

qpub

# ‘QPuB’

<b>Title</b>	Quantification of Peptides using Bayesian inference
<b>Version</b>	0.1.0
<b>Depends</b>	R ( $\geq 3.5.0$ )
<b>Operating system</b>	Linux, macOS, Windows
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<b>License</b>	GNU General Public License v3.0
<b>URL</b>	<a href="https://github.com/QuantSysBio/QPuB">https://github.com/QuantSysBio/QPuB</a>
<b>Date</b>	2019-08-01

## Description

The mass spectrometry ion peak area of peptides is linearly related to the absolute amount of the peptides through a proportionality constant called conversion factor [4]. QPuB (Quantification of Peptides using Bayesian inference) employs Bayesian statistical inference based on Markov chain Monte Carlo (MCMC) sampling to learn the posterior distributions of the conversion factors for the peptide products without further experimentation.

## Requirements

This tool requires the following R packages: R.utils, tictoc, sys, tmvtnorm, matrixcalc, corpcor, ggdmc, dqrng, coda, mcmcse, matrixStats.

## Installation and updates

No installation required. For updates check our GitHub.

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## References

Henze, S., Paul, D., Mansurkhodzhaev, A., Henklein, P., Textoris-Taube, K., Urlaub, H., Mishto, M., and Liepe, J. (2019). Quantification of in vitro peptide hydrolysis and protease-catalyzed peptide splicing using bayesian inference. Under review.

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# Nomenclature

## Sets of numbers

Symbol	Description
$\mathbb{N}$	natural numbers
$\mathbb{Z}$	integers
$\mathbb{Z}_{>0}$	positive integers
$\mathbb{R}$	real numbers
$\mathbb{R}_{\geq 0}$	non-negative real numbers
$\mathbb{R}_{>0}$	positive real numbers
$\mathbb{R}^d$	$d$ -dimensional real field

## Statistics & probability

Symbol	Description
$\text{Var}[\delta]$	variance of $\delta$
$\mathbb{E}[\delta]$	expectation of $\delta$
$\mathbb{P}(x)$	probability of $x$

## Acronyms

### Immunology

MHC	major histocompatibility complex
-----	----------------------------------

### Techniques

MS	mass spectrometry
----	-------------------

### Algorithms

QME	Quantification with Minimal Effort ( <a href="#">Mishto et al., 2012</a> )
MCMC	Markov chain Monte Carlo
M-H	Metropolis-Hastings ( <a href="#">Metropolis et al., 1953</a> ; <a href="#">Hastings, 1970</a> )

# 1 | Introduction

The central dogma in molecular biology describes how proteins are generated inside a cell. Protein dynamics are, however, tightly regulated not only by the rate of protein synthesis, but also by protein degradation through proteases. The resulting (poly)peptides from protease digestions can be further degraded into single amino acids and recycled for protein metabolism. Proteases can also produce functional peptides, which regulate signalling processes. One example is the antigen presentation pathway of the immune response. Peptides produced through various proteases, such as proteasome, metalloproteases, and others, are subsequently transported to the cell surface where they are displayed on MHC-I/II molecules, to ensure an efficient immune response.

Understanding the dynamics of protein degradation and peptide production requires quantitative information. This can be obtained through mass spectrometry (MS) measurement of protein or polypeptide digestions *in vitro* with purified proteases. Mass spectrometry, however, is only semi-quantitative, because the MS signal, i.e. the extracted ion peak area, is strongly influenced by the characteristics, e.g. sequence and charge, of the measured peptides. The MS ion peak areas resulting from different peptides can therefore not be directly compared (Bassani-Sternberg et al., 2015; Cox et al., 2014; de Graaf et al., 2014; Liepe et al., 2016, 2019). To circumvent this, labelling techniques have been developed. While labelling techniques resulted in great advance in understanding protein metabolism, they still only provide relative measures of protein / peptide abundance. Absolute quantification of peptides using MS can be achieved through titration of every peptide of interest using synthetic peptide equivalents. This is, however, very laborious and cost inefficient when quantifying many peptides.

