

10.07.2017 | PRESSEMITTEILUNG: 083/2017

Bessere Therapien dank Medizininformatik

BMBF fördert Medizininformatik mit über 150 Millionen Euro / Wanka: "Patientinnen und Patienten noch besser beraten und behandeln"



Bundesforschungsministerin Johanna Wanka und Alexander Hörbst mit den Vertretern der vier Konsortien, die für eine Förderung vorgesehen sind. v.l.: Alexander Hörbst (Vorsitzender des Gutachterkreises), Klaus A. Kuhn (DIFUTURE), Markus Löffler (SMITH), Roland Eils (HiGHmed), Johanna Wanka, Hans-Ulrich Prokosch (MIRACUM)

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MEHR ZU:

→ zurück zur Übersicht

Pressereferat

Pressemitteilungen

Bildmaterial



LINK

➤ Medizininformatik-Initiative: Digitale Vernetzung im Gesundheitssystem stärken




VIDEO



Medizininformatik: Ein Schatz, den es zu heben gilt



ZUM THEMA MEDIZININFORMATIK UND DEN GEFÖRDERTEN

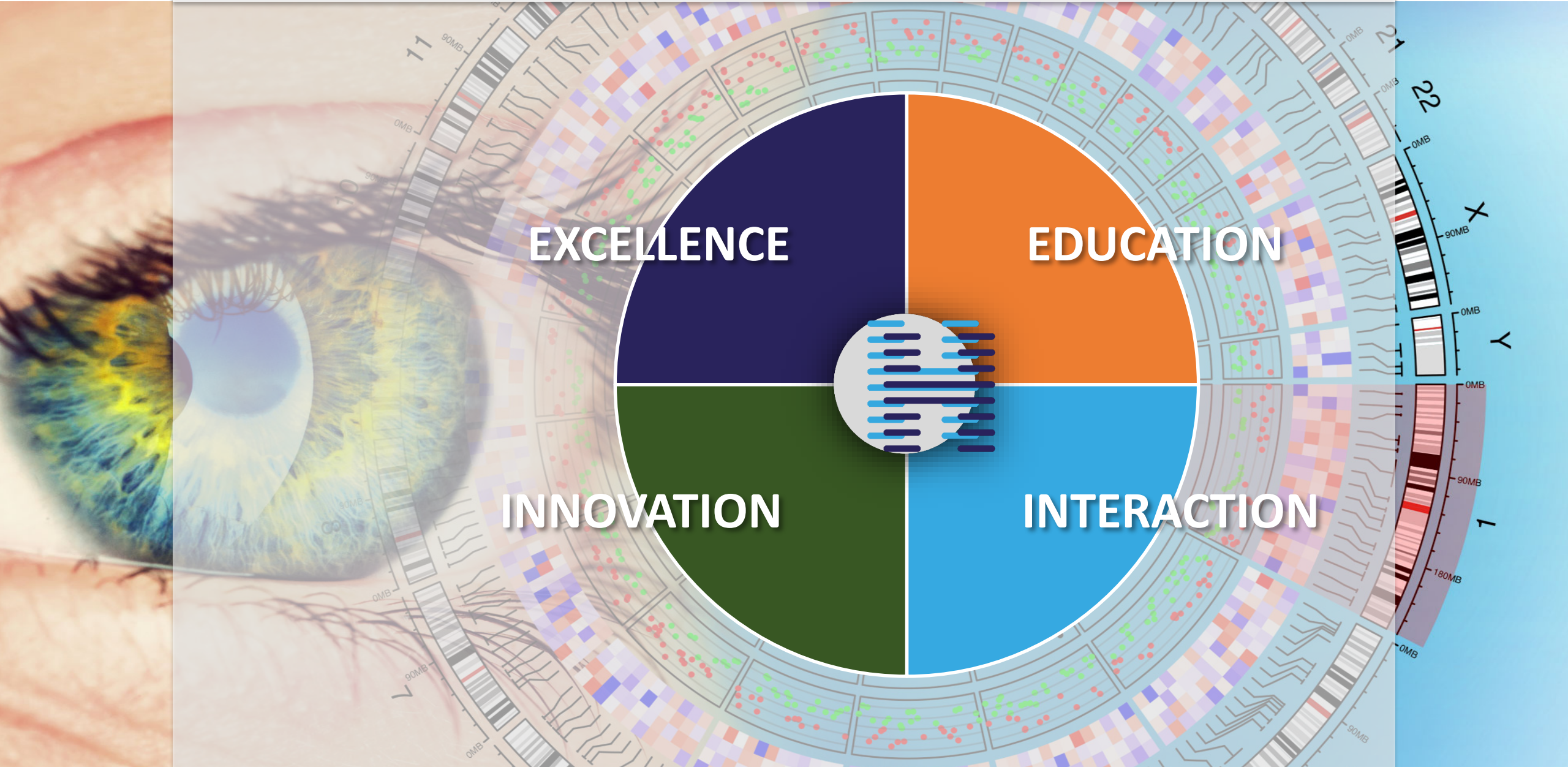


i2b2/tranSMART@HiGHmed:
Migration of intensive care unit (ICU) data into a medical research data mart.

