Systems biology

Probabilistic framework for integration of mass spectrum and retention time information in small molecule identification

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Abstract

Motivation: Identification of small molecules in a biological sample remains a major bottleneck in molecular biology, despite a decade of rapid development of computational approaches for predicting molecular structures using mass spectrometry (MS) data. Recently, there has been increasing interest in utilizing other information sources, such as liquid chromatography (LC) retention time (RT), to improve identifications solely based on MS information, such as precursor mass-per-charge and tandem mass spectrometry (MS²).

Results: We put forward a probabilistic modelling framework to integrate MS and RT data of multiple features in an LC-MS experiment. We model the MS measurements and all pairwise retention order information as a Markov random field and use efficient approximate inference for scoring and ranking potential molecular structures. Our experiments show improved identification accuracy by combining MS² data and retention orders using our approach, thereby outperforming state-of-the-art methods. Furthermore, we demonstrate the benefit of our model when only a subset of LC-MS features has MS² measurements available besides MS¹.

Availability and implementation: Software and data are freely available at https://github.com/aalto-ics-kepaco/msms_rt_score_integration.

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Supplementary information: Supplementary data are available at Bioinformatics online.

1 Introduction

The identification of small molecules, such as metabolites or drugs, in biological samples is a challenging task posing a bottleneck in various research fields, such as biomedicine, biotechnology, environmental chemistry and drug discovery. In untargeted metabolomics studies, the samples typically contain thousands of different molecules, the vast majority of which remain unidentified (Aksenov et al., 2017; da Silva et al., 2015). Liquid chromatography (LC) coupled with tandem mass spectrometry (MS²) is arguably the most important measurement platform in metabolomics (Blaženović et al., 2018), due to its suitability to high-throughput screening, its high sensitivity and applicability to a wide range of molecules. Briefly explained, LC separates molecules by their differential physicochemical interaction between the stationary and mobile phase, which results in retention time (RT) differences and MS separates molecular ions by their mass per charge (MS¹). Subsequently, MS² can be used to fragment molecules in a narrow mass window and to record the fragment intensities (MS²-spectrum). In an untargeted metabolomics experiment, large sets of MS features (MS¹ and RT, plus optionally MS²), are observed, corresponding to the different molecules in the sample. Metabolite identification concerns then the structural annotation of the observed MS features.

In recent years, numerous powerful approaches (Nguyen et al., 2018a; Schymanski et al., 2017) to predict molecular structure annotations for MS² spectra have been developed (Allen et al., 2014; Brouard et al., 2016; Dührkop et al., 2013, 2019; Nguyen et al., 2018b, 2019; Ruttkies et al., 2016, 2019). Typically, these methods output a ranked list of molecular structure candidates, that can be shown to human experts, or further post-processed, e.g. by using additional information available for the analysed sample. Sources of additional information include, e.g. RT (Bach et al., 2018; Ruttkies et al., 2016; Samarakweera et al., 2018), collision cross-section (Plante et al., 2019) or prior knowledge on the data generating process, such as the source organism’s metabolic characteristics (Rutz et al., 2019). RT, i.e. the time that a molecule takes to elute from the LC column, is readily available in all LC-MS pipelines, and is frequently
used in aiding annotation (Stansstrup et al., 2015). A basic technique is to use the difference between the observed and predicted RT (Domingo-Almenara et al., 2019; Samaraweera et al., 2018) to prune the list of candidate molecular structures. A major challenge for utilizing RT information, however, is that the RT of the same molecule can vary significantly across different LC systems and configurations, necessitating system specific candidate RT reference databases and RT predictors. Different approaches have been proposed to tackle this challenge, such as using physicochemical properties (e.g. partition coefficient, LogP) as RT proxies (Hu et al., 2018; Ruttkies et al., 2016), RT mapping across LC systems (Stansstrup et al., 2015) or predicting retention orders, which are largely preserved within a family of LC systems (e.g. reversed phase) (Bach et al., 2018; Liu et al., 2019). Using LogP as an RT proxy is simple to implement, but only models the hydrophobic separation effects of the LC system. RT mapping, on the other hand, is limited to pairs of LC systems in which the same molecules have been measured. Retention order prediction can overcome those drawbacks, by learning the LC system’s separation directly from RT data of multiple systems (Bach et al., 2018).