To overcome this limitation, algorithms have been developed that aim to estimate for each peptide a conversion factor that relates the MS ion peak area to absolute peptide amounts. Those algorithms make use of the conservation of mass in closed *in vitro* systems by estimating conversion factors for each peptide that minimise the mass deviation of amino acids between degraded substrate and generated peptide products. For less specific proteases, such as the proteasome, many peptide products can be observed and for all of them conversion factors need to be estimated. This results in a parameter estimation problem with a high dimension search space, that imposes a challenge for most optimisation routines.

We developed a tool to overcome those problems using Bayesian inference. The algorithm, named QPuB (Quantification of Peptides using Bayesian inference), employs a generalised adaptive Metropolis (AM) algorithm with global adaptive scaling to estimate the full posterior distribution of conversion factors. Here, we present an R package, which implements QPuB in a flexible and user friendly manner.

In this manual we provide installation guides, an overview about the package and step-by-step examples on how to use QPuB. We furthermore provide an appendix that describes the working principles of QPuB and gives an overview about the parameter estimation techniques used in the implementation.

## 2 | Elements of QPuB

QPuB is organized into three modules namely **INPUT**, **ALGORITHM**, and **OUTPUT** (see Figure 2.1). The **INPUT** module takes the MS signal intensities of the substrate and all major peptide products. Along with that, the algorithm also requires the specification of the protease used, for e.g. whether the protease is an endo- or an exopeptidase. As optional inputs, users can provide the titration measurements as well as the time point sequence following which the respective intensities will be compared (see Section 2.3.1). In addition, the **INPUT** module must be provided with a .txt file called **input.txt** that contains values of all the parameters (numerics as well as logicals) required to execute the algorithm and generates the results afterwards.

Upon receiving all the input parameters, the **ALGORITHM** module of QPuB invokes an adaptive Metropolis (AM) sampling algorithm (see Appendix B) to generate samples from the posterior densities of the conversion factors.

As the sampling proceeds, the **OUTPUT** module generates the histograms (excluding burn-In) and traces (including burn-In) of the Monte Carlo samples and as well as the residual plots for each conversion factors. Moreover, trace plots for the nuisance parameters such as the punishment parameter and the variance in the data, are also generated. At the end of the simulation, the Monte Carlo samples are saved as **.RData** format and a file containing the summary statistics of the chain is generated. In case the titration data is provided in the beginning, the **OUTPUT** module also calculates the absolute amounts of the products from their intensities and the estimated conversion factors using the Eq. (2.1.1) and generates the corresponding plot.