Paris, October 5, 2017, i2b2/tranSMART 2017 European Meeting

B Baum, CR Bauer, G Nußbeck, Ulrich Sax

The HiGHmed Approach



EXCELLENCE

EDUCATION

INNOVATION

INTERACTION

The HiGHmed Approach



EXCELLENCE

EDUCATION

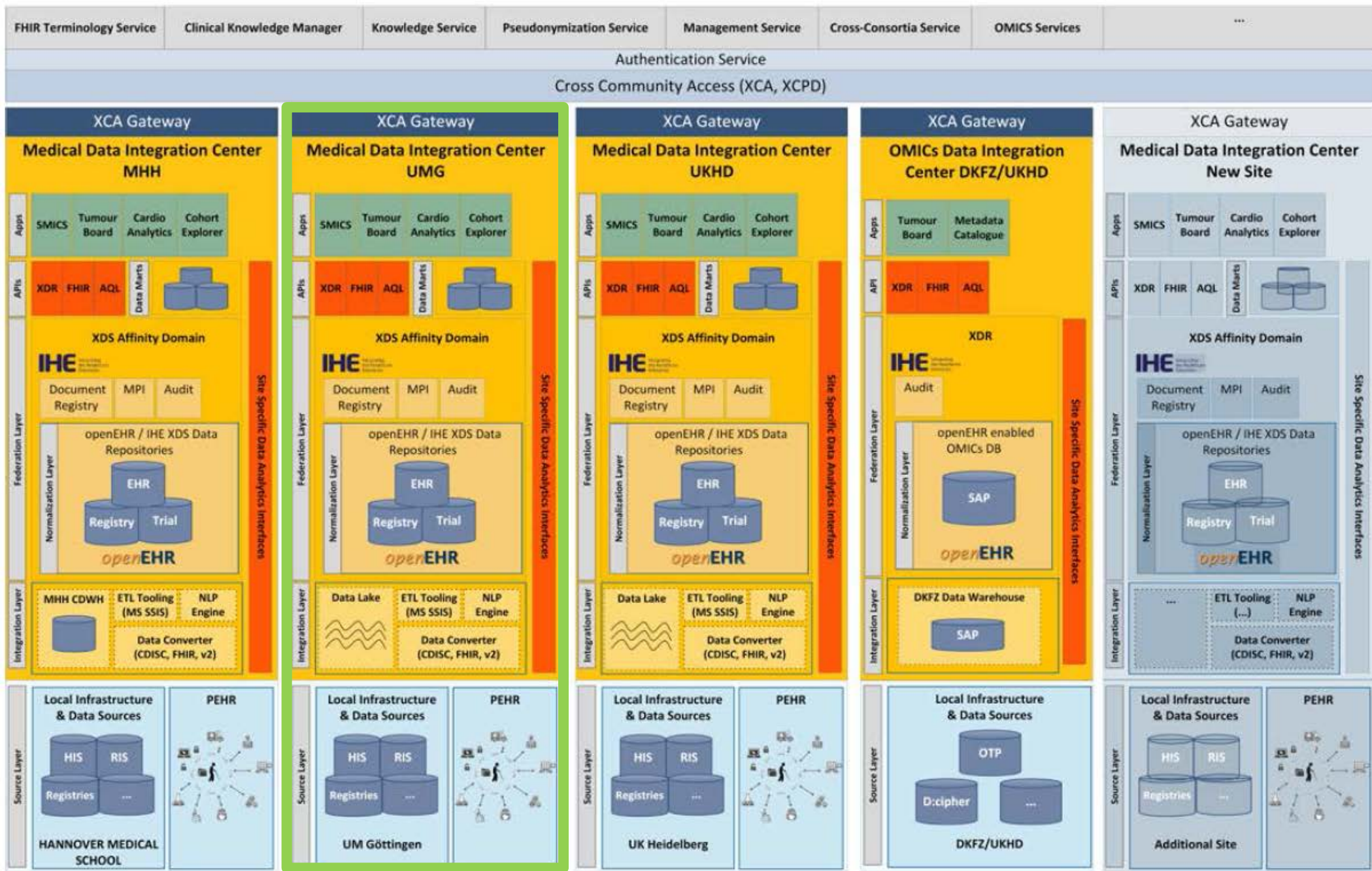
INNOVATION

INTERACTION

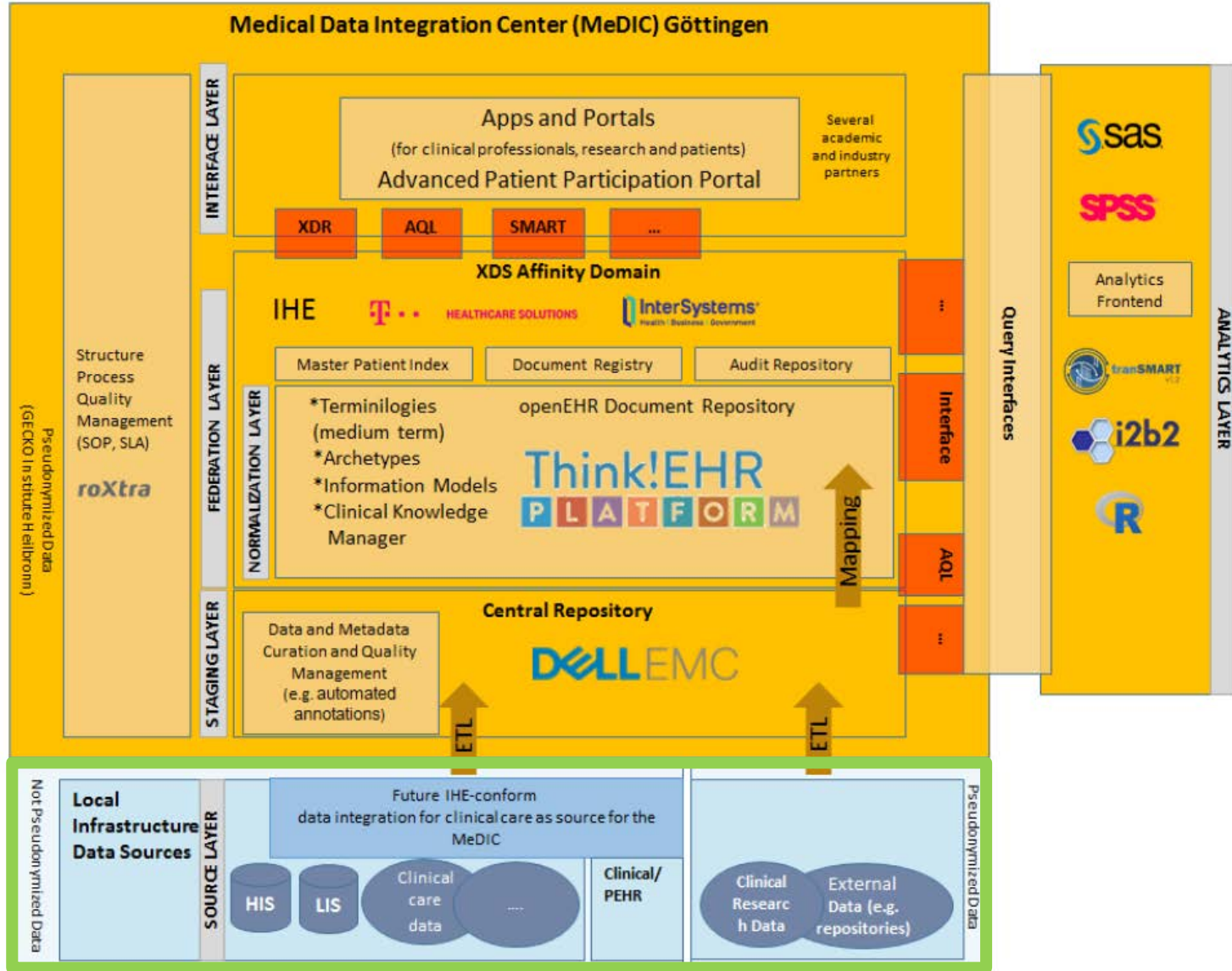


Interaction

- Systematic use of open platforms following **FAIR principles**
- Permanent adoption of **national standards (NSG)** and **interaction** with other MI-consortia
- Open standards** for health information exchange → Personal cross-Enterprise Health Record (PEHR)
- Platform for **cross-enterprise data analysis** combining openEHR and IHE XDS
- Data scientists** and data **stewards** to work with clinicians for data structuring
- Emphasis on **patient involvement**

