Mass Spectrometry based Protein Quantification

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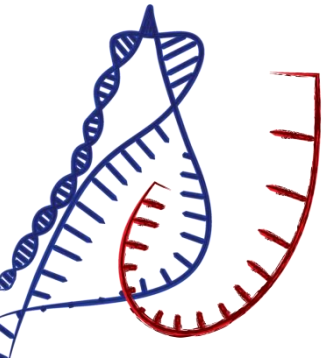
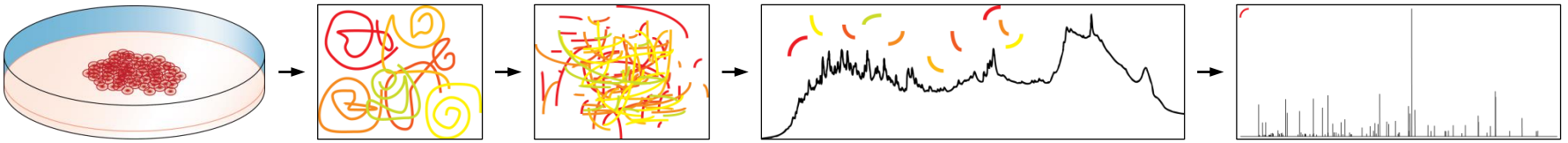
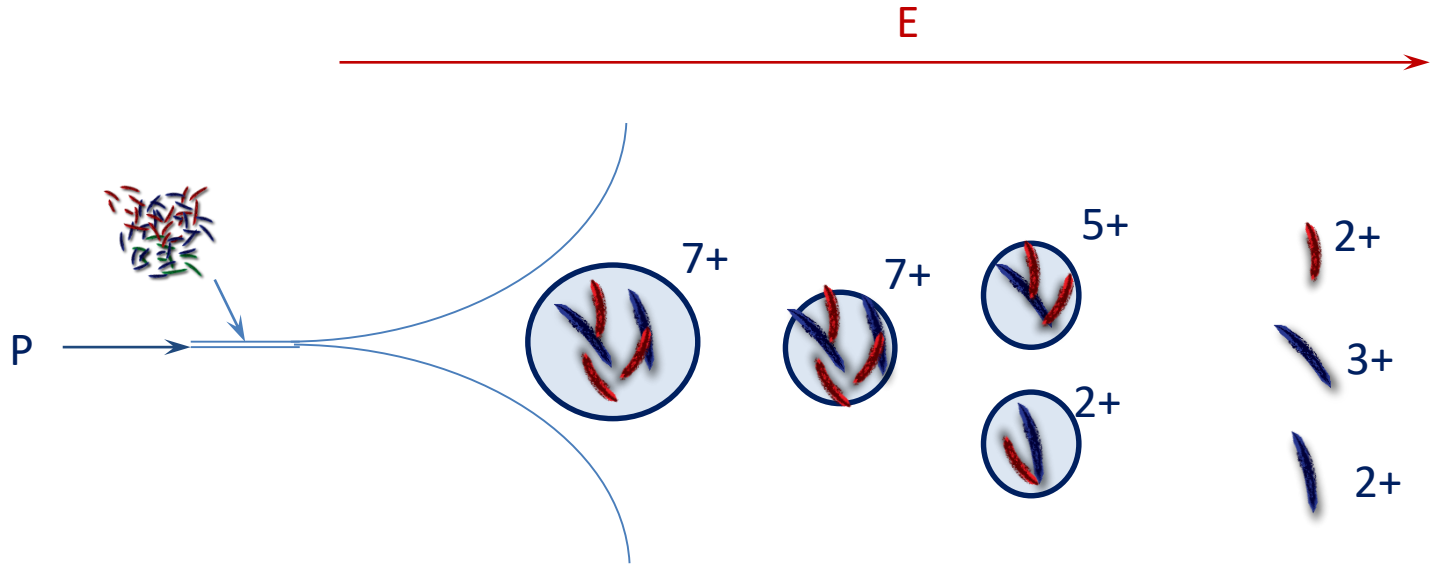


