Byonic vs. FragPipe: Comparing Performance and Efficiency in Proteomics Workflows

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The need for comparison…

- Proteomics research relies on **advanced search engines** to process complex mass spectrometry data. **Byonic** and **FragPipe** are two widely used platforms, each with **unique strengths**.

- A metadatabase with 20 projects and over 90 samples from different origins was run on Data Dependent Acquisition (**DDA**) in both software.

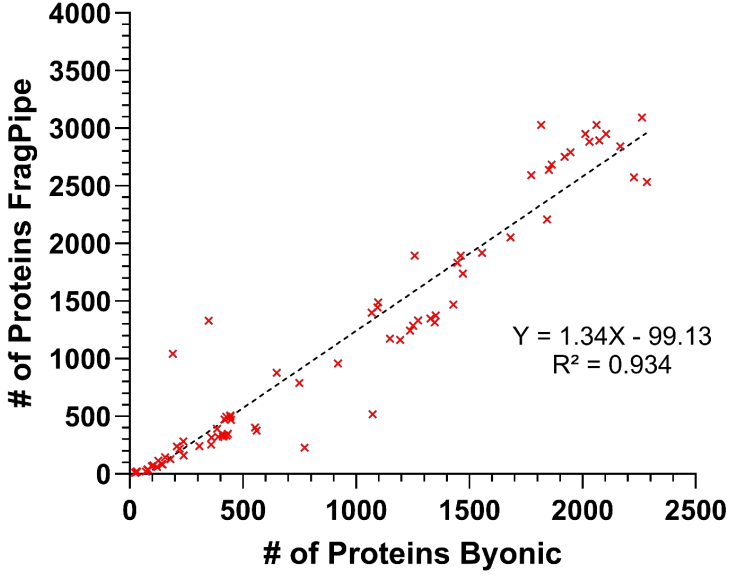
- Exploring how **sample origin** and **preparation** impact **discovery rate** for each platform.

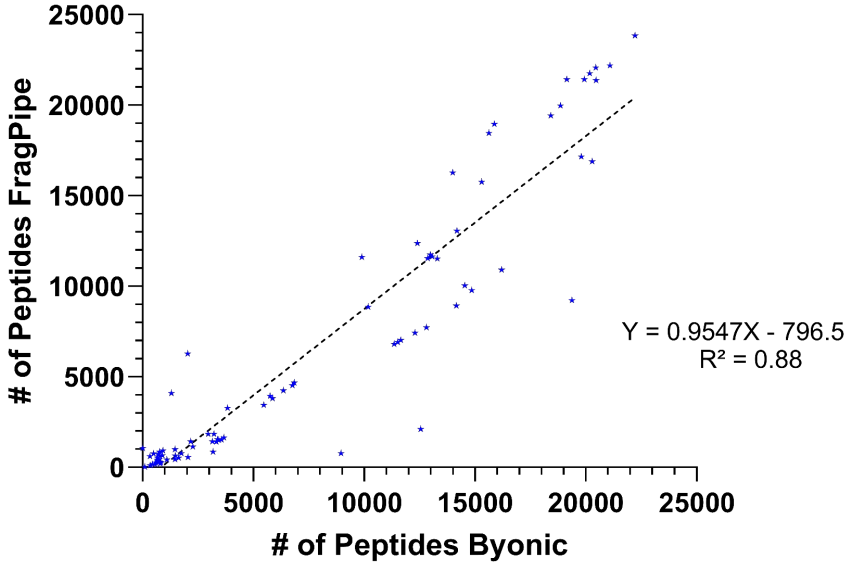
- Giving concrete answers to **when** each platform **works best** for core life.