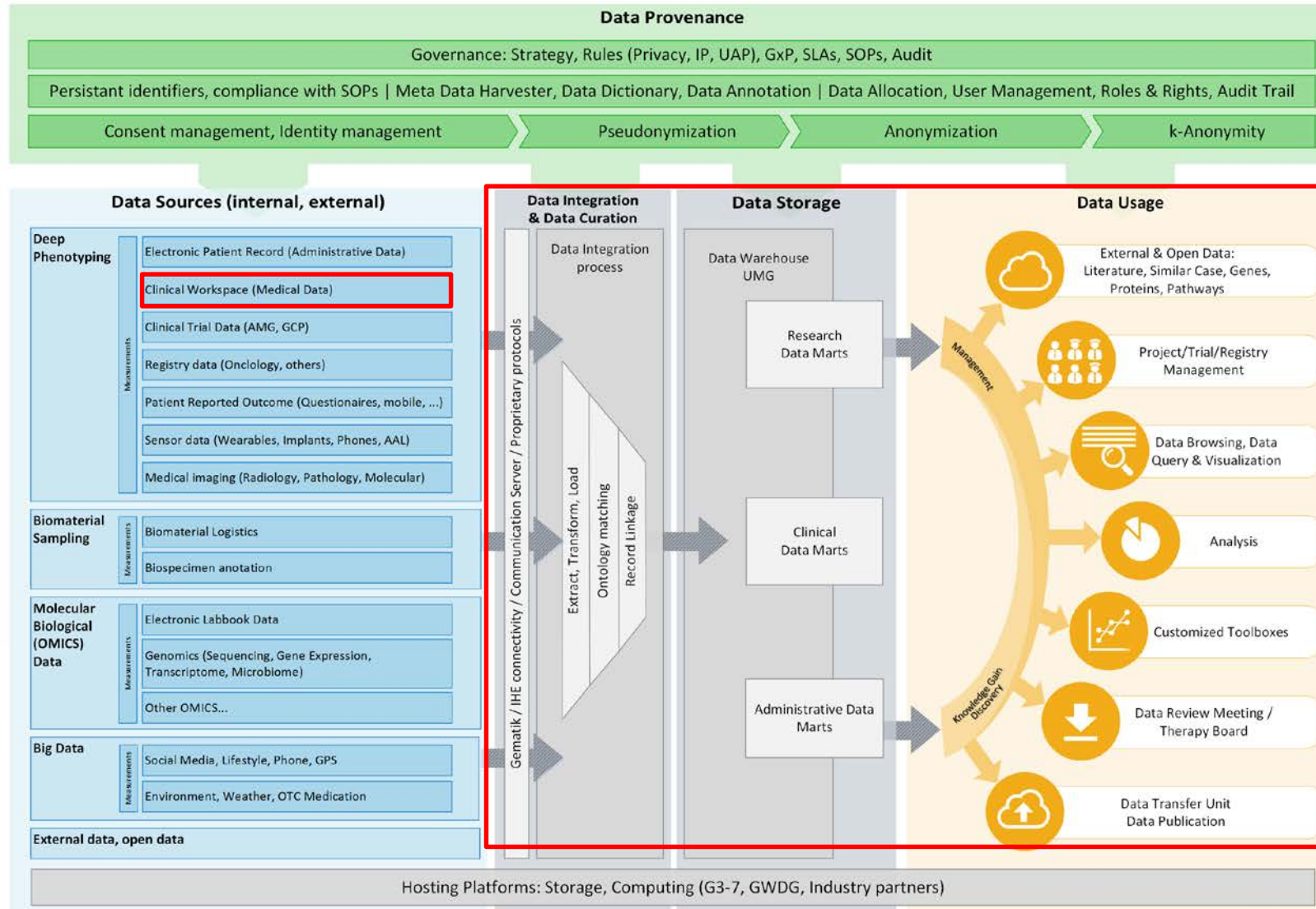


UMG MeDIC



Data management pipeline

UNIVERSITÄTSMEDIZIN GÖTTINGEN UMG



Introduction

- Retrospective evaluation and analysis of ICU data
 - Data from 2015/2016
 - 7000 Patients
 - 200 Million Facts
- Stored in ICCA (Philips)
 - Not easily accessible
 - No cross-patient query
 - No sorting or filtering

- Goal: Migration of ICU data into a clinical research data mart
- **Goal: make data accessible for Infection control use case of HiGHmed (MI-I, BMBF)**

tranSMART vs. ICCA

Navigate Terms

- [-] Across Trials
- [-] Internal Studies
 - [-] ICCA
 - [-] Aerztl. Aufnahme ANAE
 - [-] Anamnese
 - [-] Patientendaten
 - [-] Alter
 - [-] Art der Aufnahme / SAPS II
 - [-] Aufnehmender Arzt
 - [-] BMI
 - [-] Chron. Leiden (SAPS II)
 - [-] Geburtsdatum
 - [-] Groesse
 - [-] KOF
 - [-] Pat.-Typ
 - [-] Stationsaufnahme ANAE
 - [-] Art der Aufnahme
 - [-] ASA Klassifik.
 - [-] Aufnahme von
 - [-] Aufnahmeindik.
 - [-] Aufnahmezeit
 - [-] aus ext. Klinik
 - [-] aus UMG
 - [-] Trauma
 - [-] Wiederaufn. ICU
 - [-] Zuw. Stationnr.
 - [-] Aerztl. Aufnahme ANAE-AWR
 - [-] Aerztl. Verlegungsbericht ANAE
 - [-] Antrag auf Anschluss-Rehabilitation
 - [-] Beatmung
 - [-] Blasenspuelung
 - [-] Ergotherapeutischer Befund
 - [-] Ergotherapie
 - [-] Haemofiltrationsprotokoll
 - [-] Infektionsverlauf
 - [-] Konsil Chirurgie
 - [-] Konsil Innere
 - [-] Konsil Neurochirurgie
 - [-] Konsil Psychiatrie
 - [-] Konsil Spezial

Ärztl. Aufnahme ANAE

Warnhinweise Hygiene (ausschl. autom. Übermittlung durch Patientendaten)

Patientendaten

Aufnehmender Arzt

Stationsaufnahme ANAE

Geburtsdatum

Alter

Größe

Gewicht* (Aufnahme)

Körper-Masse-Index

Körperoberfläche

Art der Aufnahme (SAPS II)

Chron. Leiden (SAPS II)