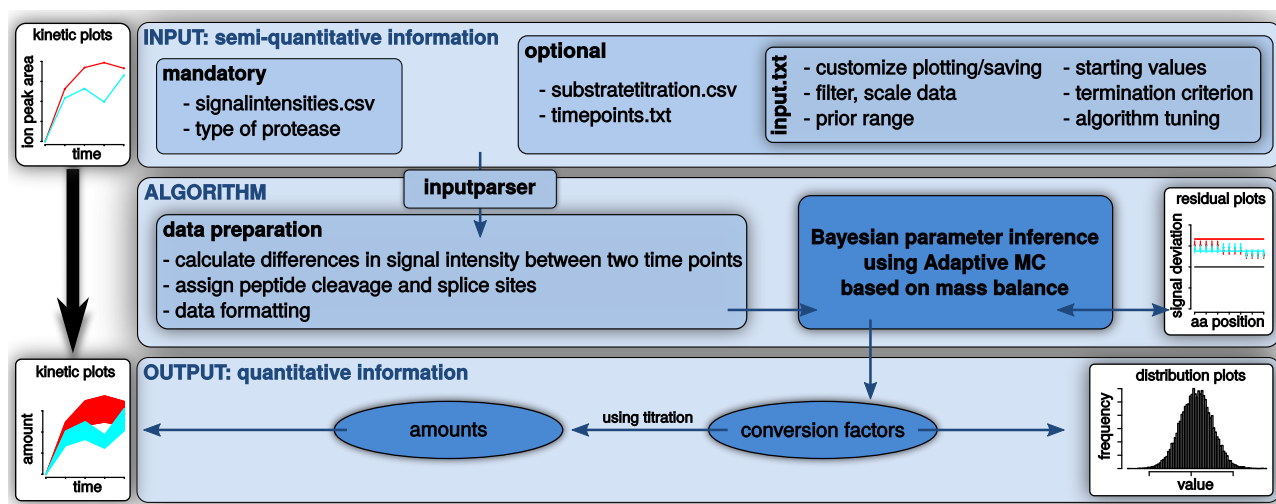


Figure 2.1: Schematic of QPuB package

## 2.1 Principles of QPuB

QPuB is based on the following two principles:

- Linear correlation between the signal intensities and the amounts.
- Mass conservation of peptide products over time assuming the *in vitro* system of digestion as a closed system.

Below, we explain in detail the two principles mentioned above.

### Linear correlation

This principle is based on (Peters et al., 2002, Figure 1), where the authors experimentally observed a linear relationship between the signal intensity  $s_i \in \mathbb{R}^+$  of a product  $i$  and its concentration  $c_i \in \mathbb{R}^+$ . Mathematically, the relationship translates to the following:

$$c_i = v_i s_i, \quad i \in [1, P] \quad (2.1.1)$$

where  $v_i \in \mathbb{R}^+$  is the conversion factor for the  $i^{\text{th}}$  product and  $P$  is the number of products. The conversion factor of the substrate is set to 1 for convenience.

### Mass conservation

The second principle that we make use of is the law of mass conservation. Since we consider a closed system of *in vitro* digestions, we know that each amino acid present in the solution at time  $t = 0$  is still present at any time  $t > 0$ . However, depending upon the precision of the mass spectrometer, small peptide products may remain undetected. This systemic loss of mass has to be accounted for. On the other hand, a gain of mass is impossible, because no amino acids are created during the digestion. Formally, the sum of amino acids of the products should be equal to the amount of substrate degraded since the beginning, for every amino acid position and for every time points:

$$\sum_{i=1}^P c_i(t) b_{ia} = c_0(t) - c_0(0) = \Delta c_0(t) \quad \forall a, t, \quad (2.1.2)$$

where  $a$  denotes the amino acid position,  $t$  denotes the time points, and  $c_i(t)$  denotes the concentration of product  $i$  at time  $t$ . The factor  $b_{ia} \in [0, 1]$  is the probability that the product  $i$  contains amino acid  $a$ . The amount of substrate degraded since time  $t = 0$  is  $\Delta c_0(t)$ . Now, substituting the expression for  $c_i$  according to equation (2.1.1), we have

$$\sum_{i=1}^P v_i s_i(t) b_{ia} - \Delta c_0(t) = 0 \quad \forall a, t. \quad (2.1.3)$$

Since this difference should be zero for every  $a$  and  $t$ , also the sum over all  $a$  and  $t$  must be zero:

$$\sum_{t=1}^T \sum_{a=1}^A \left[ \sum_{i=1}^P v_i s_i(t) b_{ia} - \Delta c_0(t) \right] = 0. \quad (2.1.4)$$

The left-hand side then gives us our objective function, which should be as close to zero as possible. In total, our aim thus is to find values for the conversion factors that minimize the difference between our simulation results and the true amount of products:

$$\min_{v_i \in \mathbb{R}^+} \sum_{t=1}^T \sum_{a=1}^A \left[ \sum_{i=1}^P v_i s_i(t) b_{ia} - \Delta c_0(t) \right]. \quad (2.1.5)$$

Instead of finding the sole minimizer of (2.1.5), QPuB uses a Bayesian approach to obtain a full distribution of possible values.



