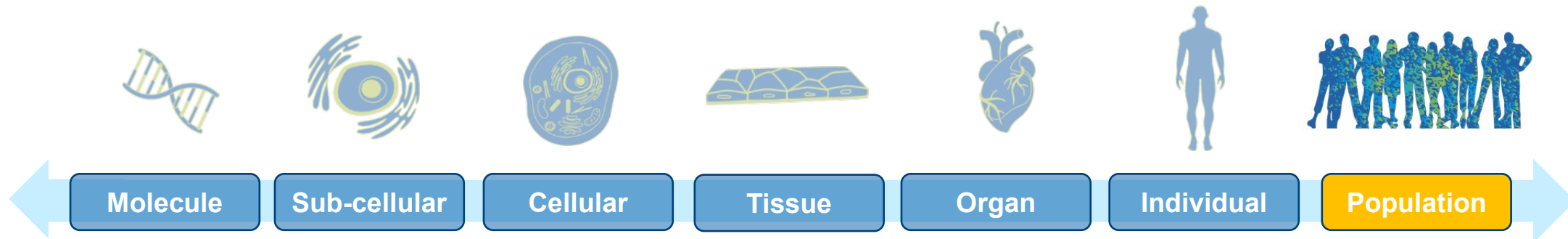
Organ level: spatial organization in 3D

- Relative positions of cells in an organ;
- Expression of markers for different cell types in different regions of the organ;
- Heterogeneity, development, internal organization.



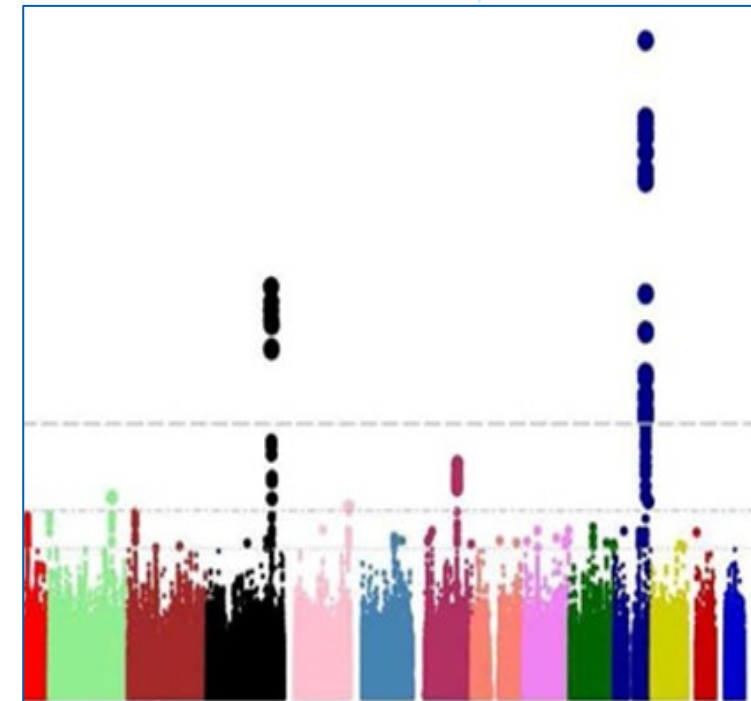
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What can we learn from each data type?



Population level: distribution and impact of genetic variants

- Correlation with disease prevalence, response to therapy, etc;
- Population health;
- Personalized medicine.



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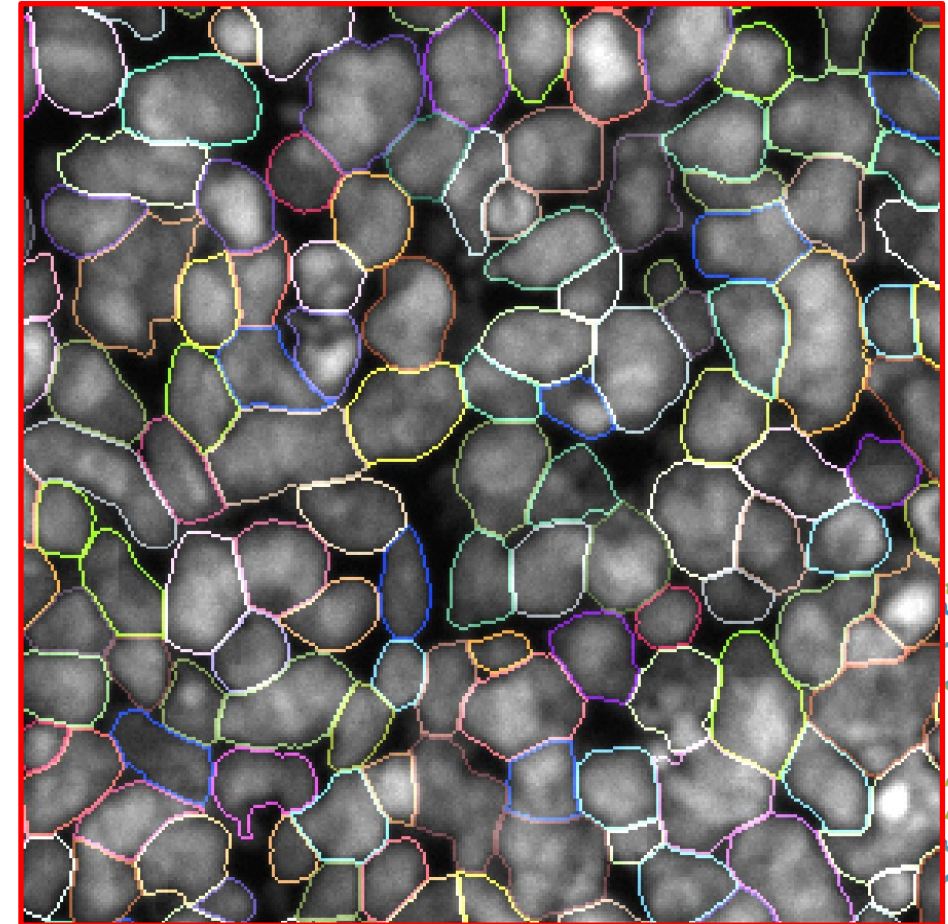
- Infrastructural Units
- **IU1:** Bioimage Analysis
- **IU2:** Omics Analysis
- **IU3:** DevOps and Web development

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- IU1 – Bioimage Analysis

Main services provided:

- High-quality image analysis solutions including quality control (QC), denoising and image restoration, segmentation, and basic quantification.
- Development of image analysis tools that are released as open-source to the broader community and included in the service portfolio.