Patiententyp

Nächste Angehörige

Anamnese

Vorerkrankungen

Abteilungsdiagnose

KH-Aufnahmediagnose

Liegedauer

Dauer-/Vormedikation

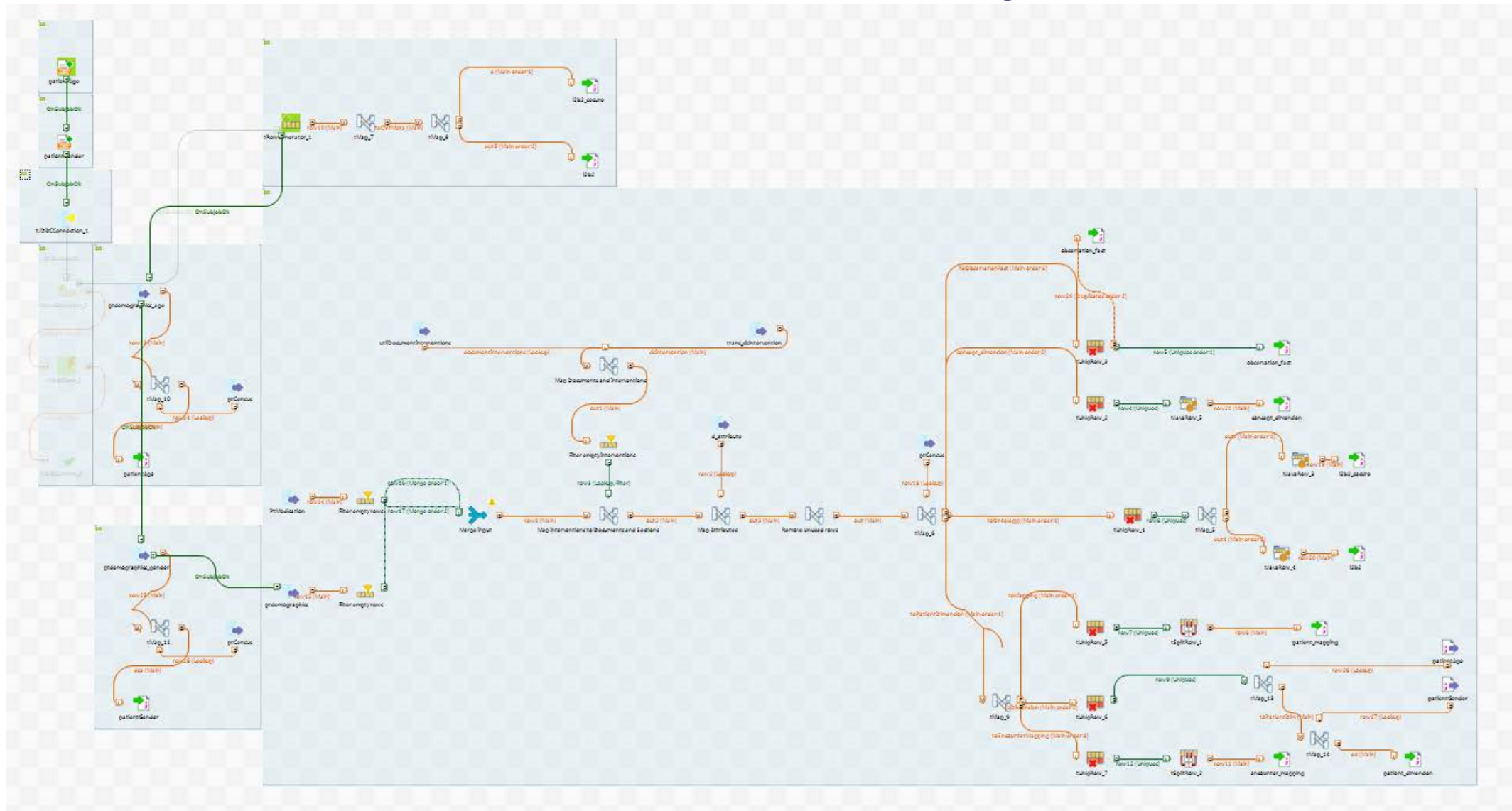
