Mass Spectrometry Analysis of Proteins Using Electron Transfer Dissociation

Statistical Model

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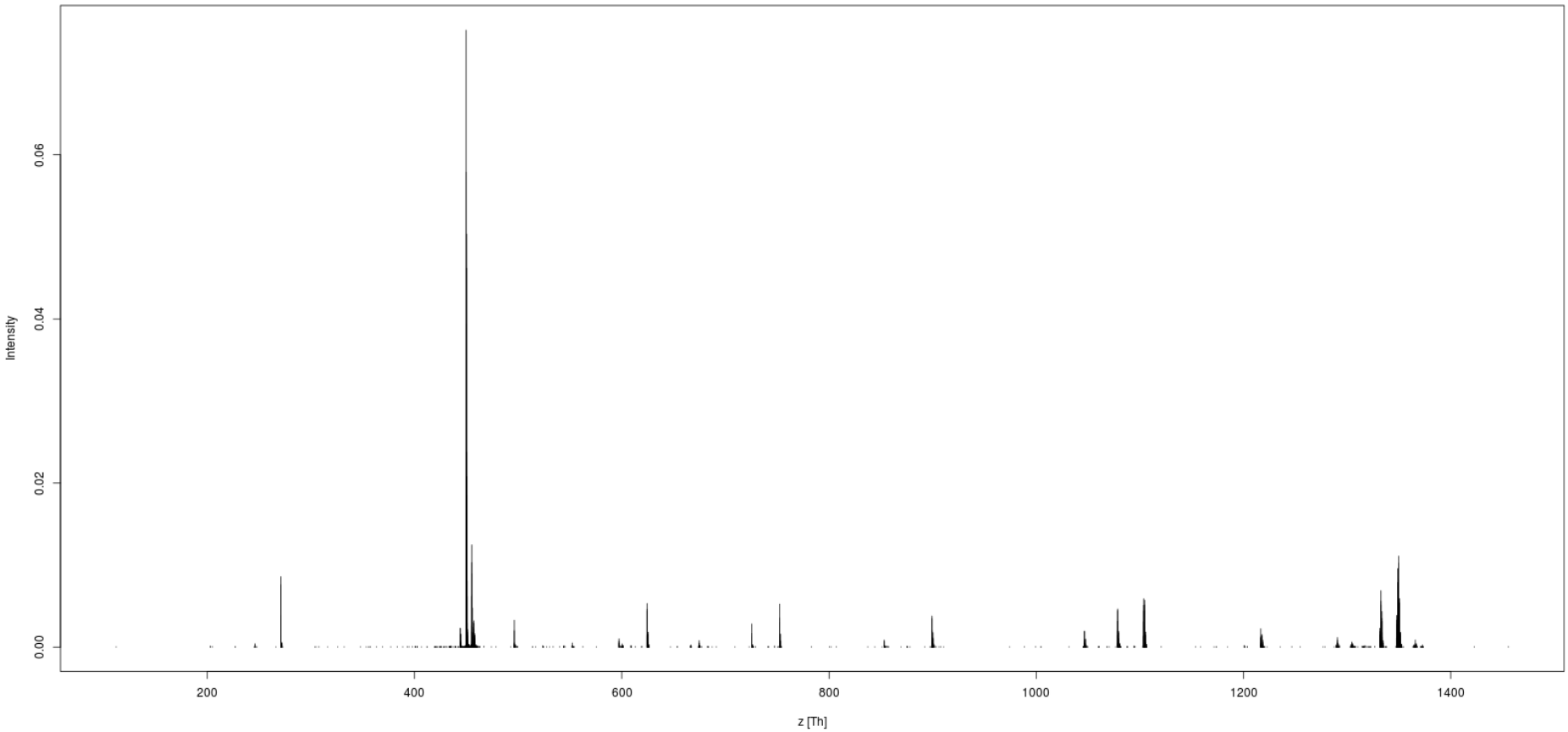
Data from a Mass Spectrometer



