

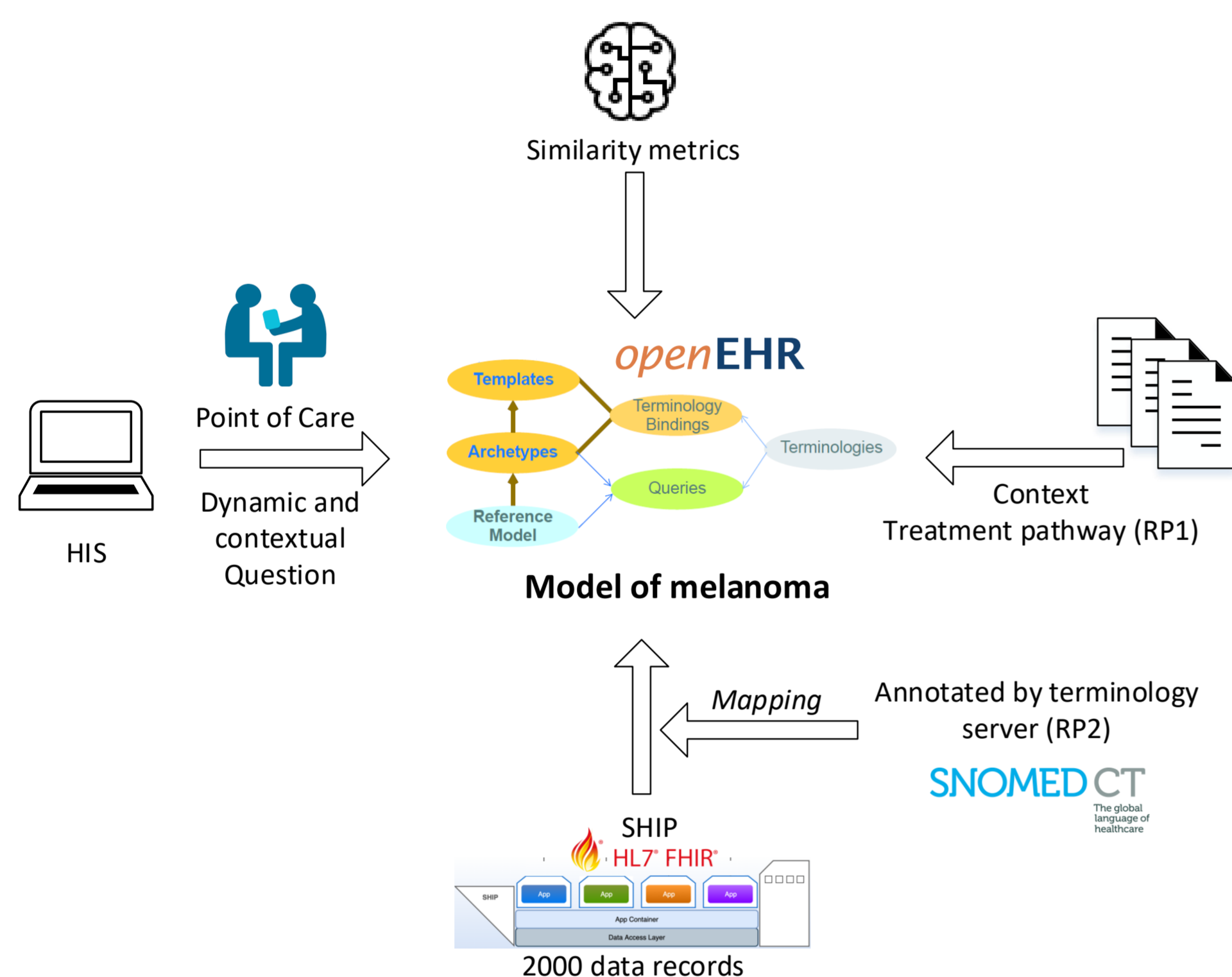
RP8 - Predictive modeling for patient similarity based on an openEHR model of melanoma

Research question

- Currently, there are no reliable predictive biomarkers available regarding primary resistance or development of resistance to therapy or the risk of (severe) side effects, especially those caused by immunotherapy
- Can a knowledge-based relevance model, developed on the basis of previous internal patient data, provide indications for this?
- How can the model be made more flexible for dynamic questions?
- How can the generated context-, patient- and user-dependent knowledge be integrated and visualized?