Therapie/Operation

Vorgeschichte

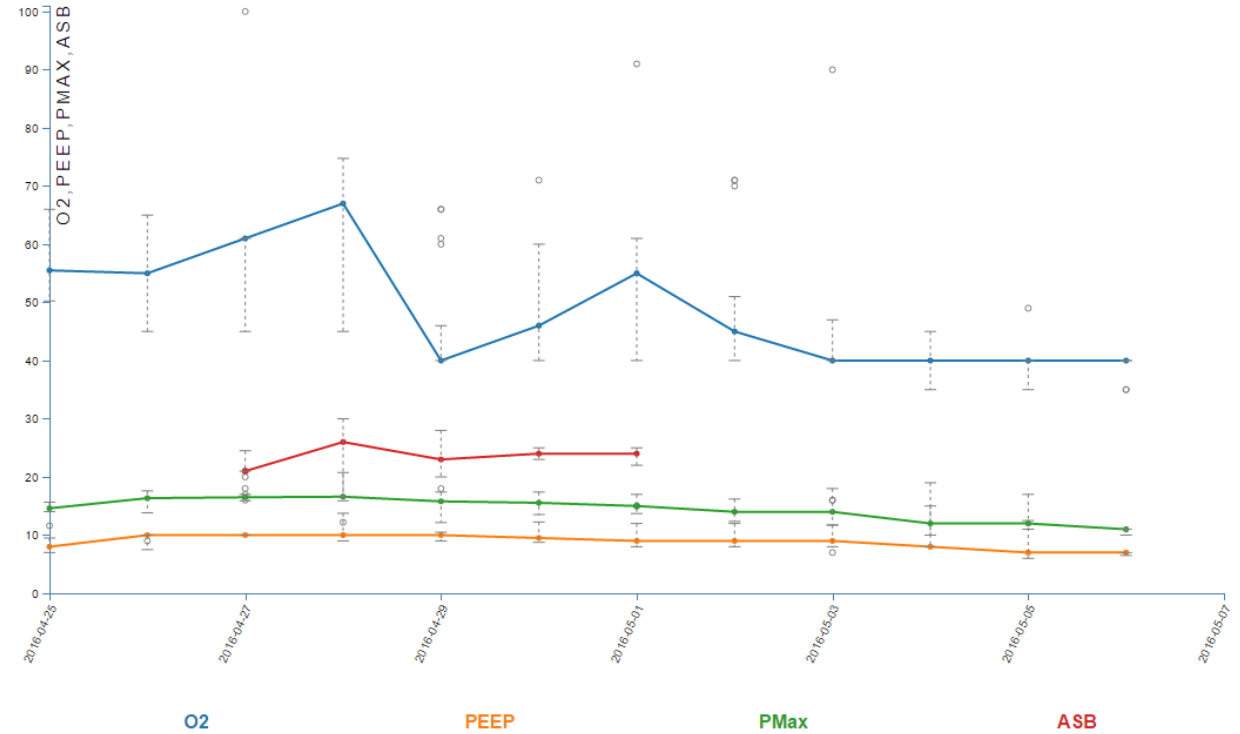
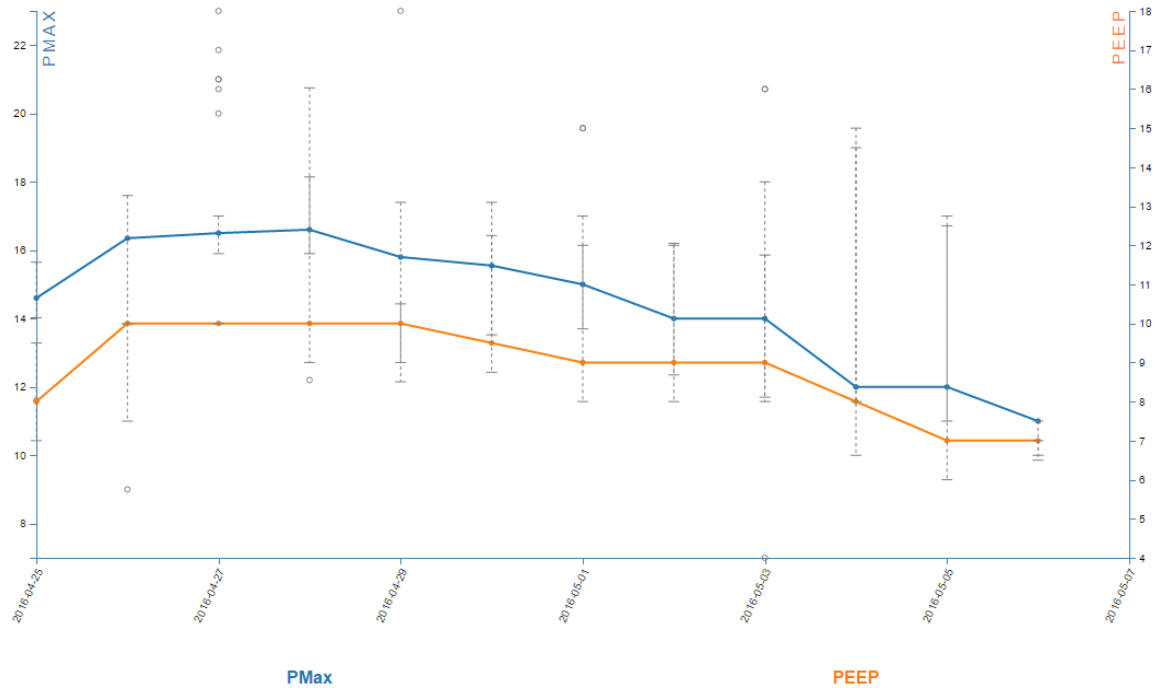
Mikrobiologische Befunde

