Hiaatanalyse (gap analysis) Genome Sequencing workgroup Datamanagement

Jeroen Belien (jam.belien@vumc.nl)
Associate professor, Amsterdam UMC, Vrije Universiteit Amsterdam
Department of pathology
Co-lead of research data IT infrastructure @BBMRI, CTO TraIT

Also on behalf of Morris Swertz and Anke Kip

Why?

- Re-use of genomic data
  - Clinical need: Personalized medicine; getting innovations faster to patients
  - Implementation of genomics (e.g. genome sequencing) in care
  - Improve Dutch research through timely national uniform implementation

- Role of ZonMw
  - Call: Development of an instruction manual (for FAIR) genomic data management
  - Start for this call: gap analysis

Assignment gap analysis

- **Inventory: meta data standards** for sequencing processes and data (this also concerns data for Health Technology Assessment) in the context of research into care applications in rare diseases and oncology.
- **Gaps and recommendations:** Based on the inventory, the gaps are described concisely and recommendations are made as to how these gaps can be addressed.
- **Advise for follow-up projects:** The report will include whether and how projects can be deployed from ZonMw (for example via a subsidy/call) to realize an improvement in the identified gaps.

Gap analysis: process followed

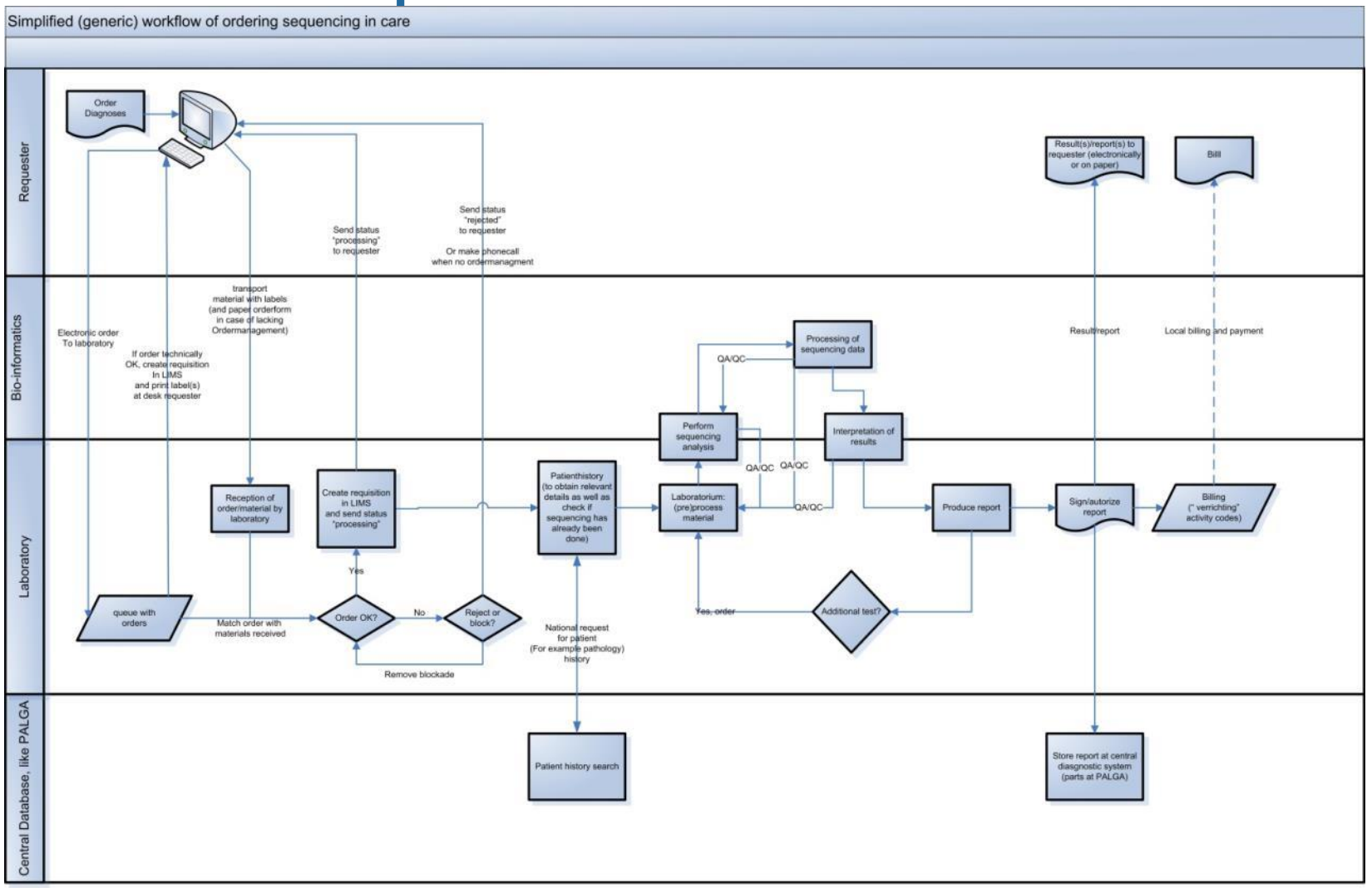
- Describe **generic process** for care (rare diseases and tumors) and / or research
- Drafting **questionnaire** regarding inventory (meta) data standards and retrieval of gaps
- **Interview** experts and ZonMw-PM projects (**20**)
  - 5 ZonMw PM projects, researchers, doctors (CG / PA)
  - Sequencing facilities, ELSI, bio-IT staff, HTA-ers
- Processing interviews and **identify gaps (129)**
- **Classify, prioritize, anonymize gaps**
- Processing to ZonMw **call (subsidy)**

