HemoPrint-Enabled Longitudinal Immune Monitoring and Transcriptomic Deconvolution for **Precision Oncology**

Ramos Varas E[†,1,2]; Vandesompele J [1,2]; Mestdagh P [1,2]
[†]presenting author
[1] Dept. of Biomolecular Medicine, Ghent University
[2]OncoRNALab, Cancer Research Institute Ghent (CRIG), Ghent, Belgium

HemoPrint

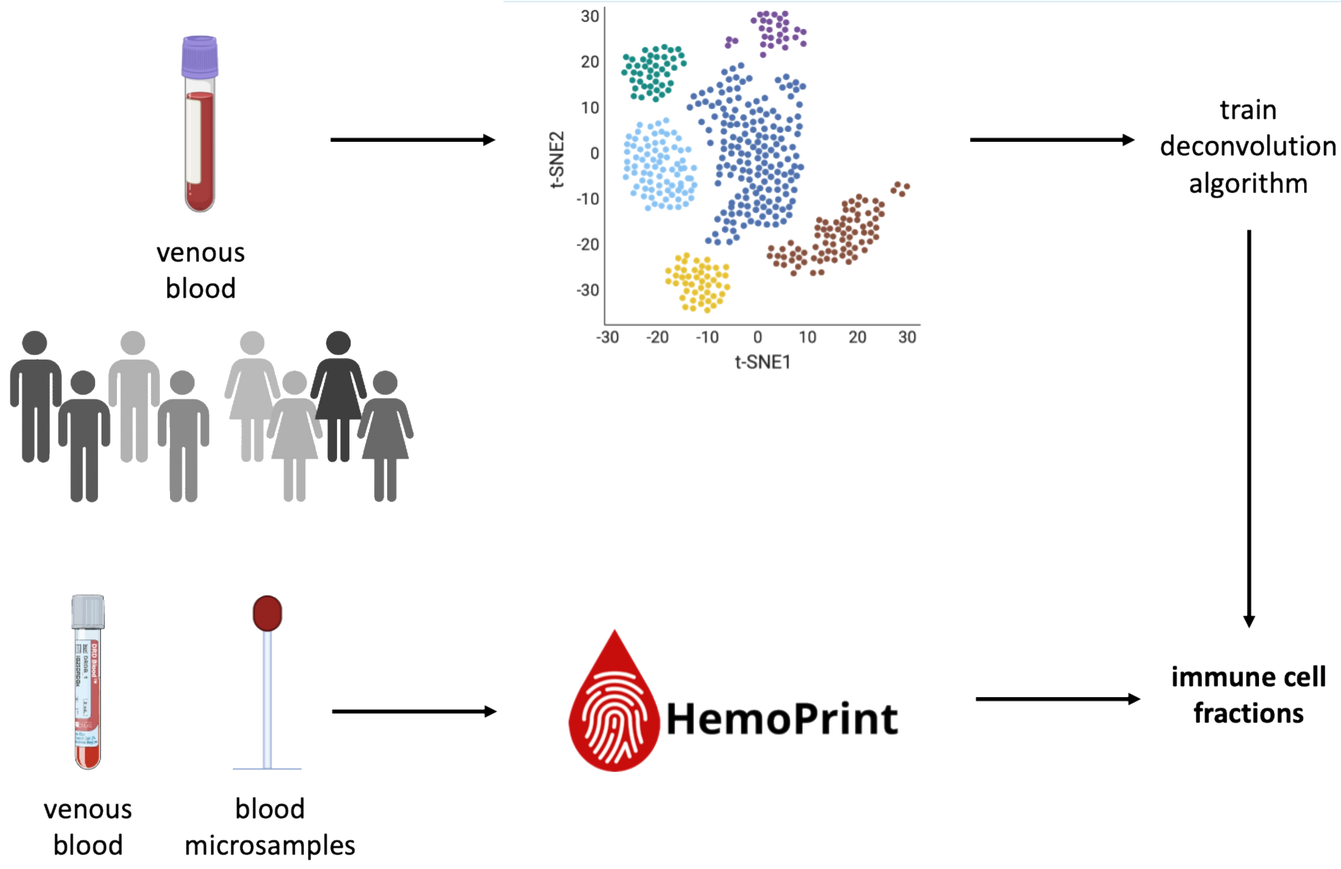
High-throughput and **cost-efficient** platform for blood transcriptomics.