This study proposes a probabilistic framework to integrate MS1 or MS2-based annotations with predicted retention order for improved small molecule identification given a set of MS features measured within one LC-MS run by building on the work by Bach et al. (2018) and Del Carratore et al. (2019). The latter proposed a probabilistic approach for integrating different types of additional information to MS1 data, including RT information. We too define a probabilistic approach, but differ in how RT is handled. Where Del Carratore et al. (2019) use absolute RT information, we follow Bach et al. (2018) and propose pairwise Markov random field for molecules eluting within the same LC-MS run. In contrast to the work done by Bach et al. (2018), our model makes use of pairwise retention order information between all MS features rather than only the ones adjacent in terms of their RTs, resulting in more accurate annotations. Furthermore, our model allows to rank all candidate lists, instead of just returning the most likely candidate assignment for each MS feature, as done by Bach et al. (2018).

Our framework models the score integration as an inference problem on a graphical model, where the edges correspond to retention order predictions, the nodes correspond to MS features and the node labels correspond to candidate molecular structures, scored by a MS2 based predictor, such as CSI: FingerID (Dühkop et al., 2015), MetFrag (Ruttkies et al., 2016) or IOKR (Brouard et al., 2016), or in the absence of MS2 information, MS1 precursor mass deviation. This graph is fully connected, which makes exact inference an NP-hard problem. To solve this challenge, we resort to approximate inference, in particular spanning tree approximations (Marchand et al., 2014; Pletscher et al., 2009; Su and Roussu, 2015; Wainwright et al., 2003).

2 Materials and methods

2.1 Overall workflow

We assume data arising from a typical LC-MS-based experimental workflow (including chromatographic peak picking, and alignment): MS features consisting MS1 measurement and the associated RT. A subset of these will include an MS2 spectrum. In the following, we present our score-integration model in the most general form in which it is provided with MS features and a set of possible candidate molecular structures. The candidate list can be generated, e.g. by querying molecular structures from a structure database, such as ChemSpider (Pence and Williams, 2010), that have the same mass as the observed MS feature. In addition, we assume that to each candidate structure a score is assigned by either a MS2-based predictor, or, if no MS2-spectrum is available, a score based on the mass deviation of the candidates from the MS mass. For all molecular candidates associated with the different MS features, the retention order is predicted. Here, we use the Ranking Support Vector Machine (RankSVM)-based predictor by Bach et al. (2018). The candidate structure scores and predicted retention orders are integrated through a probabilistic graphical model (described in the following). This allows us to rank the molecular candidate structures by their inferred marginal probabilities, given both the MS and RT information.

More formally, the output of an LC-MS experiment is given as a tuple set \( D = \{ (x, t, C_i) \} \), with \( x \in X \) being the spectrum of feature \( i \) (either an MS2 or a spectrum containing only a single peak at the mass of the precursor ion if no MS2 information is available), \( t_i \in \mathbb{R}_{>0} \) being its RT, and \( C_i = \{ m_1, \ldots, m_n \} \subset M \) being the associated molecular candidates. Here, \( m_i \in M \) represents a molecular candidate structure and \( n_i \) is the number of molecular candidates for the \( i \)th MS feature. Figure 1 shows an overview of our workflow.

2.2 Probabilistic model

Let \( G = (V, E) \) be an undirected graph, in which each node, \( i \in V \) represents one observed MS feature, and with an edge for all MS feature pairs \( E = \{ (i, j) | i \neq j \} \). The edge-set \( E \) does not contain any parallel edges. The number of MS features is denoted with \( N \), i.e. \( |V| = N \). We associate each node \( i \) in the vertex set with a discrete random variable \( z_i \) that takes values from the space \( \{ 1, \ldots, n_i \} \). Intuitively, \( z_i \) defines which candidate has been assigned to the \( i \)th MS feature. The full vector \( z = \{ z_i | i \in V \} \) corresponds to the molecular structure assignment to each MS feature in the LC-MS experiment, and it takes values from the set \( Z = \mathbb{Z}_N \times \cdots \times \mathbb{Z}_N \). In this work, we consider \( Z \) to be fixed and finite for a given set of MS features, due to our definition of the molecular candidates sets, which assumes that we can restrict the putative annotation for a given MS feature.