Tandem Mass Spectrometry





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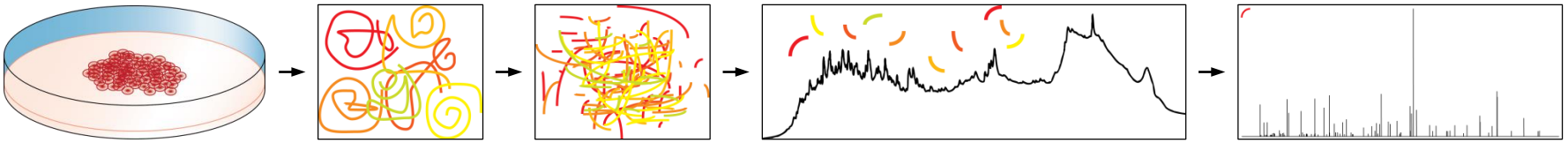
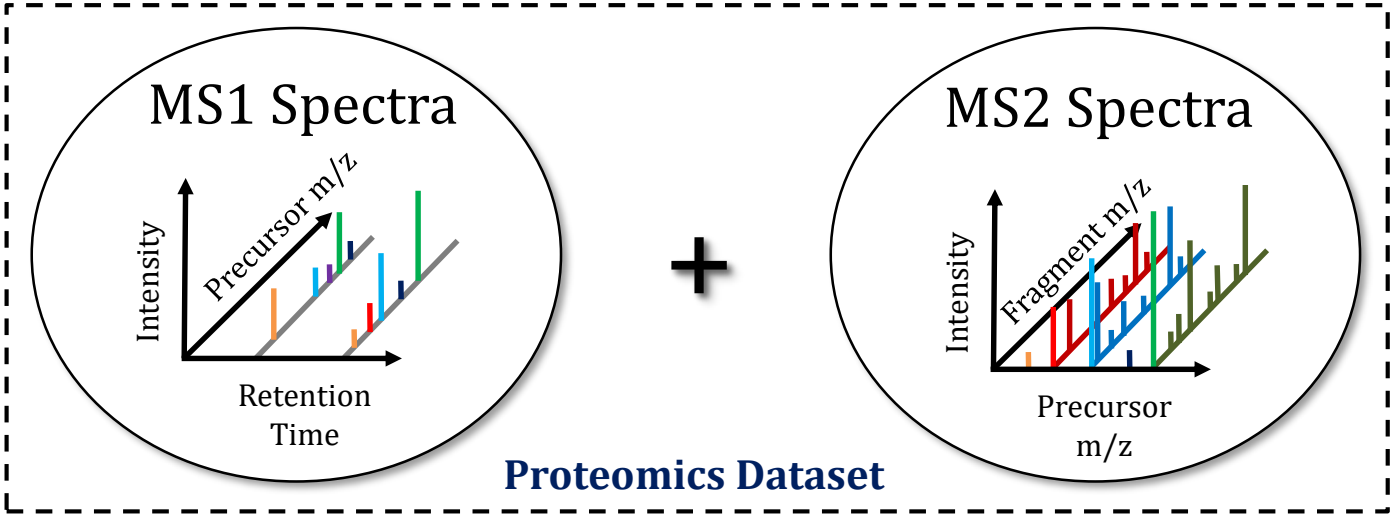
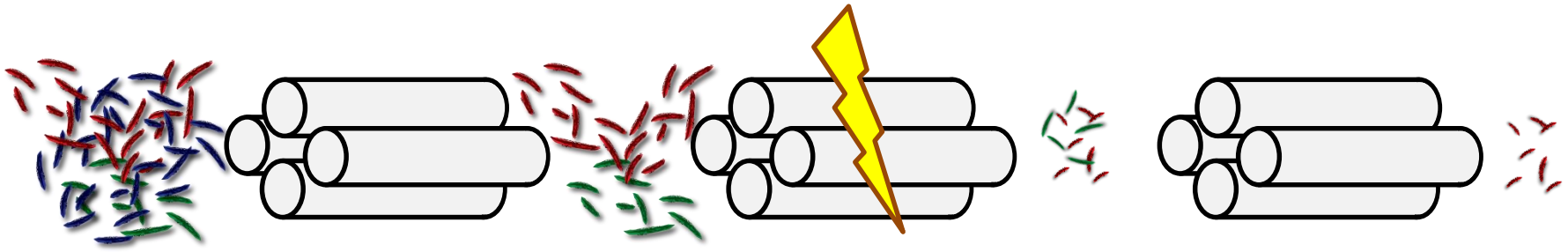
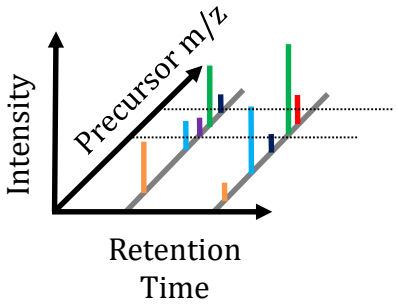
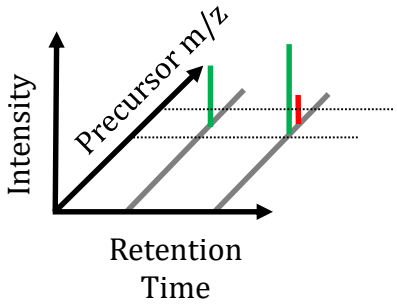


