

1. INTRODUCTION

The combination of a separation technique with high-resolution mass spectrometry is the gold standard in chemical analysis. While instruments can be tune and/or resulting datasets filtered to only analyse specific ions resulting from known components (**targeted analysis**), such instruments can analyse thousand of chemicals spanning. Being able to process all the information resulting from the separation and without any prior knowledge or assumption (**untargeted analysis**) is extraordinarily appealing and central to differential metabolomics analysis.

But classical chromatography peak picking approaches are inefficient, and specialised computerised tools must be designed. In full scan mode (MS1), such tools aim to (1) detect chromatographic-like peaks in the dataset (2) measure figure or merits as accurately as possible and (3) recognise peaks belonging to same ions between multiple datasets. Many freeware and software have been proposed, each balancing **computing speed**, **accuracy** and **completeness**.

2. WHY FINNEE?

Finnee stand for **Find the Needle**, it is a **MATLAB toolbox** [1] that aim to mine for peaks near the limit of quantification and uses chromatographic signal processing rules to insure good measurement of the peak's **chromatographic moments**. The toolbox includes many algorithms allowing to modify single datasets. For each transformation all spectra is recorded in a binary files allowing checking for data integrity. The toolbox is aimed to be versatile allowing easily to design, test and compare different algorithms

3. IN-DEPTH CORRECTIONS OF EACH DATASET[2]

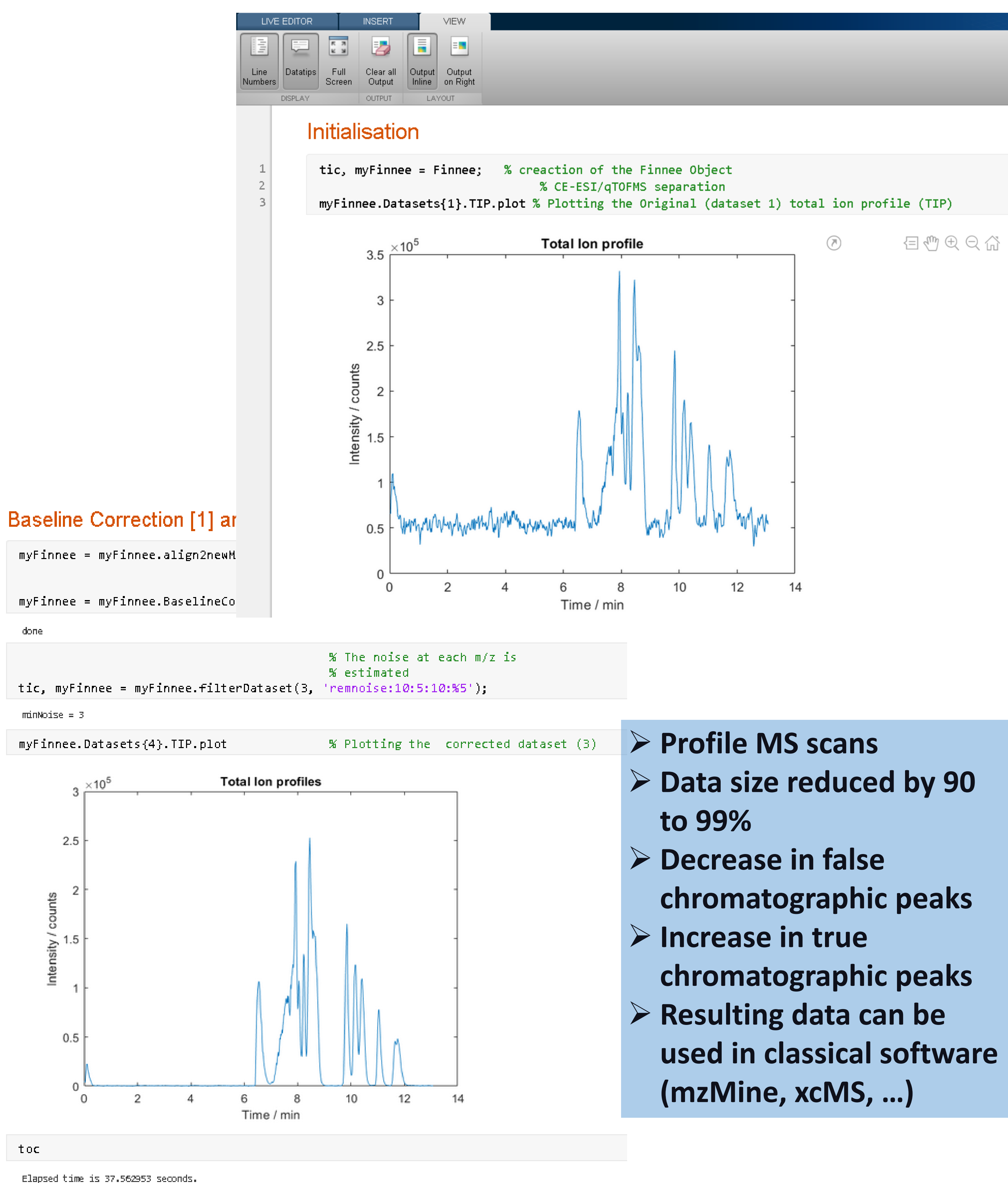


Figure 1. Matlab code and figure allowing to correct each dataset