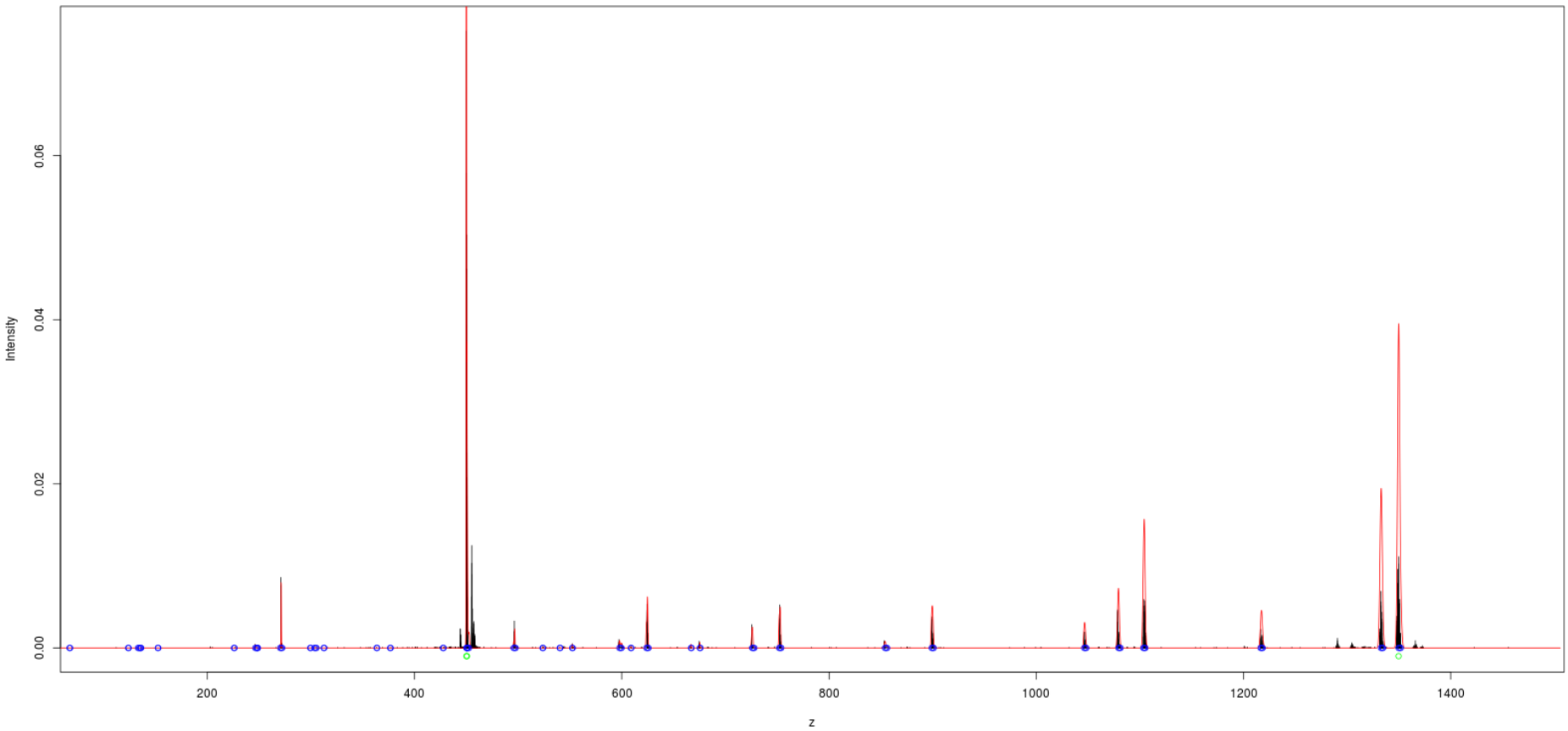
Today's Agenda

- Understanding ETD statics
- Next step : understand dynamics
- Quantitative approach : potential characterisation of peptides through the use of MASS SPEC. But not certain yet how to do it.

Project MassTodon: Debriefing

- Answers to:
  - What results from applying several actions on many molecules of a given type? Actions such as
    - Cleavage of peptide bond
    - Lost of proton
    - Gain of electron
  - Which reaction trails are most probable?
- Maturity?
  - Non-optimised reactions enumeration.
  - Non-calibrated fitting procedures.
- But who cares? To some extent - it works (for one substance).

Theoretically Explained Spectrum



Today's Agenda

1. What is our motivation?
2. Statistical Modelling
3. Generating DAGF
4. Generating DAGF
5. What remains to be done?

The Multinomial Model

Polymer as a sequence of Amino Acids

Additional Events: ETD, HTR, ETnoD, PTR

Possible Cleavages and Their Distributions

Statics: Directed Acyclic Graph of Formulas

- What can be discerned?
- Certain Trails

Statics: Directed Acyclic Graph of Formulas

Whole lotta of things to do.

- Algorithmically
  - Optimise the DAG generation
    - Take into account numerous repetitions.
    - Example : PTR->ETnoD = ETnoD->PTR.
  - Calibrate fitting procedures: stick spectra more jazzy among chemical homies, and the hood does not give a shit about approximations.


Ingvar Eidhammer, Kristian Flikka, Lennart Martens, Svein-Ole Mikalsen, *Computational Methods for Mass Spectrometry Proteomics*. Wiley-Interscience, 2007.


Igor Kaltashov, Stephen J. Eyles *Mass Spectrometry in Biophysics: Conformation and Dynamics of Biomolecules*. Wiley-Interscience, 2005.


Prof. Gavin E. Reid *Mass Analyzers*. Lecture slides from the First International Mass Spectrometry School, 2013.