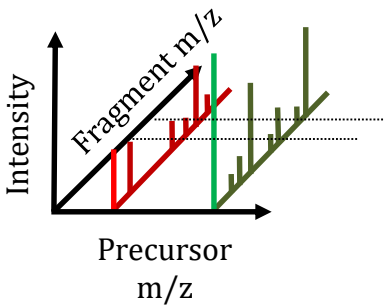


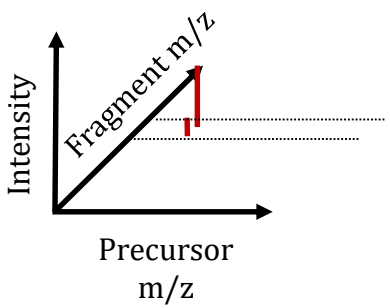
Targeted Quantification

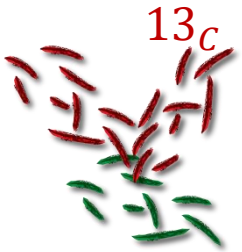






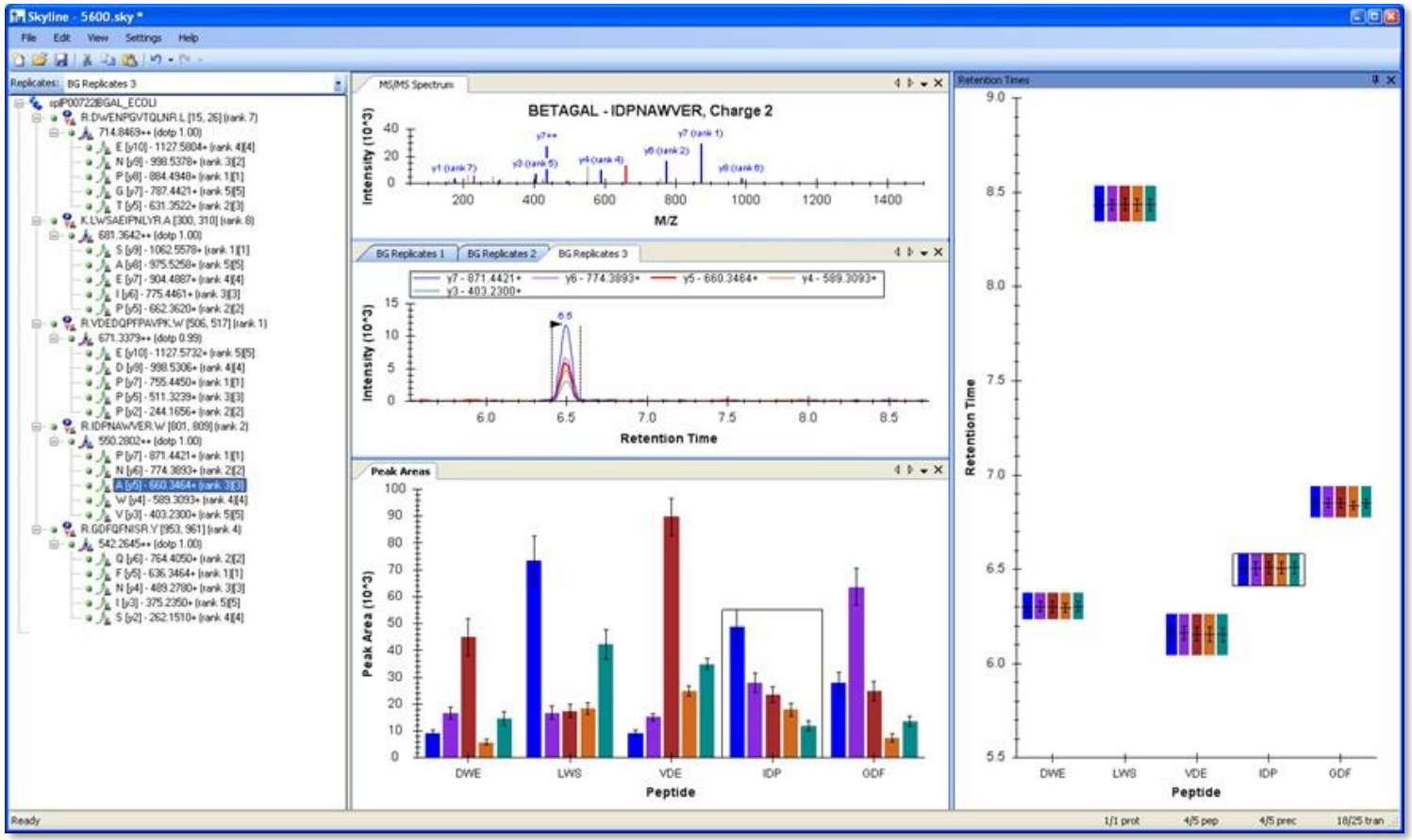




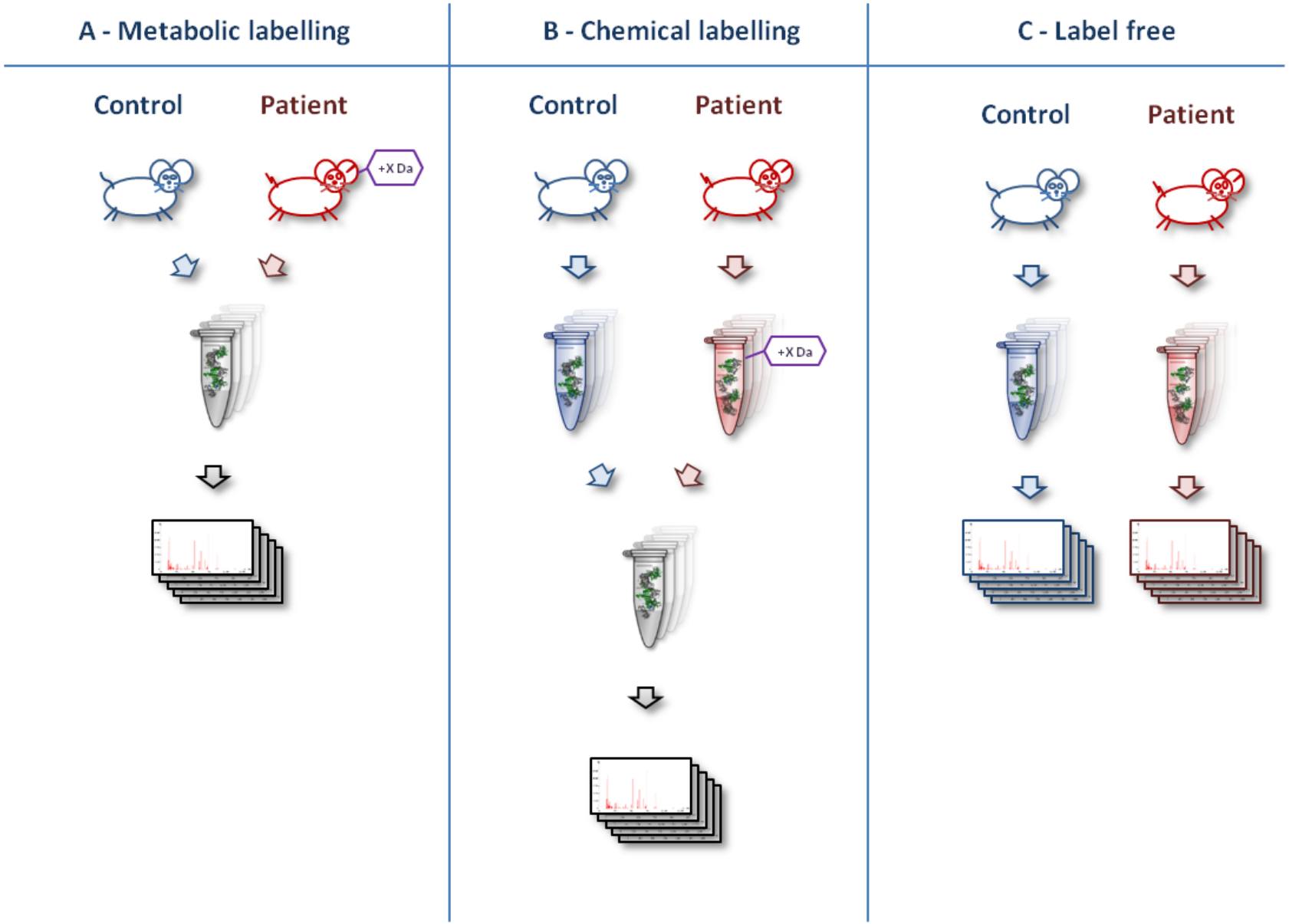


Heavy peptides are spiked as internal control

