

tesorai platform: AI-enhanced analysis of mass spectrometry data yields higher identifications and faster insights with an intuitive chat interface

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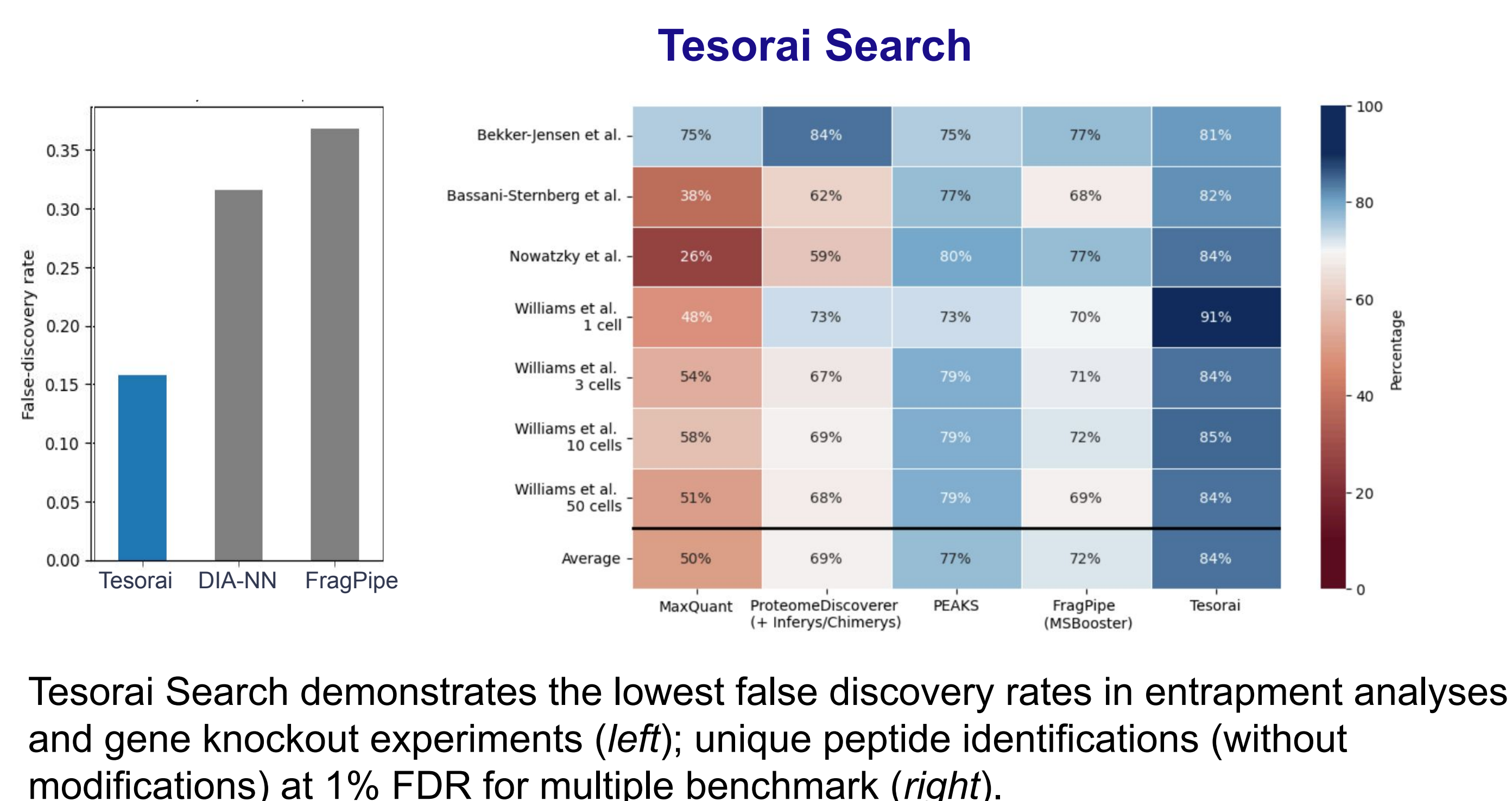
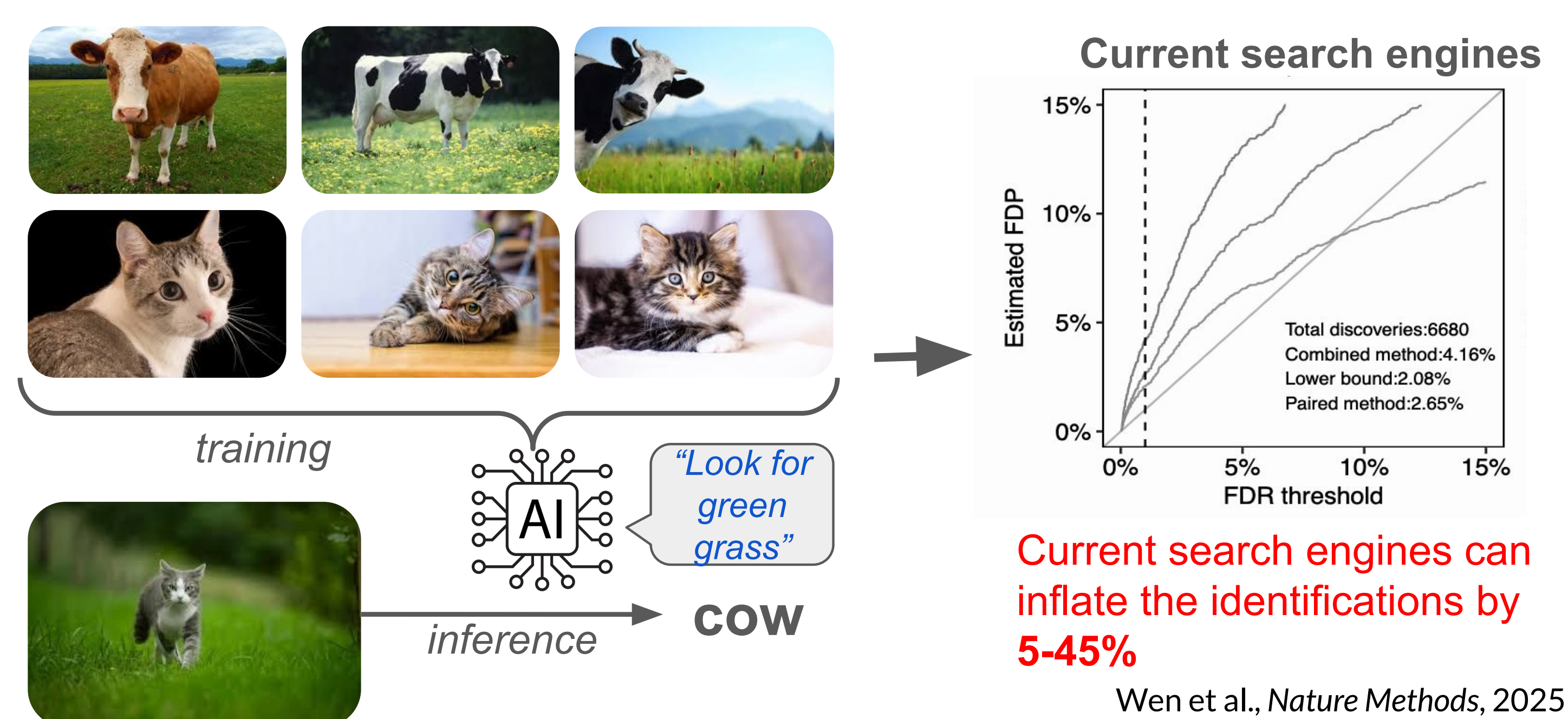
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Abstract

