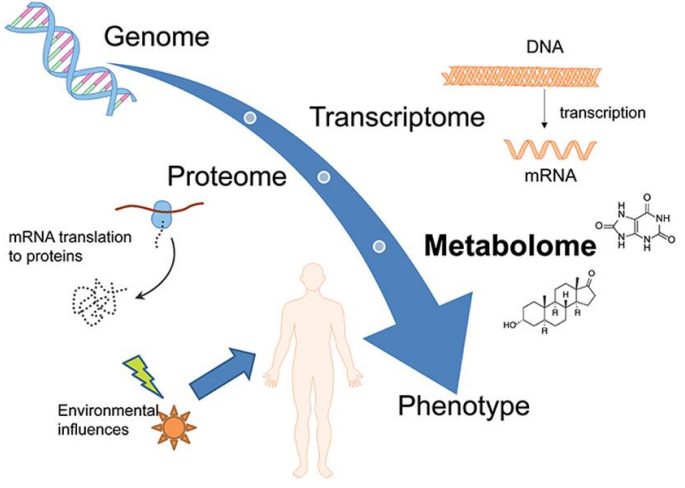
Evaluating NGS-based Olink Technology and mass spectrometry-based workflows for plasma and serum proteomics

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A joint state-of-the-art research and training facility of the ETH Zurich and the University of Zurich. With the latest technologies and key expertise for Omics research, the FGCZ carries out research projects and technology development in collaboration with the Zurich Life Science research community.

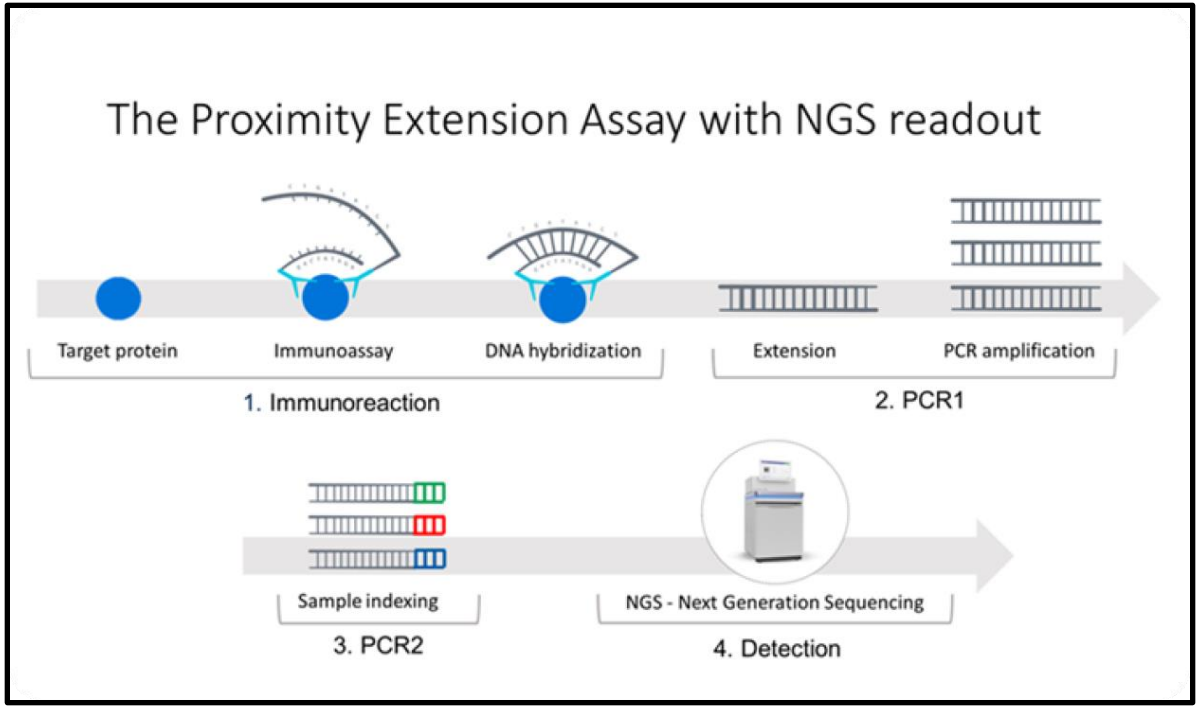
Challenges:

- Analysis of liquid biopsies like serum and plasma is one of the key challenges in clinical proteomics
- LC-MS analysis which is the gold standard, requires expert knowledge and specialized analytical equipment, making access limited to researchers.
- Complexity and high dynamic range in plasma protein concentrations are challenging for MS-based proteomics
- Probe-based workflows coupled to NGS, like Olink are promising alternatives enabling high sample throughput and low cost.