Capillary blood microsampling is a user-friendly alternative for blood samples collection compatible with recurrent sampling and large-scale studies.

Deconvolution algorithms allow estimation of cell fractions from bulk RNA-sequencing data.

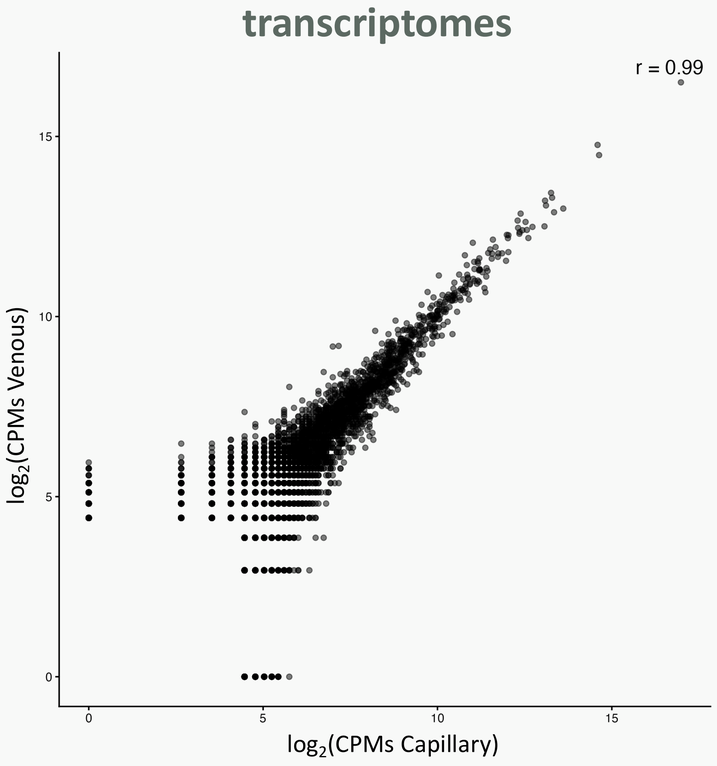
Materials & Methods

- **Samples collection:** Venous blood in EDTA and DRD (InActiv Blue) tubes and capillary microsamples were collected from healthy donors (n = 8)
- **single-cell RNA sequencing (scRNA-seq):** Whole venous EDTA blood (2 mL) was processed to generate single-cell reference profiles
- **Bulk RNA-seq:** DRD-blood and capillary microsamples were processed using HemoPrint protocol
- **Deconvolution:** SQUID algorithm was trained on the scRNA-seq reference dataset to learn cell-type-specific expression signatures, and applied to bulk data from DRD-blood and capillary microsamples
- **Validation:** Leave-one-out cross-validation at donor level for both sample types
- **Evaluation:** Predicted vs. reference cell-type proportions