2.2.1 Markov random field

The probability distribution of \( z \) is given as a pairwise Markov Random Field (MRF) (MacKay, 2005):

\[
p(z) = \frac{1}{Z} \prod_{i \in V} \psi_i(z_i) \prod_{(i,j) \in E} \psi_{ij}(z_i, z_j),
\]

composed of node \( \psi_i \) and edge \( \psi_{ij} \) potential functions, and omits higher-order cliques (hence the term pairwise). Above, \( \psi_i : Z_i \rightarrow \mathbb{R}_{>0} \) is the potential function of node \( i \) measuring how well the \( i \)'s candidate matches the measured MS information, and \( \psi_{ij} : Z_i \times Z_j \rightarrow \mathbb{R}_{>0} \) encodes the consistency of the observed retention orders for MS feature \( i \) and \( j \) and the predicted retention order of their candidates \( z_i \) and \( z_j \) and \( Z = \sum_{z \in Z} \prod_{i \in V} \psi_i(z_i) \prod_{(i,j) \in E} \psi_{ij}(z_i, z_j) \) is the partition function (MacKay, 2005).

2.2.2 Node potential function \( \psi_i \)

For each candidate \( m_r, r \in Z_i \), we predict a matching score \( \theta_r = f(x, m_r) \in \mathbb{R} \) expressing how well it matches the observed MS1 or MS2 spectrum \( x \). For that, we assume a pre-trained model, such as CSI: FingerID (Dühkop et al., 2015), MetFrag (Ruttkies et al., 2016) or IOKR (Brouard et al., 2016). We use the latter two in our experiments as representative MS2 scoring methods (Section 3.3). MetFrag performs an in silico fragmentation of \( m_r \) compares these fragments peaks with the observed ones in \( x \) and outputs a matching score. IOKR, on the other hand, can be used to directly predict a matching score \( f(x, m) \) for any (MS2 feature, molecular structure)-tuple. All matching scores \( \theta_r \) are normalized to the range \([0, 1]\). Finally, we express the potential of a molecular candidate \( m \), given the spectrum \( x \), as follows:

\[
\psi_i (z_i = r) = \max(\theta_r, c),
\]

where \( c > 0 \) is a constant used to avoid zero potentials. In our experiments, we select \( c \) such that it is 10 times smaller than the minimum of all non-zero scores across all candidate sets.

2.2.3 Edge potential function \( \psi_{ij} \)

For each candidate pair \((r, s) \in Z_i \times Z_j \) associated with the MS pair \((i, j)\), we compute how well the candidates’ predicted retention order...
is aligned with the observed one defined by the RTs \( t_i \) and \( t_j \). To this end, we apply the framework for retention order prediction developed by Bach et al. (2018). The edge potential \( \psi_i(z_i = r, z_j = s) \) is defined as follows:

\[
\psi_i(z_i = r, z_j = s) = \sigma \left( \text{sign}(t_i - t_j) \cdot w^T (\phi_r - \phi_s) \right),
\]

where \( w \in \mathbb{R}^{F_m} \) is the RankSVM’s parameter vector, and \( \phi_r, \phi_s \in \mathcal{X}_m \) are the feature vectors of the candidates’ molecular structures, and \( \sigma : \mathbb{R} \rightarrow (0, 1) \) is a monotonic function mapping the predicted preference value difference to a value between zero and one. In our experiments, we consider two mapping functions:

- **Sigmoid**: \( \sigma_{\text{sigmoid}}(x) = \frac{1}{1 + \exp(-\varepsilon x)} \)
- **Step Function**: \( \sigma_{\text{step}}(x) = 1, \text{for } x \geq \varepsilon, \quad \varepsilon = 10^{-10}. \)

The different functions can be interpreted as follows. The **sigmoid** makes full use of the information from the RankSVM margin, i.e. the score of each candidate pair depends on the preference score difference. In this work, we consider \( k \) as a hyper-parameter of our method that needs to be estimated from data (Section 3.5). The step-function, on the other hand, only differentiates between aligned and not aligned pairs.

### 2.2.4 Weighing of Information Sources

To control the contribution of each information source, i.e. MS information and retention orders, we introduce a modification on the potential functions:

\[
p(z) = \frac{1}{Z} \prod_{i \in V} \psi_i(z_i) \prod_{(i,j) \in E} \psi_{ij}(z_i, z_j) \quad ^D
\]

with \( D \in [0, 1] \). A \( D \) value close to one, e.g., will result in a score mainly based on the observed retention orders. In our experiments, we explain how this hyper-parameter can be estimated in practice (Section 3.5).