Here, we assessed the **depth**, **reproducibility**, and **biological relevance** of proteomic data obtained from Olink Reveal and LC-MS methods using the same set of samples.

Olink Reveal

- Targeted version of Olink
- >1,000 proteins

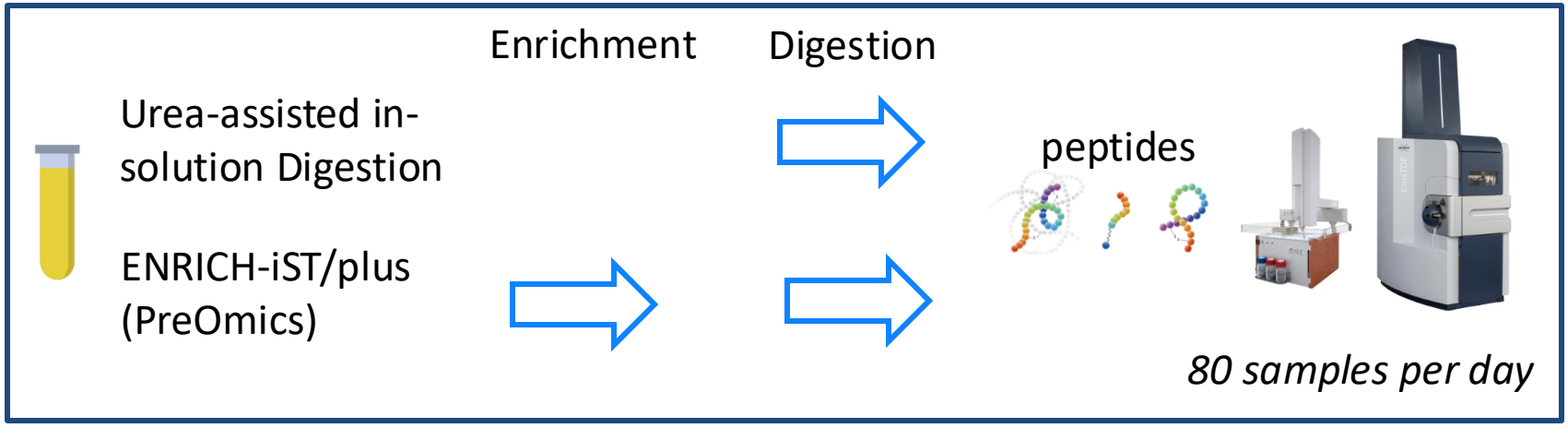


Advantages

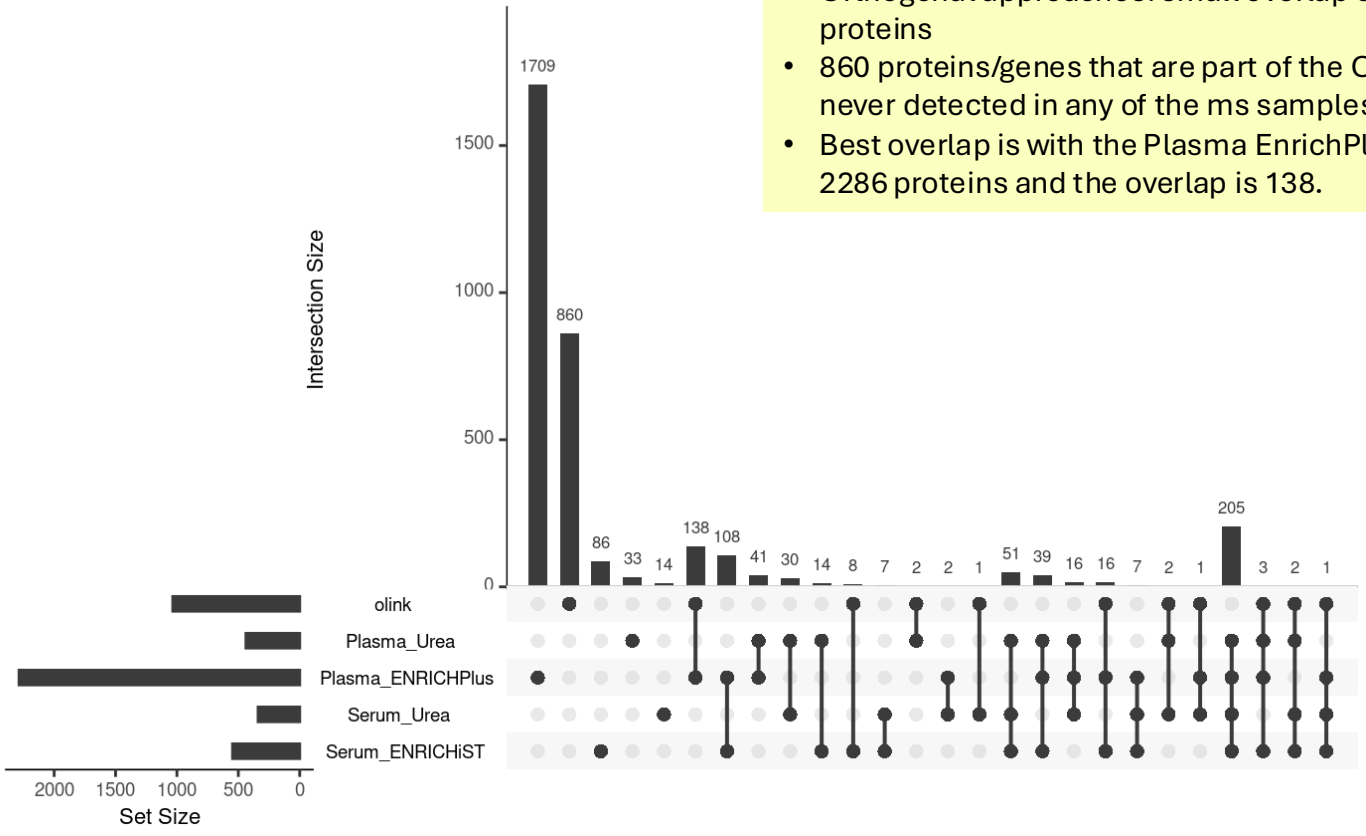
1. No CapEx
2. Very fast workflow, can process hundreds to thousands of samples per week.
3. Low input amount 4ul
4. Cheap- similar price range to RNAseq

LC-MS

- Urea-assisted in-solution digestion
- ENRICH-iST/plus procedure (PreOmics)



Preliminary Results:



- Orthogonal approaches: small overlap of detected proteins
- 860 proteins/genes that are part of the Olink set, are never detected in any of the ms samples
- Best overlap is with the Plasma EnrichPlus which detects 2286 proteins and the overlap is 138.

Workflow Comparison:

	Cost/sample (incl. bioinfo)	Throughput (sample prep & LC-MS)	Coverage (proteins)	Targeted	Isoforms
Urea-based	<50-100 CHF	~1 plate/day	400-600	N	Y
ENRICH-iST	150-200 CHF	~0.5 plate/day	1500-2000+	N	Y
Olink Reveal	120-150 CHF	5-10 plates/day	1000	Y	N

Results:

- Olink Reveal and urea-assisted LC-MS methods achieved the most reproducible results
- ENRICH-iST/plus led to higher protein coverage but at higher costs
- MS-based proteomics: price-per-sample depends on LC-MS throughput, (cheaper than Olink Reveal at a throughput of 60-100 samples-per-day)
- All solutions proved to be easily automatable.
- This study offered valuable insights into the collaborative dynamics involved in conducting a proteomics study using genomics instrumentation.