Gap analysis: results

- I know what trip wires are (crashed with folding-bike over non-visible dog outlet line)

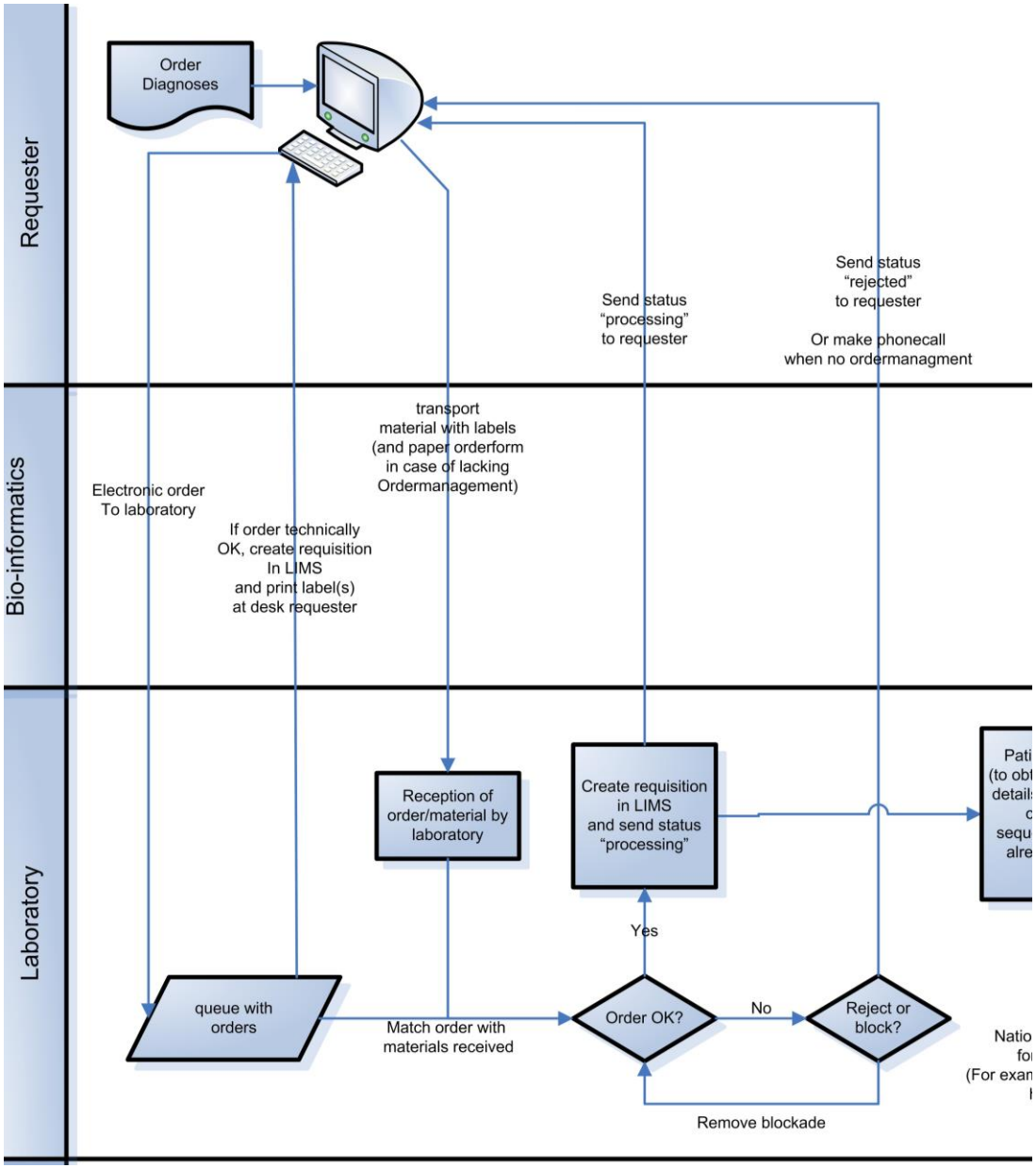
- Gap analysis has not yielded a tripwire, at most a variety of detectable hurdles