## Calculation of the concentrations

Once a distribution for the conversion factor of every peptide product is obtained, the concentrations can be calculated. If the titration data is provided by the user, we fit it using a linear model  $y = mx + b$  according to Eq. (2.1.1), where  $y = s_i$  and  $x = c_i$ . Because the conversion factor of the substrate is set to 1, the expression for the concentrations of the substrate takes the following form

$$c_0 = \frac{s_0 - b}{m}. \quad (2.1.6)$$

Using the slope  $m$  and intercept  $b$  of the substrate, the concentration of product  $i$  can be calculated as follows:

$$c_i = \frac{v_i s_i - b}{m}. \quad (2.1.7)$$

## 2.2 The software

As a package QPuB contains the following R scripts:

Scripts	Functionalities
<b>runQPuB</b>	<ul style="list-style-type: none"><li>• the main routine which is invoked using command line arguments (see Chapter 4 and 5)</li></ul>
<b>inputparser</b>	<ul style="list-style-type: none"><li>• create output folder</li><li>• parse input specifications from a text file or set defaults</li><li>• read the experimental data</li><li>• read the time points to compare, if provided</li><li>• read the titration data file, if provided</li></ul>
<b>datapreparation</b>	<ul style="list-style-type: none"><li>• filter data</li><li>• plot input signal kinetics</li><li>• assign cleavage and splice sites of peptide products</li><li>• create position probability matrix</li><li>• calculate the change in MS signal intensities between time points</li><li>• scale the data</li></ul>

### **MCMCroutine**

- run the random walk adaptive Metropolis algorithm with generalized adaptive scaling (Andrieu and Thoms, 2008)
- definition of the prior distribution
- definition of the likelihood function
- definition of the proposal distribution

### **additionalfunctions**

- contains all functions needed during and after the QPuB routine
- during:
  - plot distributions and history of parameters
  - plot current mass deviation
- after:
  - provide summary of the parameter chain
  - calculate absolute concentrations of all reagents based on the titration data if provided
  - plot kinetics of the absolute concentrations

Utilities of the scripts mentioned above are explained in the next section.

## **2.3 Dissecting the modules**

In this section, we will present a detailed description of the necessary input, algorithms and output routines of QPuB.

### **2.3.1 Input**

Mandatory input to the QPuB routine are the experimental data and some input parameters. Optional input include the substrate titration and a file of time points to be compared. For input folder structure see Section 2.3.2.

#### **Experimental Data (Mandatory)**

The data provided must be a kinetic data from mass spectrometry, i.e. signal intensities of an *in vitro* digestion over a few hours time for all major products. We strongly advise to provide more replicates for more certainty. For each replicate, a separate data file of a **.csv** format that contains the amino acid sequences and the numeric values, must be provided. In that file the first column must contain the sequences and all other columns must contain the signal intensities over time. Each row of the file corresponds to one peptide product. The first row must always contain the substrate. The header must contain numeric type time points having the same unit. The user has the flexibility to name the **.csv** files.

```
sequence,0,0.5,1,1.5,2,3,4
RTKAWNRQLYPEW,8.89E+11,5.55E+11,2.75E+11,1.38E+11,8.35E+10,2.01E+10,3.38E+09
RTKAWNR,6.02E+08,2.68E+10,3.67E+10,3.92E+10,4.70E+10,5.41E+10,4.14E+10
RTKAWNRQ,5.58E+07,6.40E+08,9.25E+08,8.88E+08,1.18E+09,1.23E+09,7.77E+08
QLYPEW ,1.14E+10,2.87E+11,4.30E+11,4.94E+11,5.55E+11,6.34E+11,5.14E+11
RTKAWNRQL,1.06E+07,2.43E+08,3.90E+08,4.23E+08,4.54E+08,3.99E+08,2.91E+08
...
```

## Parameters (Mandatory)

The input parameters are specified in a text file named **input.txt**. This name is mandatory and **must not be changed**. There are numerical as well as logical parameters. Logical parameters can be set to TRUE or FALSE. Other possible ways of spelling: **True**, **true**, **T**. The feasible values for the numerical parameters are defined below. Numbers may be formatted in decimal (2000000) or exponential notation (2e6, 20e5), but should not contain asterisk notation '\*' (2\*10\*\*6) or the caret notation '^' (2\*10^6).