Mass spectrometry (MS)-based proteomics enables high-throughput identification and quantification of proteins in complex biological systems. As data volumes grow, three key demands have emerged: (1) search algorithms that avoid overfitting and provide accurate false discovery rate (FDR) estimates; (2) a scalable and user-friendly platform that can process thousands of files in hours rather than weeks; and (3) a versatile, capable, and easy-to-use solution for downstream analyses.

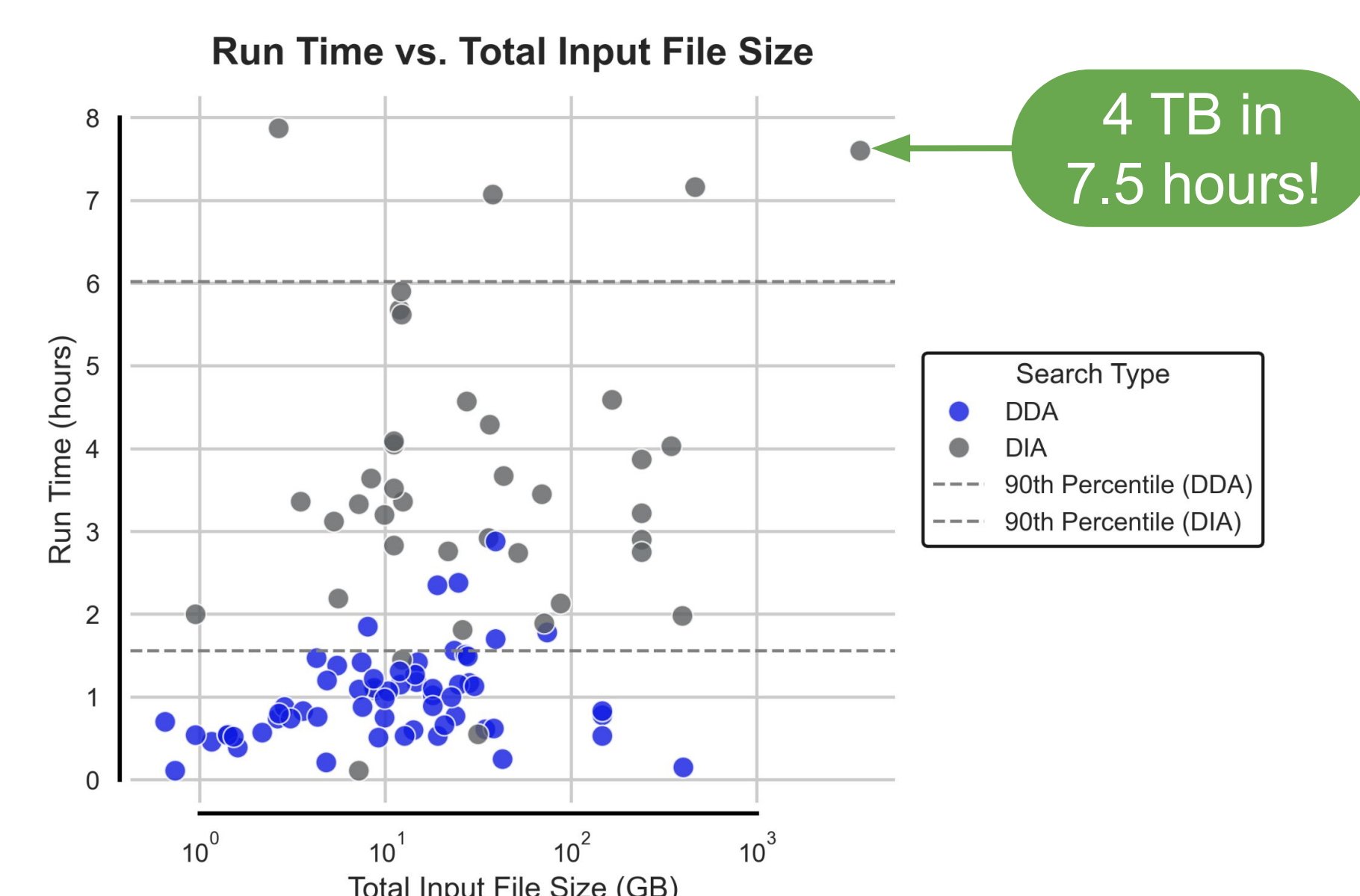
Tesorai Search addresses key bottlenecks in MS-based proteomics by integrating high identification accuracy and sensitivity with a scalable and low-barrier interface. Early user reports indicate substantial time savings—ranging from several days to weeks per dataset. By leveraging recent advances in AI, the platform enables users, including those with limited computational experience, to process raw MS data and perform differential analyses within an hour and with best-in-class tools.