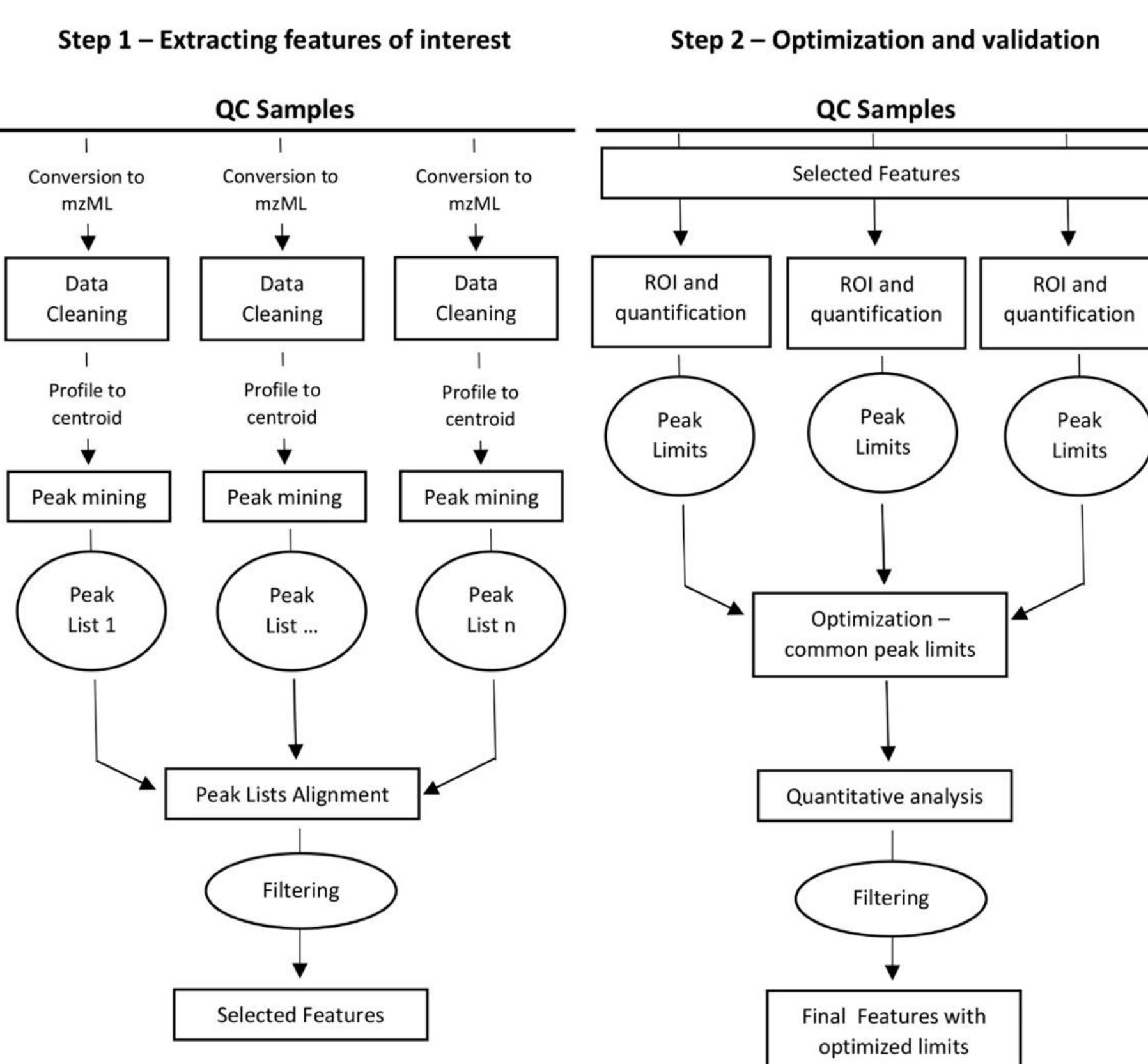
4. PEAKLIST AND VISUALISATION[3]

Getting the peaklists



Figure 2. Centergram representation

5. ALIGNMENT OF MULTIPLE DATASETS, UNTARGETED AND TARGETED ANALYSIS [4]



TWO STEPS APPROACH FOR UNTARGETED ANALYSIS

1. Untargeted analysis with QC samples only
 - List of potential markers recognised by m/z and time
2. Targeted analysis with QC samples and unknown
 - Improve analysis
 - Gain of time
 - **Parallel analysis**

6. CONCLUSIONS AND REFERENCES

Finnee is **open source**, **free to use** and available in Github, Zenodo and Matlab central (<https://github.com/glerny/Finnee2016>). More information can be found in the Github wiki and in the Finnee Blog (<https://finneeblog.wordpress.com/>). A new version is being developed to use parallel computing on distributed servers.

- [1] Erny et al. *Finnee - A Matlab toolbox for separation techniques hyphenated high resolution mass spectrometry dataset*, Chem. Int. Lab., **2016**, 155, 138-144.
- [2] Erny et al. *Background correction in separation techniques hyphenated to high-resolution mass spectrometry—Thorough correction with mass spectrometry scans recorded as profile spectra*, J. Chrom. A, **2017**, 1492, 98-105.
- [3] Erny et al. *Algorithm for comprehensive analysis of datasets from hyphenated high-resolution mass spectrometric techniques using single ion profiles and cluster analysis*, J. Chrom. A, **2016**, 1429, 134-141
- [4] Erny et al. *Mining for Peaks in LC-HRMS Datasets Using Finnee – A Case Study with Exhaled Breath Condensates from Healthy, Asthmatic, and COPD Patients*, ACS Omega, **2020**, 26, 16089–16098

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