In the following we discuss the contents of **input.txt** distinguishing low level and advanced level input parameters. For datasets with a small number of peptide products, we provide default values for most of the parameters such that there is only one or two mandatory inputs that the user must specify.

```
#####
# INPUT FILE FOR QPUB PACKAGE
#####

# WARNING: THIS FILE MUST NOT BE RENAMED!
# Mandatory name: input.txt

#####
# LOW LEVEL INPUT
#####

##### MANDATORY INPUT

# mechanism of the underlying enzyme: 'endopep', 'exo pep'
enzyme: 'endopep'

# amount of substrate loaded for kinetics (if titration provided)
loaded: 200
```

The user must choose between exopeptidase 'exo pep' and endopeptidase 'endopep' to specify the nature of the protease. In case the substrate titration is provided, the second mandatory input is the amount of substrate loaded in the kinetics. The unit must be identical to the titration data file.

```
##### OPTIONAL INPUT WITH DEFAULTS

### DIAGNOSTIC PLOTS
# plot distribution and history of parameter chain
plot_chain: TRUE
# plot residuals: mass deviation in current iteration
plot_residuals: TRUE
# plot every x iterations
freq_plot: 10000
```

```
# plot detailed: every 100 iterations before iteration 1000, every 1000
# iterations under iteration 10000
plotdet: TRUE
# generate vector graphics instead of flat png (default: FALSE)
vecplot: FALSE

### BACKUP
# save chain every x iterations
freq_save: 10000
```

As intermediate output, QPuB creates diagnostic plots of the Markov chain in the folder [plots.diagnostics](#) and saves the current chain of parameters to an RData-file. The user can choose whether these diagnostic plots of the Markov chain should be produced.

**Plot\_chain:** The chain is shown using a line plot of the parameter value over the course of the iterations. The resulting distribution is shown in form of a histogram with the frequency of parameter values.

**Plot\_residuals:** The residual plot depicts the mass deviation of the QPuB outcome from the true solution. Following the rule of mass conservation, the amount of every amino acid should sum up to the amount of substrate degraded between two time points to be compared, indicated by a horizontal line for each replicate. The boxplots represent the distributions of the concentrations for every amino acid, arising from the outcome distributions of the conversion factors.

**freq\_plot** and **freq\_save:** Specify the frequency at which the plots will be generated and saved, respectively. The default value is 10000. Any integer value larger equal 1 is feasible.

To inspect the behaviour of the chain in the first few iterations, the logical parameter **plotdet** is set to **TRUE**. In this case, the diagnostic plots are produced every 100 iterations before iteration 1000, and every 1000 iterations until iteration 10000. After that, the plots are produced according to the specified value for **freq\_plot**. This detailed plotting can be turned off by setting **plotdet** to **FALSE**. The diagnostic plots are saved as compressed pdf-files. All other figures are exported as **.png** format. In order to obtain the plots as vector graphics, the user needs to set the logical parameter **vecplot** to **TRUE**.

```
#####
# ADVANCED INPUT
#####

### DATA MANIPULATION
# Scale products to match order of magnitude of substrate
scaleprod: TRUE
# Filter out products which have a signal intensity
# below the threshold.
# If TRUE then threshold must be set.
filterprod: FALSE
threshold: 1e6
```

The signal intensities of the peptide products are scaled to bring the substrate and the product intensities to the same order of magnitude. In this way the prior ranges are less dependent on the specific data set. One can set the parameter **scaleprod** to **FALSE** if this scaling is not required. In this case, the prior range and the starting values have to be adjusted below.

