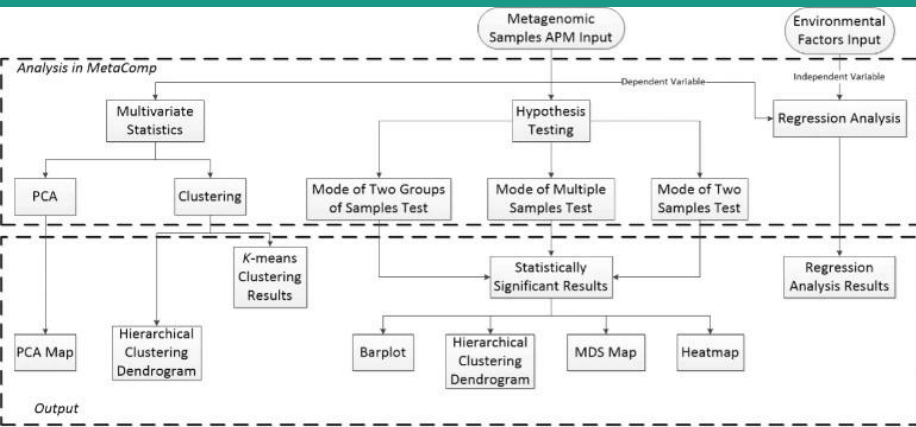


Powerful world of (meta-)genomics held back by lack of Standard Operating Procedures

A computer science-oriented analysis on automated metagenomic approaches and pipelines, their common practices, and technical shortcomings

What are the current technical shortcomings that limit the reproducibility of metagenomic analysis from a Computer Science perspective?



Identified Problems

- Too many tools → Lack of overview
- Lack of CS expertise in
 - **Setup** and usage of tools
 - Development and **maintenance** of tools

Potential Solutions

- Curated & crowdsourced **directory** or **wiki** of tools
- Integrating (more) **programming** and application usage trainings as part of curriculum
- **Software development** trainings for developers of tools
- Self-contained mashup **interfaces** like KBase