### 2.3 Ranking candidates through approximated marginals

We rank the molecular candidates using the marginals of the MRF (1). The marginal for the candidate \( r \) of MS feature \( i \) is given as:

\[
p(z_i = r) = \sum_{\{z' \in \mathcal{Z} \mid r \}} p(z').
\]

In practice, the calculation of (2) is intractable due to the size of the domain \( \mathcal{Z} \) of \( z_i \), which grows exponentially with the number of MS features, thus we will resort to approximate inference methods.

#### 2.3.1 Tree approximation of \( G \)

To enable feasible inference of (2), we approximate the MRF (1) using spanning trees of the original graphical model \( G \) (Marchand et al., 2014; Pletscher et al., 2009; Su and Rousu, 2015; Wainwright et al., 2005). In the following let \( T \) be a spanning tree of \( G \) with the same nodes, but an edge-set \( E(T) \subseteq E \), with \( |E(T)| = N - 1 \), that ensures \( T \) being a cycle-free single connected component. The probability distribution of the graphical model induced by \( T \) is given as:

\[
p(x|T) = \frac{1}{Z(T)} \prod_{i \in V} \psi_i(z_i) \prod_{(i,j) \in E(T)} \psi_{ij}(z_i, z_j). \]

As the graphical model associated with (3) is a tree, we can exactly infer its marginals through the **sum-product algorithm** (MacKay, 2005). The sum-product algorithm is a message-passing algorithm using dynamic programming that has linear time complexity in the number of MS features. See, e.g. MacKay (2005) for further details on the algorithm.

The output of the sum-product algorithm are the unnormalized marginals \( p(z_i = r|T) \) for all \( i \in V \) and \( r \in \mathcal{Z}_r \). We calculate the normalized marginals as follows (MacKay, 2005):

\[
p(z_i = r|T) = \frac{\mu(z_i = r|T)}{\sum_{r' \in \mathcal{Z}_r} \mu(z_i = r'|T)}. \]

#### 2.3.2 Random spanning trees sampling

We compare two approaches to retrieve spanning trees from \( G \). The first approach is to randomly sample spanning trees from \( G \) (c.f.
Pletscher et al., 2009; Su and Rousu, 2015; Wainwright et al., 2005). We sample the trees by applying the minimum weighted spanning tree algorithm to a random adjacency matrix. If for an MS feature pair \((i, j)\) both RTs are equal, i.e. \(t_{i}=t_{j}\), than their corresponding edge is not sampled. This is justified by the observation, that MS features with a RT difference equal zero, do not impose constraints on the retention order of their corresponding candidates.

We will refer to a sampled spanning tree as \(T_{S}\). The second approach was implicitly used by Bach et al. (2018) and corresponds to a linear Markov chain where edges connect adjacent MS features ordered by increasing RT, which can be seen as a degenerate spanning tree. In the remaining text, we refer to this tree as \(T_{chain}\).

### 2.3.3 Averaged marginal over a random spanning tree ensemble

Using tree-like graphical models for the inference is motivated by the exact and fast inference it enables us to do. However, a single tree, such as \(T_{chain}\) or a sampled \(T_{S}\), will most likely only be a rough approximation of the original probability distribution (1). Therefore, the use of random spanning tree ensembles \(\mathcal{T} = \{T_{i}\}_{i=1}^{N}\) has been proposed. In particular, Wainwright et al. (2005) show that an expectation over trees can be used to obtain an upper bound on the maximum a posteriori (MAP) estimate of the original graph, and showed that this approximation can be tight if the underlying trees agree about the MAP configuration. More recently, Marchand et al. (2014) demonstrated generalization bounds for joint learning and inference using tree ensembles. More applied work in using tree-based approximation can be found in Pletscher et al. (2009), who use majority voting and Su and Rousu (2015), who empirically study several aggregation schemes in multilabel classification.