Antibiotika

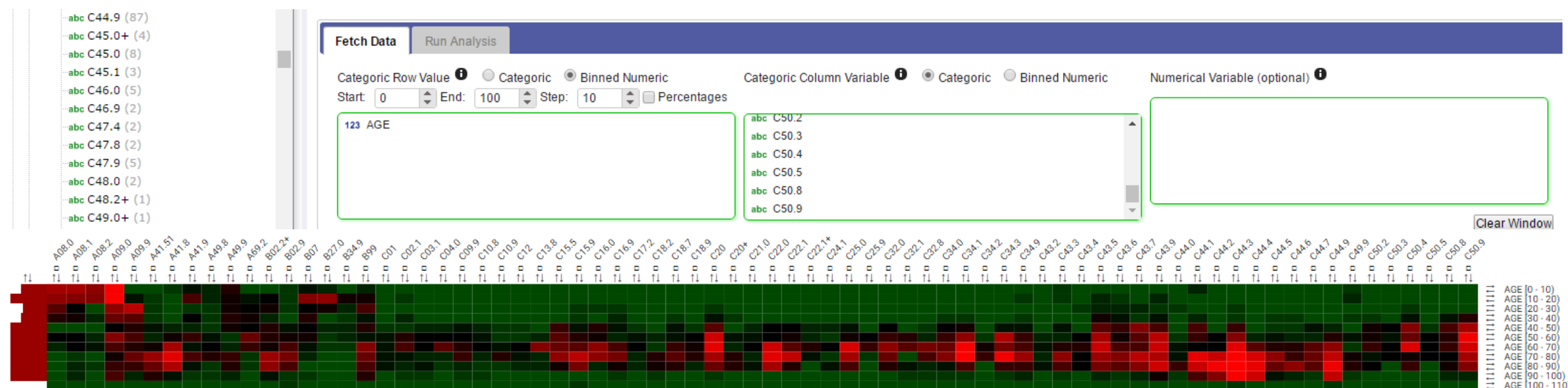
Extraction of UMG ICU data and Loading in tranSMART



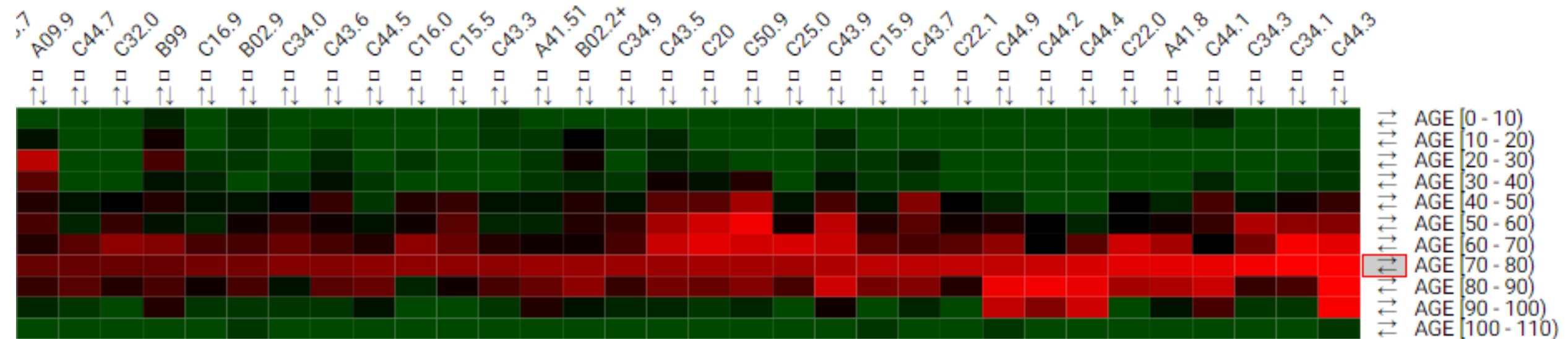
tranSMART Visualization



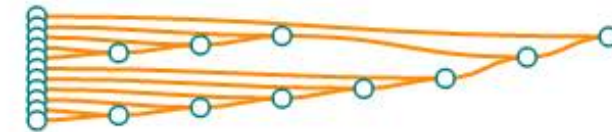
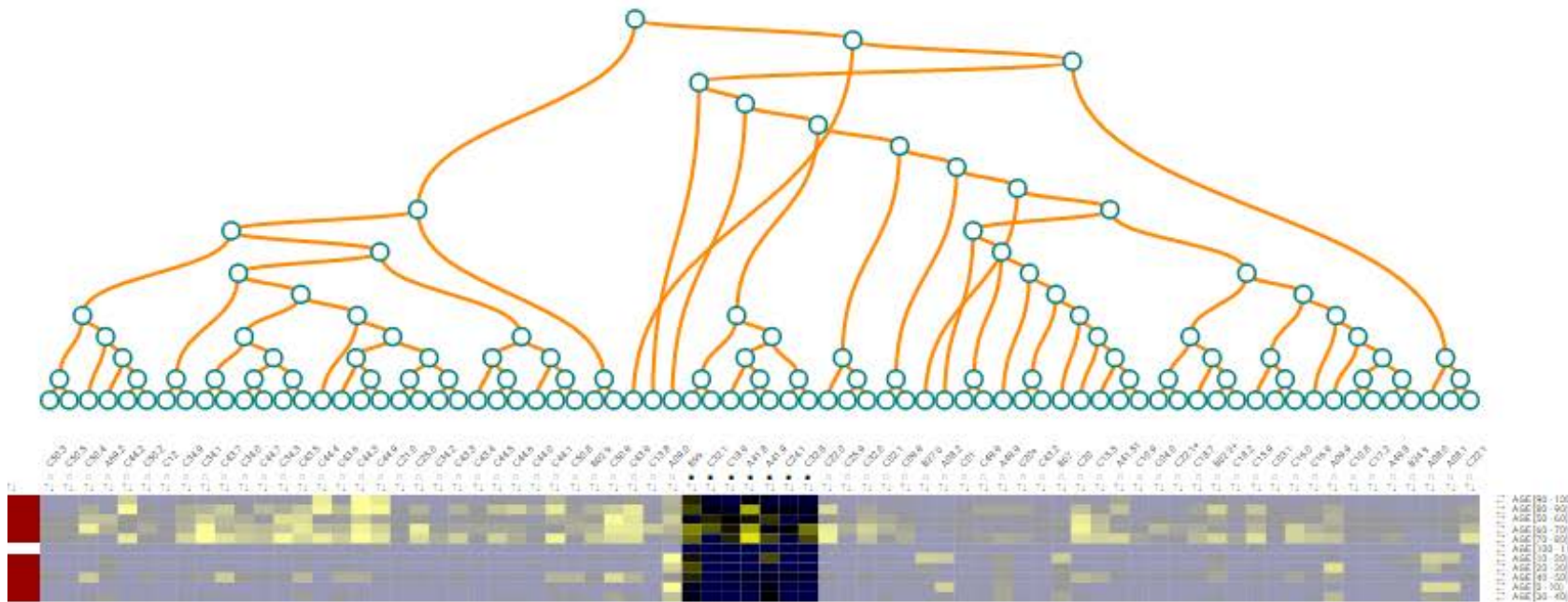
- Builds a correlation between two sets of phenotype data
- Uses patient numbers or a numerical value for weighting
- Allows to quantitate numerical values into categorical ones