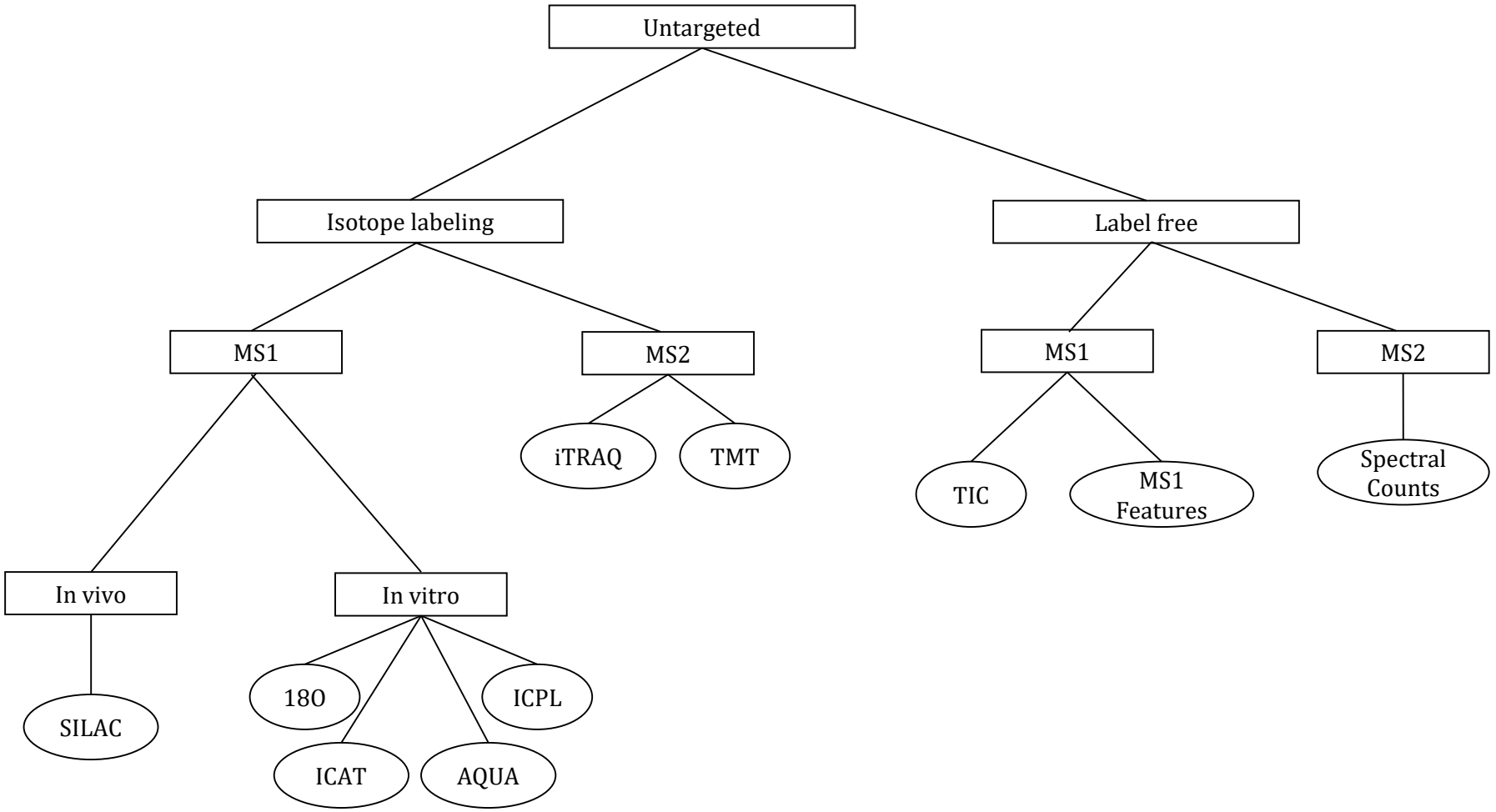
Data interpretation using Skyline



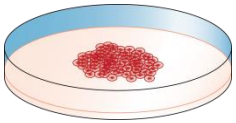
Sample Labelling and Multiplexing

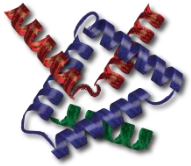


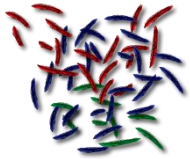
Tandem Mass Spectrometry