For large datasets, the dimension may be reduced by excluding some of the peptide products that have low intensities (**filterprod: TRUE**) below a threshold (**threshold: threshold\_value**). This filtering is pragmatic since peptides having such low intensities contribute less to the mass conversion. We propose a **threshold** value of  $10^6$  for datasets larger than 100 products.

```

### UNIFORM PRIOR DISTRIBUTION
# lower and upper bound of uniform prior range
# of conversion factors for all products
conv_lower: 1e-4
conv_upper: 1e4
# lower and upper bound of uniform prior range of the standard deviation
sigma_lower: 1e-4
sigma_upper: 1e4

### STARTING VALUES OF THE PARAMETERS
# initial values of the conversion factors of all products
conv_start: 1
# initial value of the standard deviation in the data
sigma_start: 10
# initial value of the punishment parameter. Choose a value between 0 and 1
pun_start: 0.1

```

For the prior range, choose any positive values satisfying  $\text{lower} < \text{upper}$ . If the product signals are scaled to fit the substrate (`scaleprod: TRUE`, default), then the prior range of the conversion factors is narrowed down to approximately 7 orders of magnitude centered around the value 1, which is the fixed conversion factor of the substrate. For both the conversion factors and the standard deviation, the default prior range is  $[10^{-4}, 10^4]$ .

Since the conversion factor of the substrate is set to 1 by default, we choose 1 as the starting value for the conversion factors of all peptide products. Along with that, an initial value of 10 for the standard deviation has turned out to be a reasonable choice for our examples. The user may choose any starting values in the prior range specified above. Moreover, the default starting value of the punishment parameter is set to 0.1.

The punishment parameter takes a value between 0 and 1. A value of 0 signifies strict avoidance, whereas a value of 1 imposes a zero avoidance for the mass gain.

```

### ALGORITHM PARAMETERS
# optimal acceptance rate
OptAccRate: 0.234
# track performance of the run: print acceptance rate and effective sample size
Track: TRUE
# Exponent for the sequence to realize vanishing adaptation.
# Choose a value between 0 and 1.
GammaExponent: 0.5
# Fraction of the Markov chain to consider as burn-in, 0.25 means 25% burn-in
burnFrac: 0.5

### PROPOSAL FUNCTION
# burn-in of the internal Gibbs sampler
burnGibbs: 1000
# Thinning parameter of the internal Gibbs sampler
thinGibbs: 20

```

A typical choice of the optimal acceptance rate for the Metropolis algorithm is 0.234 (Roberts et al., 1997). The user may choose any value between 0 and 1. With the setting `Track: TRUE` the current acceptance rate and the current effective sample size are printed at every 1000 iterations.

Vanishing adaptation is achieved via the so called Gamma function with exponent `GammaExponent`. Any value between 0 and 1 may be chosen, the default is 0.5. For details on the Adaptive Metropolis algorithm see the Appendix B.

When the Markov chain starts in a region of low likelihood, it will probably take a while to arrive at the region of the target distribution. Therefore, initial samples have low contribution towards the posterior distribution, and are typically discarded as burn-in. We use 50% of the chain as burn-in by default. The value of the parameter `burnFrac` decides the fraction of the samples that will be discarded as burn-in. The parameter takes a value between 0 and 1. For example, a value of 0.25 means that 25% of the samples will be discarded as burn-in.

The R function `rtmvmnorm` used in the proposal function generates proposal samples from a truncated multivariate normal distribution using a Gibbs sampler. The parameter `burnGibbs` specifies the amount of burn-in samples for the Gibbs sampler. The default value of `burnGibbs` is 1000. In addition, the degree of uncorrelated samples is taken care of by the parameter `thinGibbs` which has a default value of 20. See the respective package documentation for details.

```
### TERMINATION CRITERION
# TRUE: termination via effective sample size calculation.
# FALSE: enables the MaxIter variable, which is the maximum number of
# iterations the MCMC will run
TerminationCriterion: TRUE
MaxIter: 1e6
# iteration when to start checking the criterion
ESSiter: 10000
# Confidence level for calculating the effective sample size
# using the minESS routine
ConfLevel: 0.05
# Monte Carlo error in percent for the minESS routine
Tolerance: 0.05
```