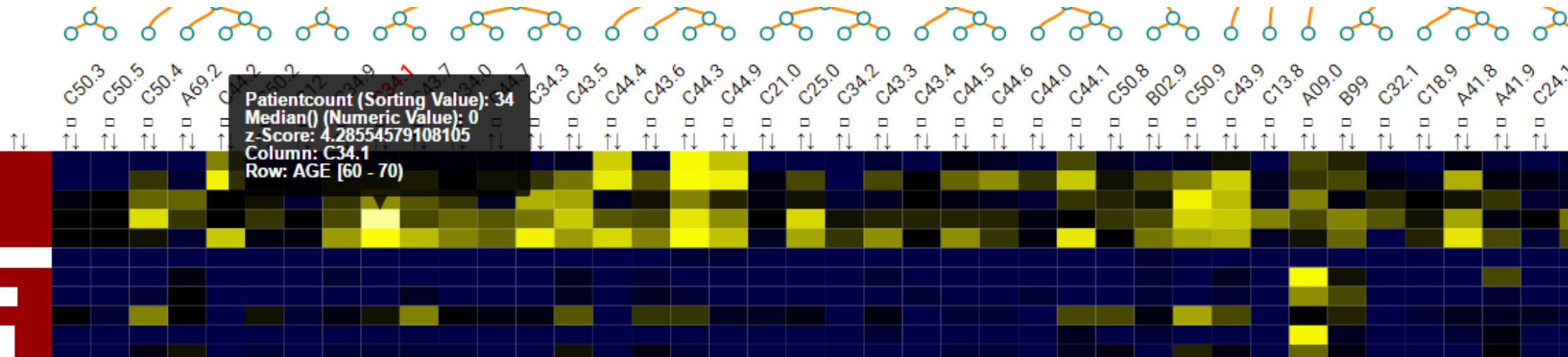
- Features same functionality like SmartRs genotype heatmap:
sorting, color sets, clustering and additional information



- Features same functionality like SmartRs genotype heatmap:
sorting, **color sets**, **clustering** and additional information



- Features same functionality like SmartRs genotype heatmap: sorting, color sets, clustering and **additional information**



Chances and Challenges

- Data Source is a medical product
- No data dictionary, dynamic labeling (!)
- Twofold Export:
 - Structure
 - Data
- Privacy challenge (solvable)
- Data Review meetings very useful for Dialogue
- IP challenge (probably not solvable)
- Important data source for MI-Initiative meDIC

Results

- Upload of most ICU data into tranSMART database
 - database partitioning for better performance done
- Dynamic creation of tranSMART search tree by uploaded data
- tranSMART search tree complies to ICCA tabs
- Timeline data not applicable in current tranSMART
 - Grouping of timeline data by patient and enumeration during ETL
 - Example: PEEP 001 = 200, PEEP 002 = 230 for patient X
 - Therefore: Actual dates of events are not used, but comparison of patient easier
 - Repeating events (modifier) and time based queries and analysis are already solved in current i2b2 released

Outlook

- Extension of timeline visualization
 - interactive zoom, scrolling, patient selection
 - additional standard statistical visualization
- More phenotype visualizations needed
- Add additional data sources to ICU data
- Continued data review meetings
- Include more data sources for local and for HiGHmed purposes

Retreat 2017: The Goettingen ML team grows rapidly!



Excellence

Associate Partners




Private and Networking Partners



Academic Partners

ROBERT KOCH INSTITUT





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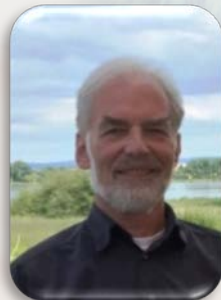
Thank you...



Roland Eils
Clinical Genomics



Björn Bergh
Clinical Information Systems



Otto Rienhoff
Collaborative Clinical Research



Michael Marschollek
Sensors and Interoperability



Ramin Yahyapour
Data Management and Analytics