State of the art

- Different approaches for the identification of similar patients in different medical disciplines [1,2] for predictive modeling, usually using only a few variables
- No consideration of the current context, the patient the course of treatment, no user-dependent visualization
- Use of international standards like SNOMED CT, openEHR, HL7 FHIR [3] to represent data, but not as a knowledge model
- Vector-based and network-based approaches for creating similarity metrics [4 - 6].

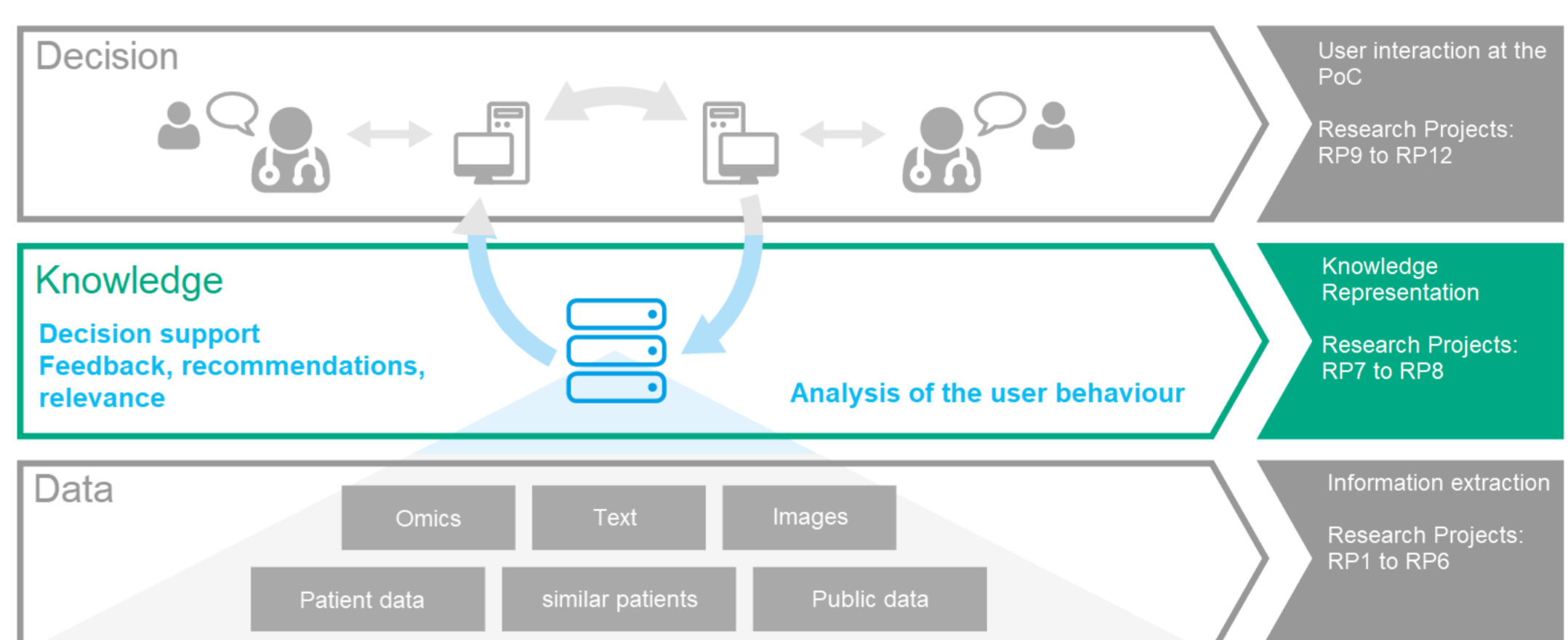


Integration

- Modelling of patient similarity also based on position on the treatment pathway and explicit knowledge about the disease (FP1)
- Visualization at the point of care based on the current context of the patient the course of treatment (FP 9)
- Enrichment of the mapping from FHIR to openEHR using the terminology server (FP2)

Solution approach:

- Use of historical patient data from 2000 data sets of the skin tumour centre from SHIP
- Transfer of FHIR resources into an openEHR model with semantic annotation according to SNOMED CT
- Development of a knowledge-based relevance model based on openEHR and context-related similarity metrics



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