Motivated by the mentioned literature, we opted to average the marginals of a random spanning tree ensemble \(T_{E}\), where for each tree \(T_{i}\) we independently retrieve the marginals using the sum-product:

\[
p(z_{i} = r | T) = \frac{1}{N} \sum_{T_{i} 
\]

### 2.3.4 Max-marginals

The exact inference on trees allows us to use the max-marginal, as an alternative to the sum-marginal shown in Equation (2). The max-marginal is closely related to the MAP estimate. For a single tree \(T\) it is given as:

\[
p_{\text{max}}(z_{i} = r | T) = \max_{\{r | z_{i} = r, \forall r \neq z_{i}\}} p(z_{i} | T).
\]

The interpretation of the two marginals (sum and max) differs slightly. Whereas the sum-marginal expresses the sum of the probabilities of all configurations \(z'\) with \(z'_{i} = r\), the max-marginal is the maximum probability that a configuration with the constraint \(z_{i} = r\) can reach. In our experiments, we compare the performance of both marginal types (Section 4.1). The max-product algorithm is used to calculate the unnormalized max-marginals \(p_{\text{max}}(z_{i} = r | T)\), which is a modification of the sum-product algorithm, in which summations are replaced by maximization. The normalized marginal can be calculated as (MacKay, 2005):

\[
p_{\text{max}}(z_{i} = r | T) = \frac{p_{\text{max}}(z_{i} = r | T)}{\max_{\{r | z_{i} = r, \forall r \neq z_{i}\}} p_{\text{max}}(z_{i} = r | T)}.
\]

By plugging Equation (5) into (4) instead of the sum-marginal, we obtain the averaged max-marginal \(\overline{p}_{\text{max}}\).

### 3.3 Run-time complexity

Calculating the marginals for an individual tree and all MS features \(i\) has run-time complexity \(O(N \cdot n_{\text{max}})\). Here, \(N\) is the total number of features and \(n_{\text{max}} = \max_{n_{\text{max}}} | Z_{i} |\) the maximum number of molecular candidates for a feature.

### 3.4 Material and experiments

#### 3.4.1 Evaluation datasets

To evaluate our score-integration approach, we use two publicly available datasets. These are described in this section and summarized in Table 1.

**CASMI 2016**

The Critical Assessment of Small Molecule Identification (CASMI) challenge is a contest organized for the computational spectrometry community (Schymanski et al., 2017). For its implementation in 2016, a dataset of 208 (MS², retention-time)-tuples was released. The dataset contains 81 negative and 127 positive ionization mode MS² spectra. The molecular candidate structure sets were extracted from ChemSpider, using a \(\pm 5\) ppm window around the monoisotopic exact mass of the correct candidate, by the challenge organizers.

**EA (Massbank)**

Massbank (Horai et al., 2010) is a publicly available repository for MS data. For the development of MetFrag 2.2, Ruttkies et al. (2016) extracted 473 (MS², retention-time)-tuples of 359 unique molecular structures from Massbank (EA dataset). The dataset is split into 154 negative and 319 positive ionization mode MS² spectra. We used the molecular candidates provided by Ruttkies et al. (2016) extracted from ChemSpider using the molecular formula (MF) of the correct candidate.

For each dataset and ionization mode, we repeatedly subsample training and test (MS², RT)-tuple sets: CASMI (negative) 50-times \(N_{\text{train}} = 31, N_{\text{test}} = 50\); CASMI (positive) 50-times \(N_{\text{train}} = 52, N_{\text{test}} = 75\); EA (negative) 50-times \(N_{\text{train}} = 45, N_{\text{test}} = 65\); and EA (positive) 100-times \(N_{\text{train}} = 50, N_{\text{test}} = 100\). No molecular structure, determined by its InChI representation, appears simultaneously in test and training. The training set is used for the hyper-parameter selection (Section 3.5) and the test sets are used to assess the average identification performance of our score-integration framework (Section 3.4).

#### 3.4.2 Training setup for the retention order predictor

To calculate the edge potentials of our MRF model (1), we use the RankSVM retention order prediction approach by Bach et al. (2018). The RankSVM model is trained using seven publicly available RT datasets. Six where published by Stanstrup et al. (2015) along with their RT mapping tool PredRet: UFZ_Phenomenex, FEM_long, FEM_orbitrap_plasma, FEM_orbitrap_urine, FEM_short and Eawag_XBridgeC18. The seventh dataset contains examples for which RTs were published as part of the training dataset for the CASMI 2016 challenge (Schymanski et al., 2017). The joint dataset covered four different chromatographic columns all using H2O → MeOH (with 0.1% formic acid as additive) as eluent. In total, the dataset contained 1248 (molecule, RT)-tuples of 890 unique molecular structures, after the same pre-processing as in Bach et al. (2018) was applied. We represent the molecular structures using Substructure counting fingerprints calculated with rcdk and CDK 2.2 (Willighagen et al., 2017). We use the MinMax-kernel (Ralaivola et al., 2005) to calculate the similarity between the fingerprints. For our experiments, we build an individual RankSVM model for each (MS, RT)-tuple subsample (Section 3.1), ensuring no molecular structure in the subsample is used for the RankSVM training.