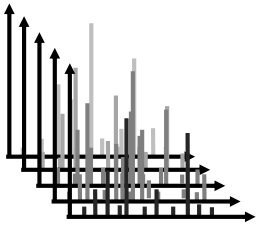


Spectrum Counting



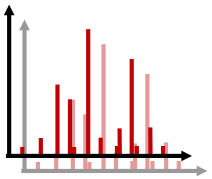






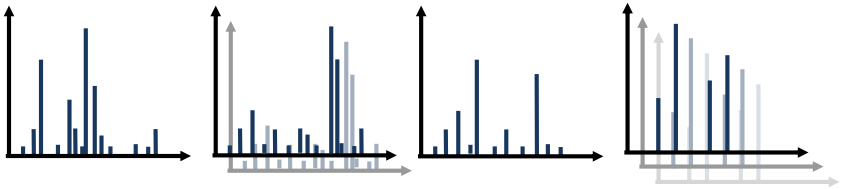
Protein R

Peptide R1



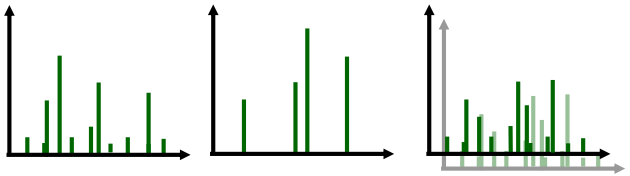
Protein B

Peptide B1 Peptide B2 Peptide B3 Peptide B4



Protein G