PROTEIN METRICS



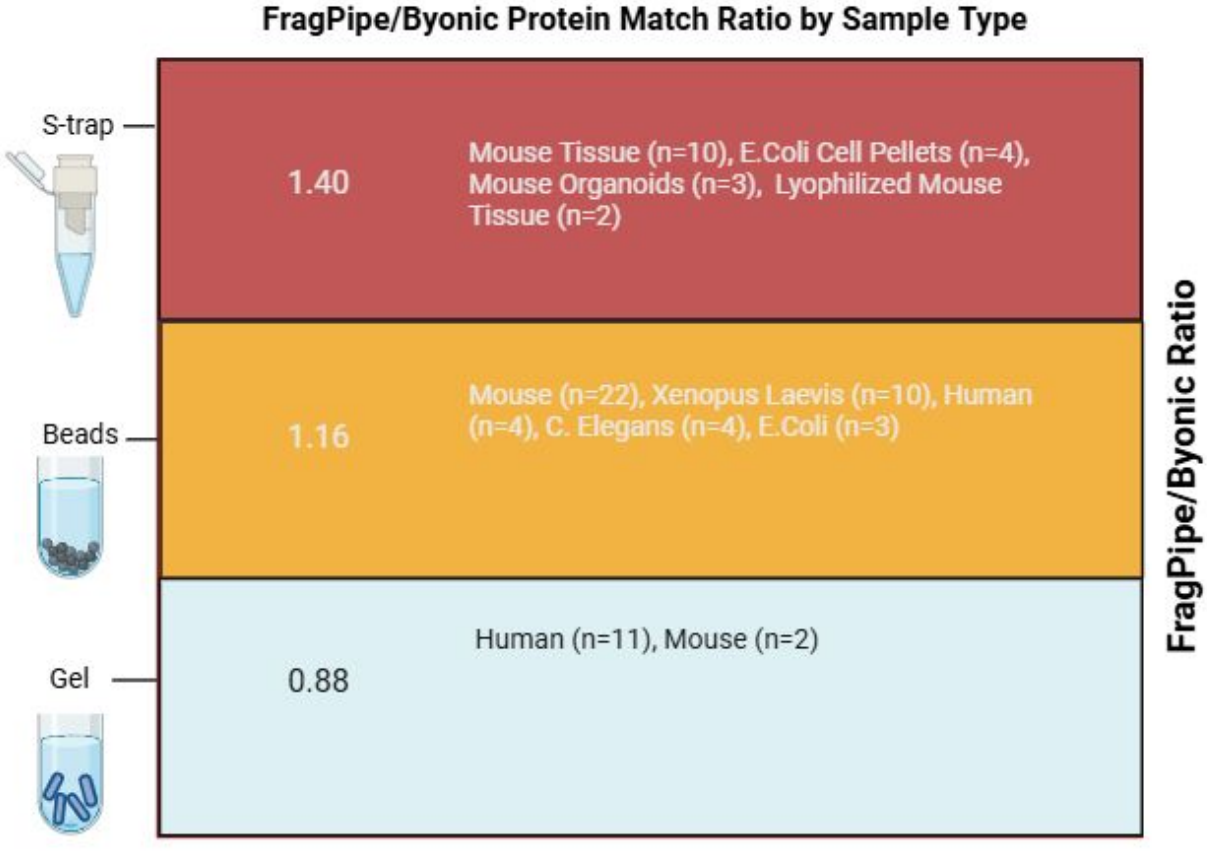
Byonic; better for peptides, FragPipe; better for proteins



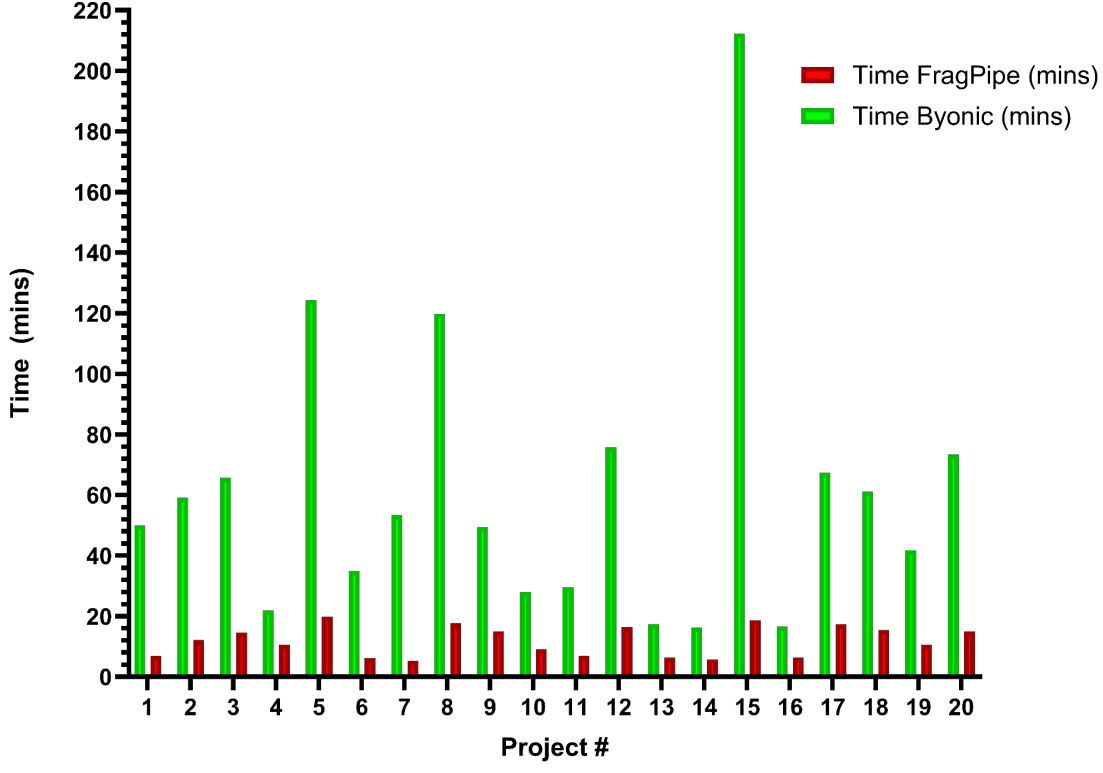


- **Strong correlation** overall.
- 35% higher discovery rate for **proteins** on **Fragpipe**.
- 5% higher discovery rate for **peptides** on **Byonic.**

Sample Workflow Matters



Processing Time across software



- FragPipe takes significantly **less time** to process data compared to Byonic.

- The explanation of the time discrepancy stems from the **batch analysis capabilities** of FragPipe.

Conclusion

- Both Platforms show **similar results** in discovery rate for proteins and peptides.
- FragPipe **excels in speed**, ideal for **high-throughput** analyses.
- Workflow choices can have a **large impact** in protein discovery.
- FragPipe is **free** and **open source**, making it more accessible.
- Both platforms excel at different things, proving that there is **no one size-fits-all solution**.

PROTEIN METRICS

FRAGPIPE

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