#### 3.4.3 MS²-based match scores from MetFrag and IOKR

We apply MetFrag (Ruttkies et al., 2016) and IOKR (Brouard et al., 2016) as representative methods to obtain MS² matching scores for the molecular structures in the candidate list of each MS² spectrum.

**MetFrag**

We use the latest MetFrag version 2.4.5 (http://msbi.ipb-halle.de/crusttkie/metfrag/MetFrag2.4.5-CL.jar) and utilize it as described in Ruttkies et al. (2016). The MS² matching scores are calculated using the FragmenterScore feature of MetFrag.
3.3.2 IOKR

Two IOKR models are trained, for negative and positive mode MS² spectra, respectively. The training (MS², molecular structure)-tuples are extracted from GNPS (Wang et al., 2016), Massbank and the CASMI 2016 training data. We remove training molecular structures that appear in our evaluation datasets (Section 3.1). This results in 3255 negative and 6773 positive mode training examples. We use a uniform combination of 16 MS² spectra and fragmentation tree (FT) kernels as input kernel (Supplementary Section S4). On the output side, we use the same molecular fingerprint definitions as Duhrkop et al. (2019) as feature representation and a Gaussian kernel those distances are derived from the Tanimoto kernel (Brouard et al., 2019) as output kernel. For all MS² spectra in our evaluation datasets, we calculate the FTs using SIRIUS 4.0.1 (Duhrkop et al., 2019) and keep the highest scoring tree for each spectra to calculate the MS² and FT kernels used by the IOKR.

3.4 Performance evaluation

In our experiments, we use the top-k accuracy to determine the metabolite identification performance, i.e. the percentage of correctly ranked molecular candidates at rank k or less. Different approaches can be used to determine the rank of the correct structure. We follow the protocol used by Schymanski et al. (2017). If multiple stereo-isomers were present in the candidate list, only the one with the highest MS²-score was retained. The correct molecular structure was found by comparing the InChIs containing no stereo information. The top-k accuracies are calculated the test sets.

3.5 Hyper-parameter estimation

The training set of each individual subsample is used to determine optimal weighting D between MS and retention order information. For that, we run the score-integration framework for a different D values, and calculate the area under-the-ranking curve up to rank 20: 
\[ \text{top20AUC} = \frac{1}{20} \sum_{i=1}^{20} \text{rank}(i) \]
where rank(i) is the number of correct structures up to rank i and N is the number of MS features. Subsequently, we select the retention order weight with the highest top20AUC (Supplementary Section S2). The optimal sigmoid parameter k is estimated using Platt’s method (Lin et al., 2007; Platt, 2000) calibrated using RankSVM’s training data (Section 3.2).

3.6 Experiments

3.6.1 Full MS² information available

We compare our approach for combining MS² and RT information for metabolite identification against the baseline, which only uses MS¹ information for the candidate ranking. This allowed us to quantify the performance gain by using RTs. Furthermore, we applied two recently published methods for the integration of MS² and RT scores and compared them to our approach. The first one is MetFrag 2.2 (Ruttkies et al., 2016), which exploits the RT information by establishing a linear relationship between the candidates’ predicted LogP values with the observed RTs. Each molecular candidate receives an additional score by comparing its predicted RT against that observed for the corresponding MS² spectra. We use the

<table>
<thead>
<tr>
<th>Dataset</th>
<th>Ionization</th>
<th>Mass spectra info.</th>
<th>Molecular candidates</th>
<th>Chromatography</th>
<th>Eluent</th>
</tr>
</thead>
<tbody>
<tr>
<td>CASMI 2016</td>
<td>Negative</td>
<td>Precursor m/z</td>
<td>81</td>
<td>74 589</td>
<td>Phenomenex Kinetex EVO C18</td>
</tr>
<tr>
<td>CASMI 2016</td>
<td>Positive</td>
<td>Precursor m/z</td>
<td>127</td>
<td>183 633</td>
<td>Phenomenex Kinetex EVO C18</td>
</tr>
<tr>
<td>EA (Massbank)</td>
<td>Negative</td>
<td>Precursor m/z</td>
<td>154</td>
<td>75 107</td>
<td>Waters XBridge C18</td>
</tr>
<tr>
<td>EA (Massbank)</td>
<td>Positive</td>
<td>Precursor m/z</td>
<td>319</td>
<td>215 893</td>
<td>Waters XBridge C18</td>
</tr>
</tbody>
</table>