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- IU3 – DevOps and Web Development

Main services provided:

- Developing and maintaining the computational tools and pipelines used by the NF.
- Creating and maintaining WebApps providing services to the scientific community.



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- Project life cycle

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- Project life cycle

1. Project kick-off



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- Project life cycle

1. Project kick-off

2. Quality assurance



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- Project life cycle

1. Project kick-off

2. Quality control

3. Methods and tools development



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- Project life cycle

1. Project kick-off
2. Quality control
3. Methods and tools development
4. Analysis



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- Project life cycle

1. Project kick-off
2. Quality control
3. Methods and tools development
4. Analysis
5. Delivery of analysis results,
data, pipelines



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- Empowering scientists

1. Project kick-off
2. Quality control
3. Methods and tools development
4. Analysis
5. Delivery of analysis results, data, pipelines

Training,
knowledge
transfer



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- Knowledge dissemination

Project results can be disseminated to the scientific community as:

- Raw and processed datasets submitted to public repositories;
- Easily accessible databases with high interoperability;
- Scientific software hosted and maintained by the facility.

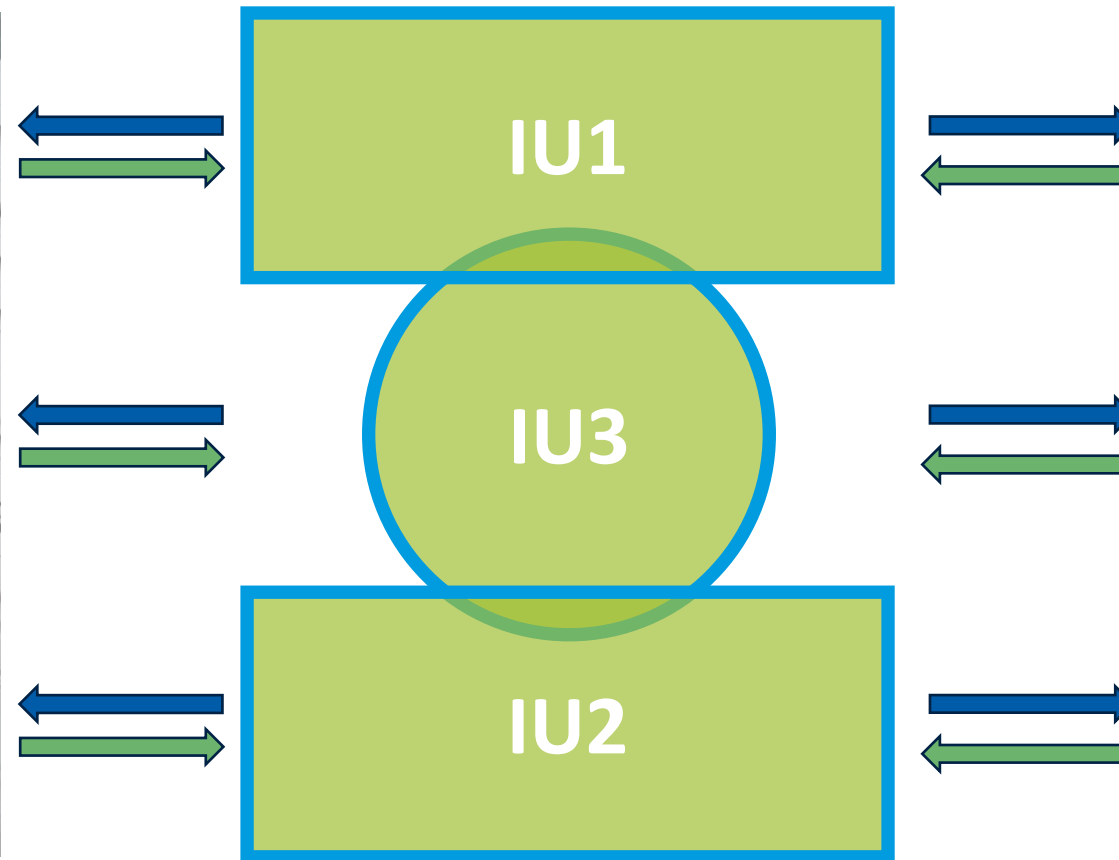


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- Computational resources
- In-house **HPC cluster**, with 2380 cores, 25 GPUs, and about 10 petabytes of storage space;
- Access to **cloud-based** computational resources;
- Planned: integration with European bioinformatics infrastructure (e.g. **ELIXIR**).



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Facility Members



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Head of National Facility for Data Handling and Analysis



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Backend/ DevOps Engineer



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Bioimage Analyst



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Senior Bioinformatics Technician



Eugenia Cammarota
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Melisande Georgia Croft
Research Software Engineer



Damian Edward Dalle Nogare
Manager Image Analysis Facility



Riccardo Roberto De Lucia
Software and Web Developer



Joran Deschamps
Image Analysis Researcher and Research Software Engineer Coordinator

Thank you

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