Peptide G1 Peptide G2 Peptide G3



Protein R

$$NSAF = \frac{3}{252} = 1.19 \times 10^{-2}$$

$$emPAI = 10^{\frac{1}{20}} - 1 = 0.12$$

Protein B

$$NSAF = \frac{7}{422} = 1.66 \times 10^{-2}$$

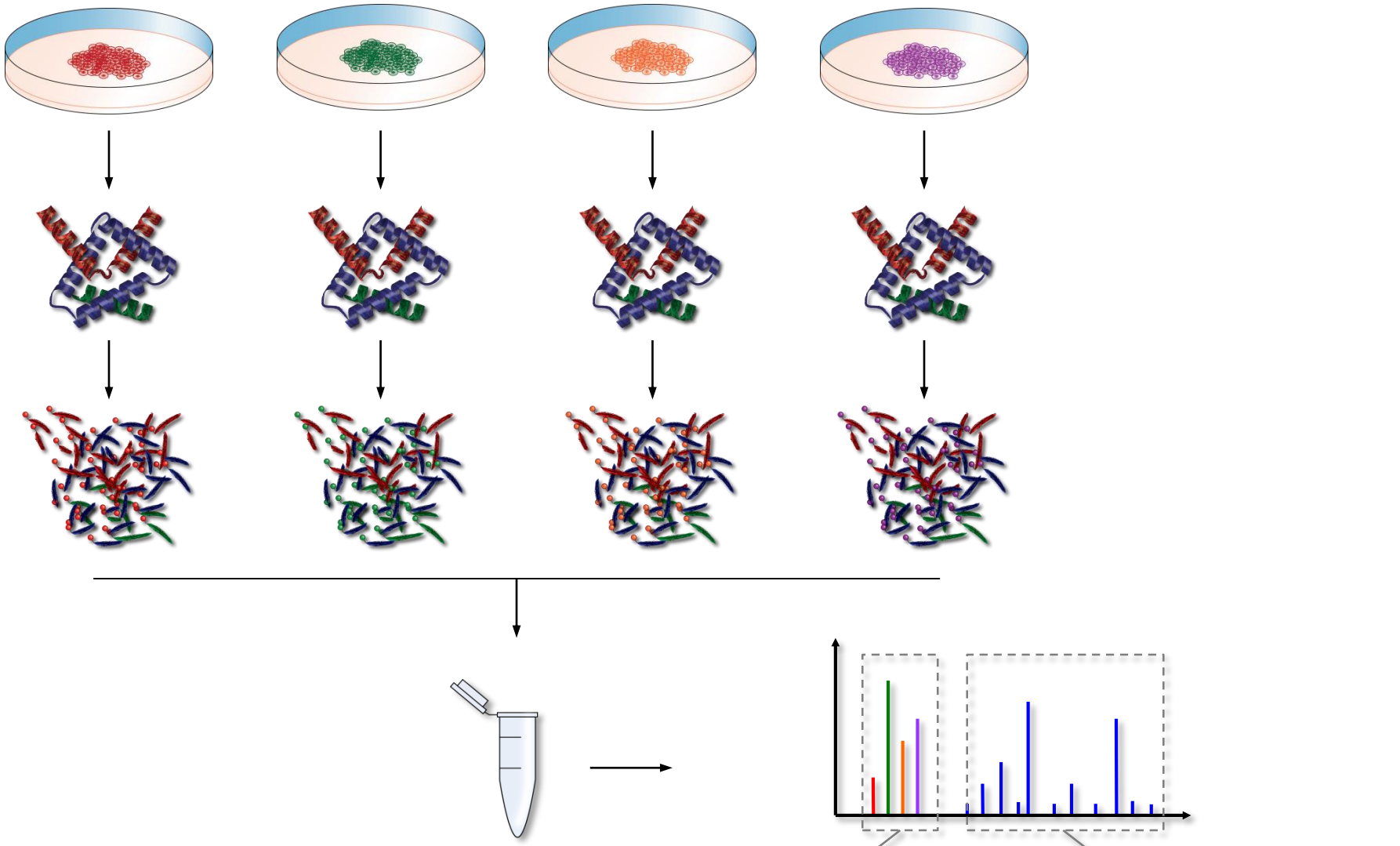
$$emPAI = 10^{\frac{4}{37}} - 1 = 0.28$$