*Extracted from ChemSpider. CASMI: ± 5 ppm window around mono isotopic exact mass of correct candidate. EA: MF of correct candidate.
Table 2. Identification accuracies (top-k) for the different datasets and ionization modes

<table>
<thead>
<tr>
<th>Dataset</th>
<th>Method</th>
<th>Negative Top-1</th>
<th>Top-5</th>
<th>Top-10</th>
<th>Top-20</th>
<th>Positive Top-1</th>
<th>Top-5</th>
<th>Top-10</th>
<th>Top-20</th>
</tr>
</thead>
<tbody>
<tr>
<td>CASMI 2016</td>
<td>MS² + RT (our)</td>
<td>15.2 (***)</td>
<td>47.2 ****</td>
<td>57.0 (***)</td>
<td>70.1 (***)</td>
<td>14.0 (***)</td>
<td>40.7 (***)</td>
<td>52.2 (***)</td>
<td>62.8 (***)</td>
</tr>
<tr>
<td></td>
<td>MS² + RT (Chain-graph)</td>
<td>13.2 (***)</td>
<td>49.4 ****</td>
<td>61.0 ****</td>
<td>69.4 ****</td>
<td>11.9</td>
<td>36.5</td>
<td>50.2 ****</td>
<td>60.7 (***)</td>
</tr>
<tr>
<td></td>
<td>MS² + RT (MetFrag 2.2)</td>
<td>14.0 (***)</td>
<td>42.0</td>
<td>55.5</td>
<td>71.2 ****</td>
<td>13.7 (***)</td>
<td>36.2</td>
<td>46.2</td>
<td>57.5</td>
</tr>
<tr>
<td></td>
<td>Only MS²</td>
<td>11.1</td>
<td>44.2</td>
<td>55.3</td>
<td>68.0</td>
<td>11.8</td>
<td>37.3</td>
<td>47.0</td>
<td>58.3</td>
</tr>
<tr>
<td>EA Massbank</td>
<td>MS² + RT (our)</td>
<td>28.7 (***)</td>
<td>61.9 ****</td>
<td>73.8 ****</td>
<td>83.6 ****</td>
<td>27.3 (***)</td>
<td>61.6 (***)</td>
<td>72.9 (***)</td>
<td>80.7 (***)</td>
</tr>
<tr>
<td></td>
<td>MS² + RT (Chain-graph)</td>
<td>27.2 (***)</td>
<td>59.5 ****</td>
<td>72.4 ****</td>
<td>81.8 ****</td>
<td>23.9 (***)</td>
<td>59.2</td>
<td>70.1</td>
<td>79.1 (***)</td>
</tr>
<tr>
<td></td>
<td>MS² + RT (MetFrag 2.2)</td>
<td>30.2 (***)</td>
<td>59.2 ****</td>
<td>73.6 ****</td>
<td>84.4 ****</td>
<td>24.0 (***)</td>
<td>59.0</td>
<td>69.5</td>
<td>77.1</td>
</tr>
<tr>
<td></td>
<td>Only MS²</td>
<td>22.8</td>
<td>57.6</td>
<td>69.5</td>
<td>78.5</td>
<td>21.2</td>
<td>59.0</td>
<td>69.7</td>
<td>77.6</td>
</tr>
</tbody>
</table>

Note: Compares our score-integration framework (MS² + RT (our)), against the baseline (Only MS²), MetFrag 2.2 with predicted RT and the Chain-graph model. The best performance for each dataset and ionization is indicated by bold-font. The stars (*) represent the significant improvement over the baseline calculated using a one-sided Wilcoxon signed-rank test on the sample top-k accuracies (P < 0.05 (*), P < 0.01 (**) and P < 0.001 (***)).
Table 5. Top-k accuracies averaged on the CASMI data (pos. & neg.) using either MetFrag or IOKR as MS²-scoper for two different candidate sets: ‘All’ molecules queried using a mass window; only those with ‘correct molecular formula’.

