



Proteomics pipeline

Cancer

WT

samples





PH,UB,AB,APMS...

Experimental

Computational .raw files

- Tool widely used
- Algorithms yield high mass accuracy and precision
- It covers a wide variety of proteomics experiments
- Simplified user interface
- It can now run on **Linux** (improved performance)



output files



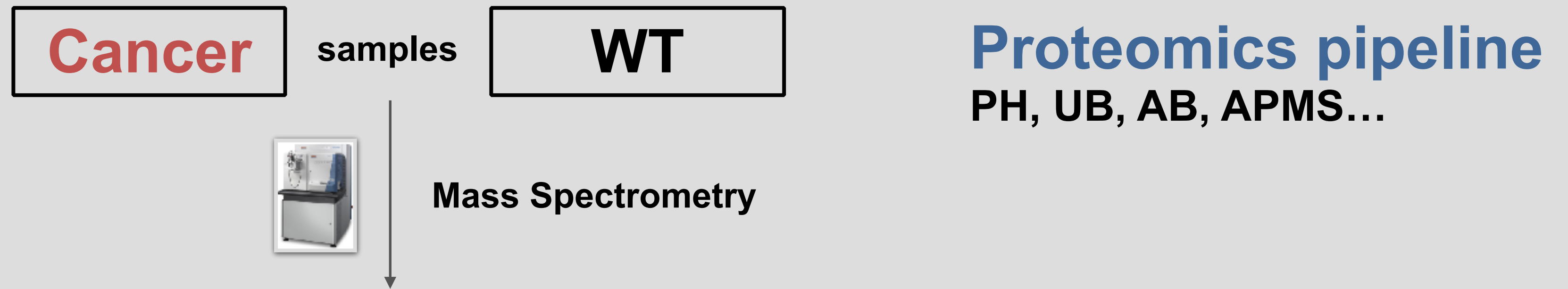
MaxQuant

Peptide Identification

Mass Spectrometry

Experimental

Computational



.raw files

output files



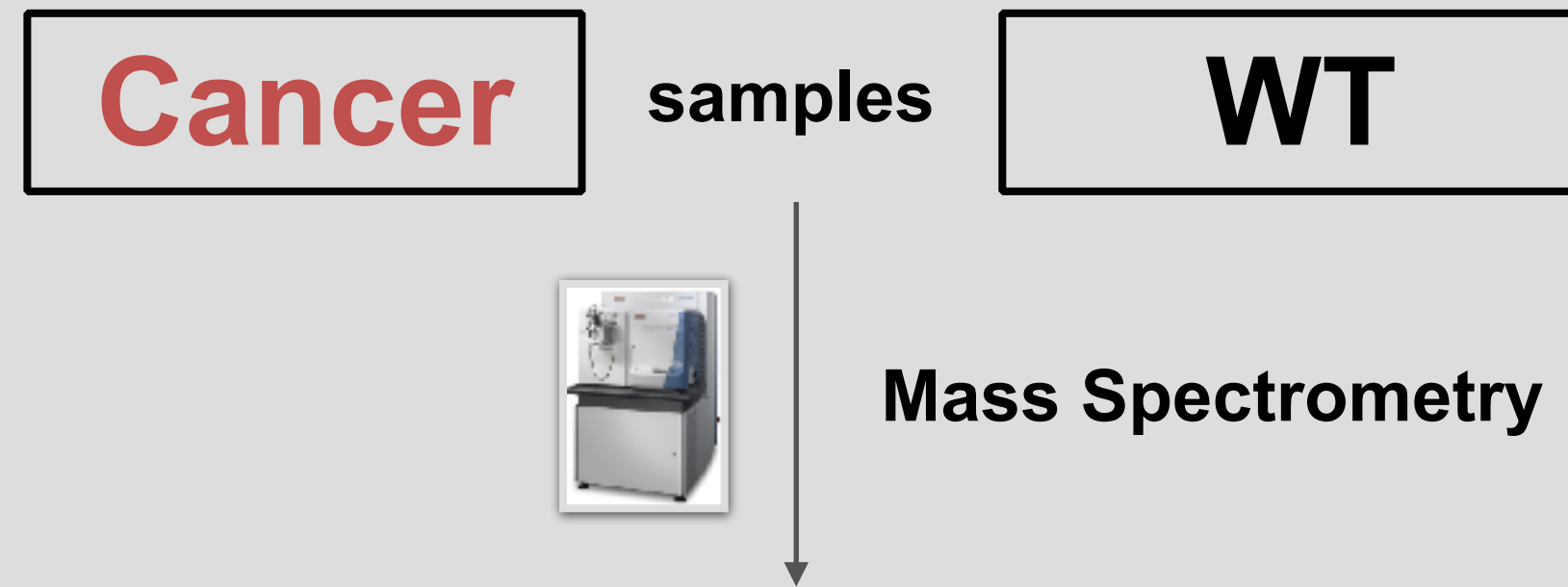
MaxQuant

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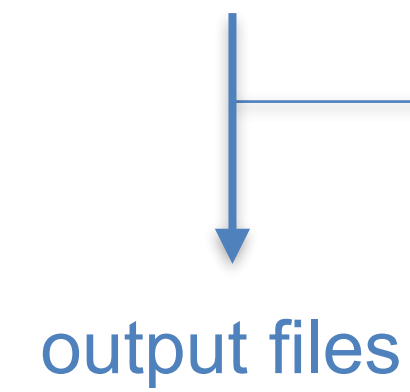
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for Mass Spectrometry
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