Results: Generic process care & research

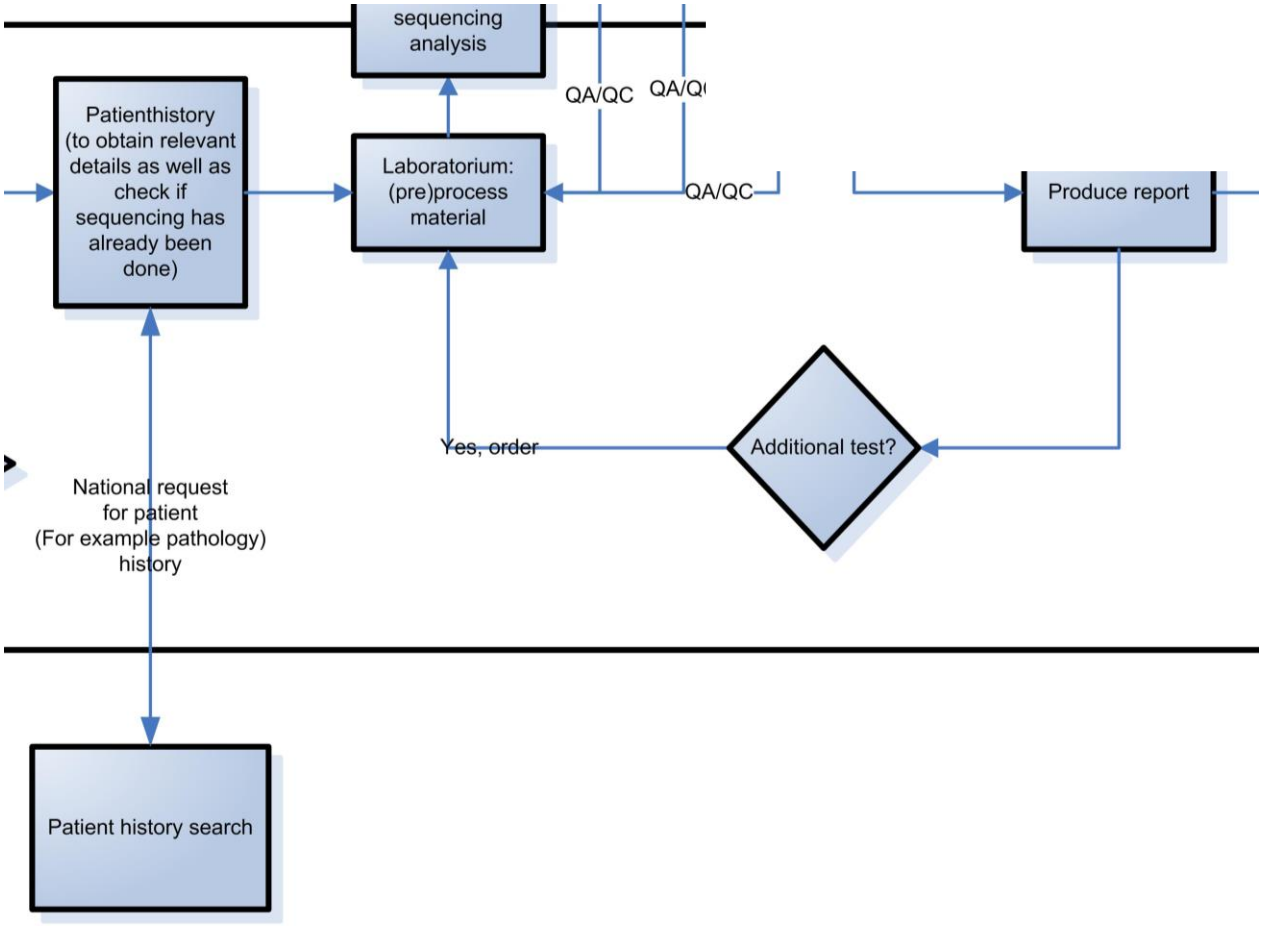


LIMS: Laboratory Information Management System
PALGA: Pathologisch Anatomisch Landelijk geautomatiseerd archief
QA/QC: check result, if necessary perform earlier step(s), etc.

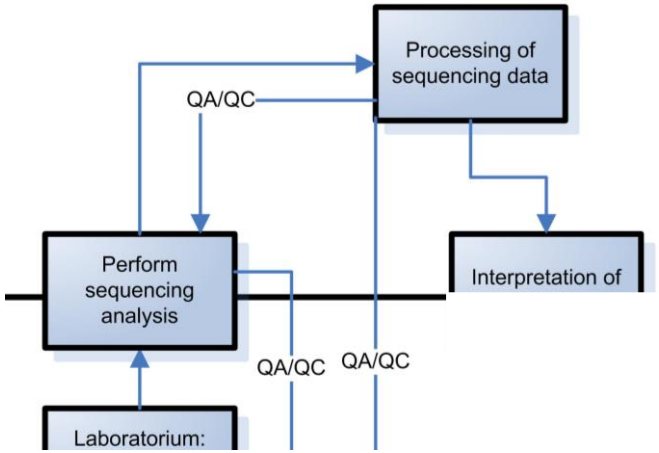
Zooming in on parts process: the request