Tesorai Search avoids overfitting and accurately estimates false discovery rates without compromising sensitivity

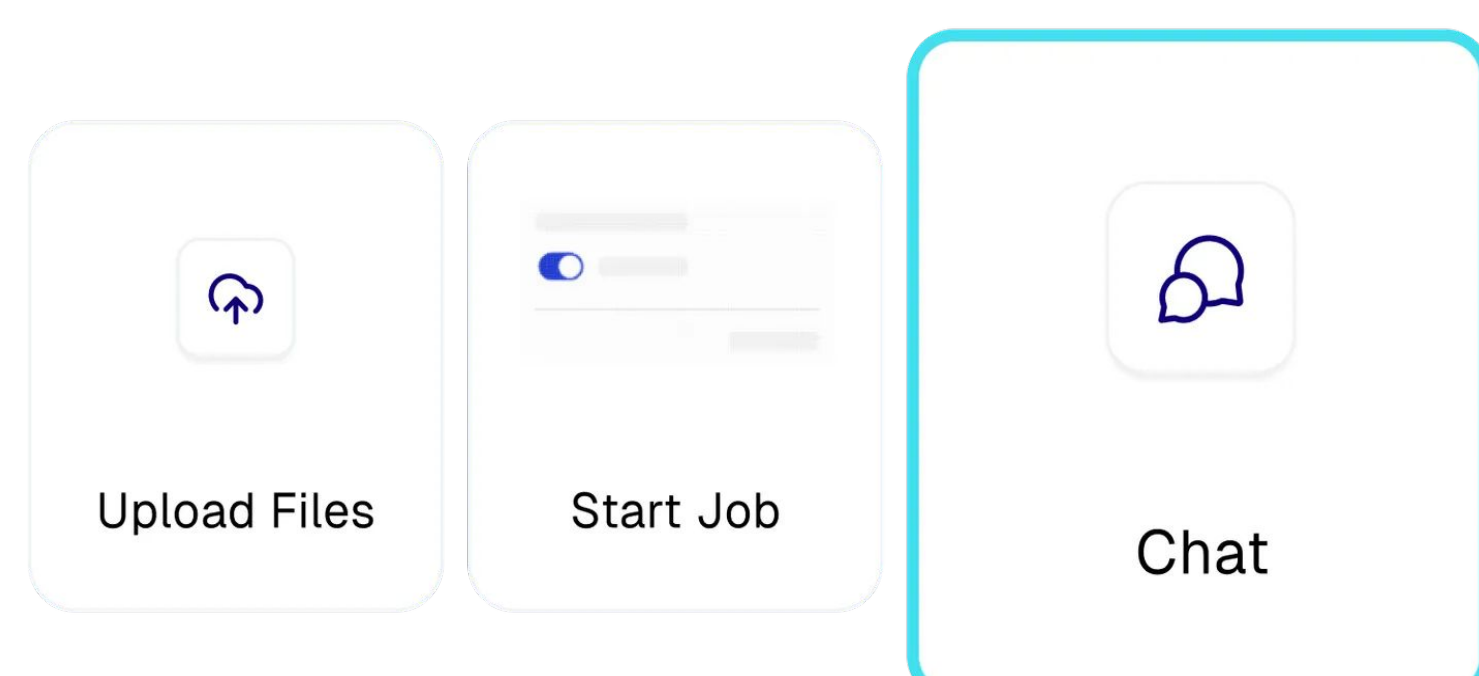


Innovative cloud engineering enables processing of large amounts of data in hours rather than days/weeks

- **Cloud-based platform** – Web-browser interface with no installation required, enabling immediate access from any operating system.
- **Simple setup with only five parameters** – Designed for usability, Tesorai Search can be configured in seconds.
- **Extremely scalable** – Efficiently processes large datasets, from individual experiments to 100s of files, including high-throughput data from timsTOF and Astral instruments.
- **Interactive dashboard** – Provides intuitive visualizations including annotated spectra, mapped protein sequences, and built-in QC metrics for rapid validation and interpretation.
- **Organization-wide sharing and collaboration** – Supports multi-user access and shared projects, enabling teams across departments or institutions to collaborate in real time.



Seamless integration with Chat for downstream analyses



- **Data deep dives** (right)
- **Unsupervised analysis** – PCA, t-SNE, heatmaps
- **Univariate differential analysis**, with data normalizations and imputations, t-test and linear models, and inclusion of covariates
- **Machine learning** – support for various standard models and calculation of feature importances
- **Gene-set enrichment analyses** – integration with knowledge graphs such as GO, protein & drug interactions, tissue expression, and more