Protein G

$$NSAF = \frac{4}{123} = 3.52 \times 10^{-2}$$

$$emPAI = 10^{\frac{3}{8}} - 1 = 1.37$$

Reporter ion based quantification



Reporter Intensities				Sequence
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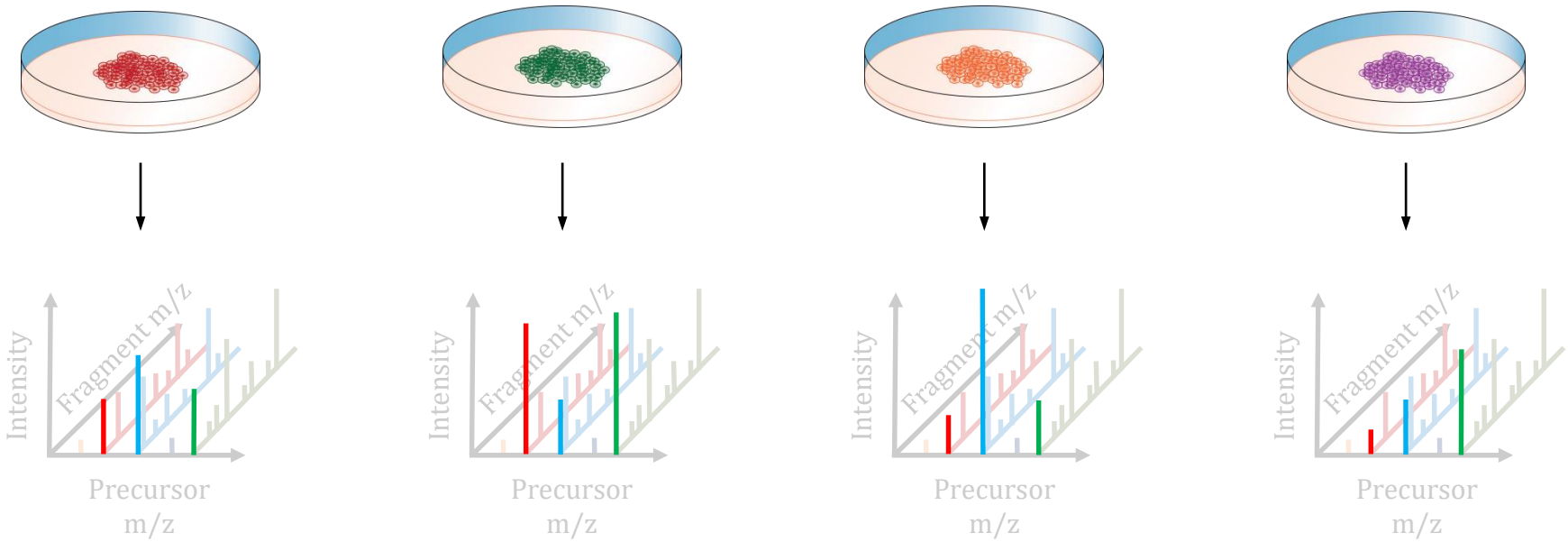
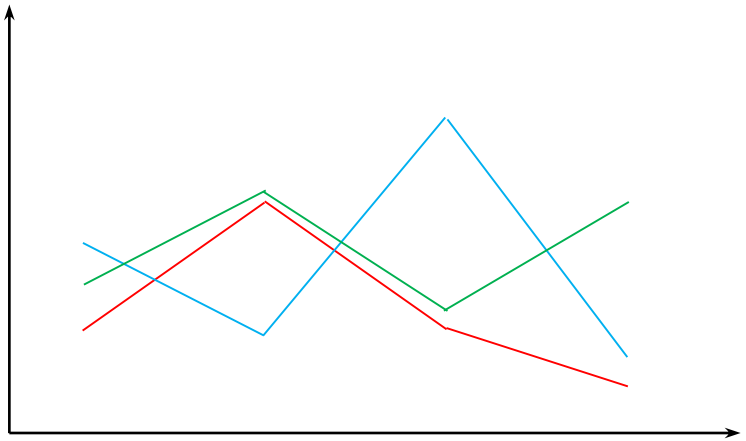
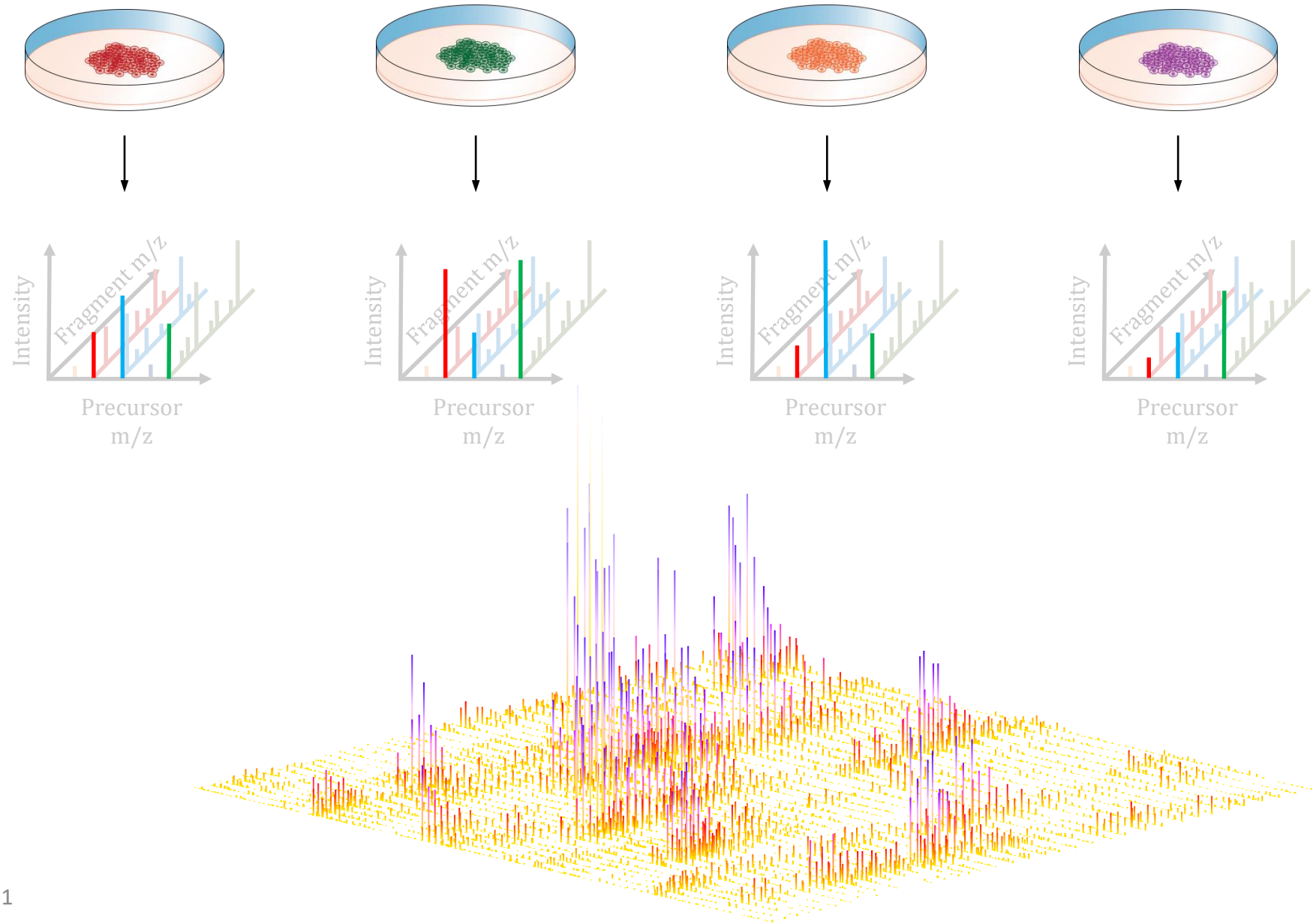
Label-free quantification





Label-free quantification