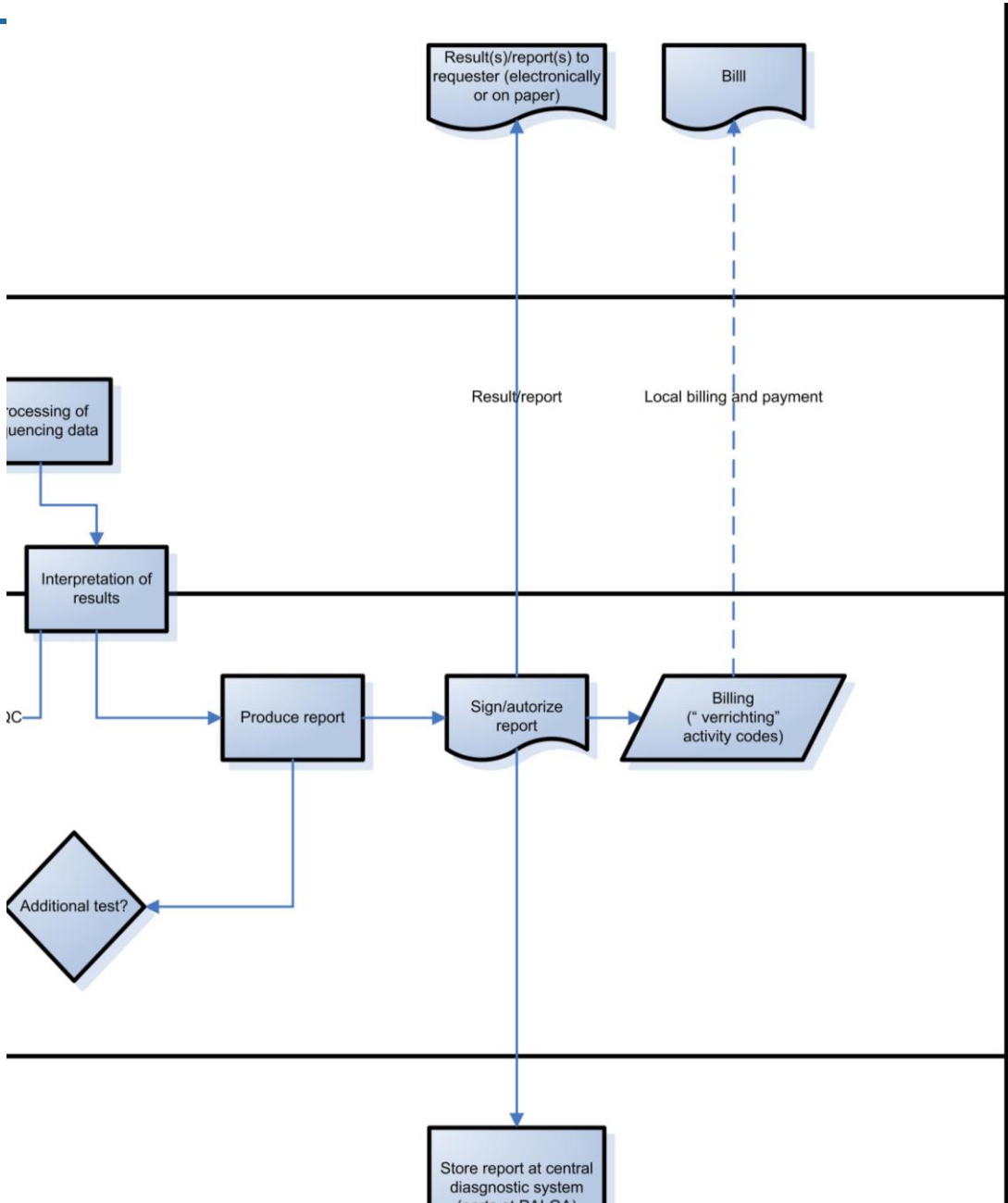
(pre)process material(s)