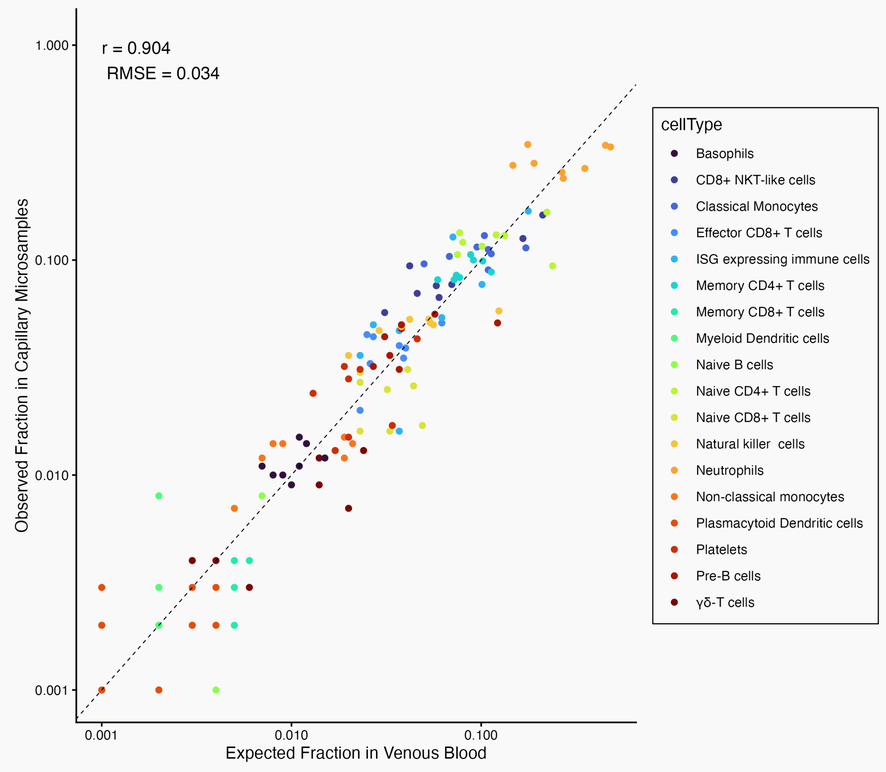
Results

Correlation of venous and capillary blood transcriptomes



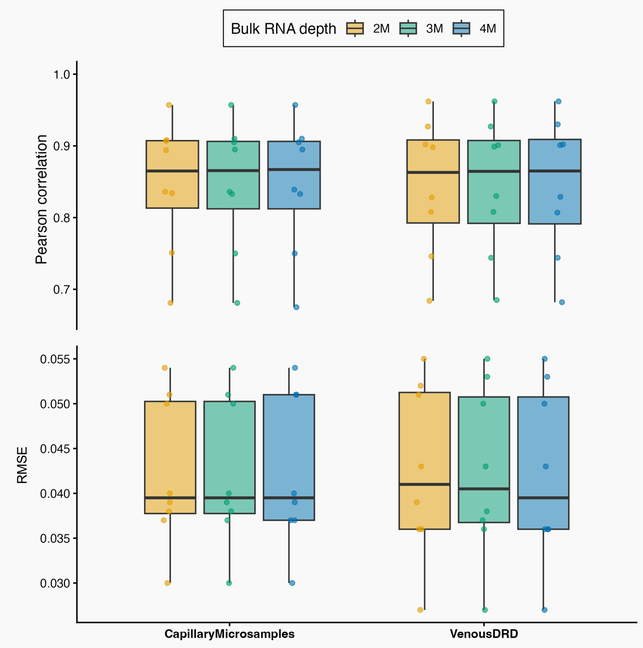
High concordance of gene expression between matched venous blood and capillary microsamples. Bulk RNA-seq profiles from a representative donor show high gene expression correlation, indicating that capillary microsampling reliably captures the venous blood transcriptome.

SQUID deconvolution



Observed vs expected cell fractions inferred by SQUID. Each point represents a cell type within a sample (colored by cell type), with axes shown on a log10 scale. The dashed line indicates perfect agreement. High concordance is observed (r = 0.904), with increased variability at low-abundance cell types.

Deconvolution accuracy



Deconvolution performance is stable across sequencing depths. Pearson correlation (top) and RMSE (bottom) are shown for capillary microsamples and venous DRD samples at 2M, 3M, and 4M reads. Points indicate individual samples.

HemoPrint unlocks scalable, minimally invasive immune monitoring for precision oncology.

HemoPrint enables accurate and minimally invasive immune profiling through transcriptomic deconvolution.

Strong concordance with single-cell references supports its use for longitudinal monitoring in precision oncology.

Future work will focus on improving sensitivity for rare cell types and validating the approach in clinical cohorts.

References

Chen DS, Mellman I. (2027) Elements of cancer immunity and the cancer-immune set point. *Nature* 18,321-330

Cobos FA et al. (2023) Effective methods for bulk RNA-seq deconvolution using scnRNA-seq transcriptomes. *Genome Biol* 24(1)

Newman AM et al. (2019) . Determining cell type abundance and expression from bulk tissues with digital cytometry. *Nat Biotechnol* 37,773-782

Shen X et al. (2024) Multi-omics microsampling for the profiling of lifestyle-associated changes in health. *Nat. Biomed. Eng* 8, 11–29

elena.ramosvaras@ugent.be