<table>
<thead>
<tr>
<th>Candidate Set</th>
<th>Method</th>
<th>MetFrag Top-1</th>
<th>Top-5</th>
<th>Top-10</th>
<th>IOKR Top-1</th>
<th>Top-5</th>
<th>Top-10</th>
<th>Top-20</th>
</tr>
</thead>
<tbody>
<tr>
<td>All</td>
<td>MS² + RT</td>
<td>14.6 (***)</td>
<td>44.0 (***)</td>
<td>54.6 (***)</td>
<td>66.5 (***)</td>
<td>26.0 (***)</td>
<td>48.0 (***)</td>
<td>60.0 (***)</td>
</tr>
<tr>
<td></td>
<td>Only MS²</td>
<td>11.4</td>
<td>40.7</td>
<td>51.2</td>
<td>63.2</td>
<td>24.4</td>
<td>46.0</td>
<td>58.4</td>
</tr>
<tr>
<td>Correct MF</td>
<td>MS² + RT</td>
<td>17.7 (***)</td>
<td>48.4 (***)</td>
<td>59.8 (***)</td>
<td>71.0 (***)</td>
<td>30.6</td>
<td>52.3</td>
<td>66.2 (***)</td>
</tr>
<tr>
<td></td>
<td>Only MS²</td>
<td>13.1</td>
<td>46.0</td>
<td>56.9</td>
<td>68.7</td>
<td>30.6</td>
<td>53.9</td>
<td>65.3</td>
</tr>
</tbody>
</table>

Note: The stars (*) represent the significant improvement over the Only MS² (see Table 2 for details on the significance test).

4.3 Missing MS²

In Figure 3, we show the identification accuracy using our score-integration framework compared to the baseline (Only MS) when only some percentage of the MS features has an MS² spectrum. The features without spectra only use the precursor mass as MS information (Section 3.6). We vary the percentage from 0% to 100% with 25%-point steps. The retention order weight \( D \) was optimized using the 100% setting. At 0%, the score-integration framework only uses the mass of the candidates and their predicted retention order for the ranking. In the absence of MS² information, we observe a high performance gain for top-20. The more MS² information we add, the smaller the gain in top-20 accuracy using the retention orders. The fact that RT is a weaker information than MS² could explain this observation. The more MS² are available, the less additional information RT can add. For the top-1, there is constant improvement for all MS²%’s.

5 Discussion

In this article, we have put forward a rigorous probabilistic framework for the integration of MS-based candidate structure and retention order predictions. Our framework allows the use of any of the popular models, such as CSI: FingerID, IOKR or Metfrag for scoring candidate structures on MS data.

Our method takes into account the retention orders of all candidate structure pairs in distinct candidate lists through an approximated fully connected MRF model. It generally achieves higher quality structural annotations of observed MS features than using a single Markov chain as implied in the Bach et al. (2018) model. It also improves on the method of Ruttkies et al. (2016), which uses predicted RTs, in three out of four experiments. For the latter approach, we believe using the RankSVM scores instead of the predicted LogP values could improve the performance. Both measures are proxies for retention behaviour and our results show that the RankSVM predicts the retention order more accurately than the LogP values (see Supplementary Table S2). We also demonstrate that our framework improves the identifications, if only a subset of the MS features come with an MS² spectrum. The framework is computationally efficient, e.g. ranking the candidates for a set of \( N = 75 \) MS features takes \( < 4 \) min (see Section S.5), and can be trained using modest-sized datasets.

The amount of improvement using RT information was shown to depend on the dataset and MS² scorer (here MetFrag or IOKR). This indicates that RT information rather fine tunes the ranking given by the MS² scorer, e.g. by better tie-breaking. The underlying factors could be ambiguities in the candidate sets that can be only be resolved by RT or molecular features that cannot be predicted by MS. Stereochemistry is an obvious factor, but annotations of stereochemistry are not always provided for the RT databases limiting the use of this information for training better retention order prediction models. Thus improved modelling of stereochemistry features is an important open problem (Witting and Boeker, 2020). A further research direction could be to include the LC system’s configuration, e.g. column or eluent, into the retention order prediction. As LC systems can be configured to separate certain molecular classes, this could provide additional information to certain molecular candidates. Also, using the LC peak shape to train a model directly predicting the retention order probabilities could be more accurate, e.g. by incorporating RT variance. However, such data are currently not part of the public RT databases.

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**Conflict of Interest:** none declared.

**References**