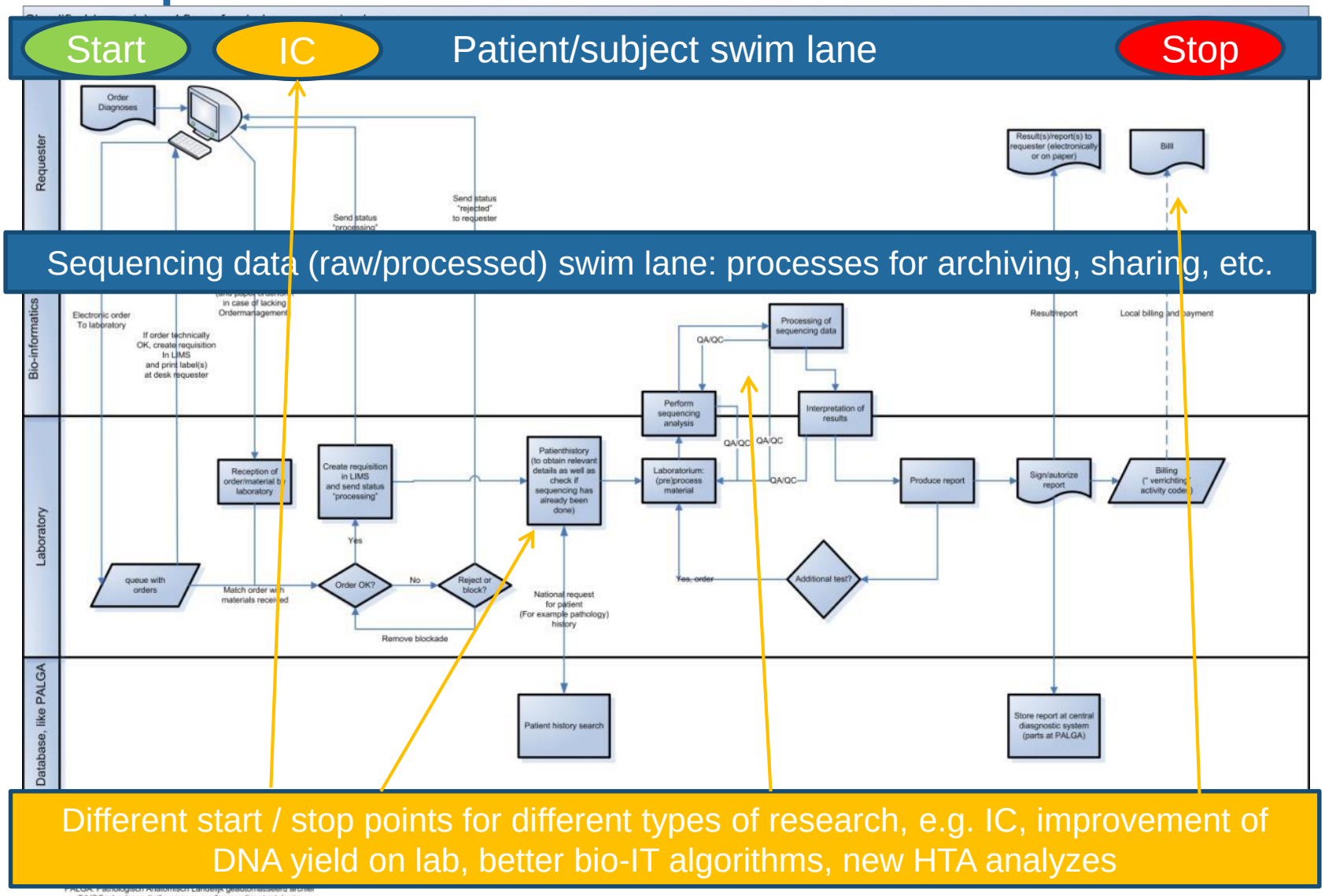
sequencing & analysis



Interpretation, reporting, and billing



Generic process care & research : modifications



Gaps highlighted: first example

- Doctor requests a cardiopanel. WGS is performed and doctor gets results/answer limited to cardiopanel only. In WGS, however, more abnormalities are found that are relevant for the patient, but they can not be included with cardiopanel request, otherwise it would be classified as screening.
  - Researcher could naively gain access to data that doctor (applicant/requester) has not seen

Gaps highlighted: second example

– Within software, the (reference) genome is often identified with self-designed strings (e.g. "chromosome1") instead of a unique identifier (NC_000001 and possibly versioned NC_000001.11). When adjustments are made to one of the programs, a problem arises further in the chain because the adjustment has not (yet) been implemented.

Gaps highlighted: third & fourth example

- Not being able to find out if someone else has already done DNA sequencing of a patient / study participant
- Unclear what can/can't be shared / (re)use(d) of (parts of) DNA data under the new GDPR (Dutch AVG) Act that is enforced since the end of May 2018. In this law, DNA (Data and derivatives thereof) belong to the special categories of personal data.

Next steps?

- Subset of identified gaps are part of the recently posted ZonMw call: Personalized Medicine Development of an instruction manual on genomic data management
- Other subset of identified gaps have a strong relationship with ELSI (Ethical, Legal and Social Implications/Issues) and have been handed to the ELSI-workgroup of ZonMw PM
- White-paper/Research-paper on the gap analysis

Thank you for your attention. We welcome any question or suggestion.

Jeroen Belien	jam.belien@vumc.nl
Anke Kip	anke.kip@lygature.org
Ilse Custers	custers@zonmw.nl
Morris Swertz	m.a.swertz@rug.nl

Special thanks goes to all persons interviewed as well as to the workgroup datamanagement of ZonMw PM