The QPuB run terminates based on the effective sample size (ESS) of the Markov chain by default. The algorithm checks for convergence every 1000 iterations after iteration `ESSiter: 10000` by default or according to the user input. Any value `ESSiter > 1000` may be chosen, in order to constitute a positive definite covariance matrix of the samples (Vats et al., 2019). `ConfLevel` and `Tolerance` are the internal parameters of the *minESS* routine. They signify the confidence level for the ESS and the fraction of the accepted Monte Carlo error in parameter estimation, respectively. Both the parameters take a value between 0 and 1. For example, a value of 0.05 for `ConfLevel` means that the calculated value of the ESS is within the 95% level of confidence (see the respective package documentation for details). For large and complex datasets, reaching the minimum number of ESS can take a very long time. Upon visual inspection, it may appear that the chain has already converged, although mathematically it might not be. In such cases, the user can opt for a termination criterion based on the maximum number of iterations by setting `TerminationCriterion` to `FALSE`, and assigning a desired number to the parameter `MaxIter`. The default value of `MaxIter` is set to  $10^6$ , meaning that the algorithm will terminate after  $10^6$  iterations. Additionally, for high dimensional problems, it may happen that the covariance matrix of the target distribution becomes singular or ill-conditioned. In such cases, routines `tmvtnorm` and `multiESS` will not work. QPuB avoids such premature termination by first inspecting the covariance matrix, and then automatically switching to the maximum iteration mode if the matrix is found to be singular.

### Timepoints (Optional)

In QPuB, not the signal intensities per se but the differences in intensities between a pair of time points are taken into account. Using the input file `timepoints.txt`, the user may specify, which time points should be compared. The name of the file is mandatory and must not be changed. If no `timepoints.txt` file is provided, the variation in signal intensity between two consecutive time points is considered by default:

```
0 1
1 2
2 3
3 4
```

The file must contain numbers arranged in two columns. QPuB calculates the difference in signal intensity of the second column compared to the first column. For each row, intensities in the first column are subtracted from the intensities in the second column.

Regardless of the unit and numeric values of the time points in the data file, the timepoints file has to be provided with the count of the time points:

number	0	1	2	3	4
hours	0	0.5	1	1.5	2
minutes	0	30	60	90	120

The user is recommended to manipulate the sequence of time point indices for comparison if certain time points are supposed to be weighted more or less than others. See Section 5.4.5 for an example.

### Titration (Optional)

To calculate absolute concentrations from the estimated conversion factors and the input signal intensities, QPuB requires the substrate titration data as input. Titration measurements are specified in a csv-file, which has the following structure:

```
"pmol","rep1","rep2"
0,8738783.03163,33850140.1962817
6.5,125855871751.115,126066103768.273
12.5,228222898282.954,252195890030.762
25,518494461424.112,513196824959.805
50,1029977038639.7,1004577689796.97
75,1323855190838.57,1263027816310.47
100,1654653991391.97,1751554906143.47
```

The first column is the amount of substrate loaded into the mass spectrometer and further columns contain the intensities in replicates. The precise column names are unimportant but a header must be provided, for example: "amount","rep1","rep2",.... The name of the file can be user defined and must be specified as one of the command line arguments, see Chapter 4 for further details. The titration data file must be located in the input folder.

The initial output of an execution using the titration data versus not using it is exactly the same. The conversion factors are unaffected. Only the content of the final folders [concentrations](#) and [plots.concentrations](#) differs. If no titration data is provided, then normalized intensities are returned. These can be used to qualitatively compare the peptide products but they don't provide absolute amounts.

### 2.3.2 The inputparser

QPuB requires a particular input folder structure. The input folder [inputfoldername](#) contains the input.txt file, the timepoints.txt file (if provided), the titration csv-file (if provided), and a [data](#) folder that contains all the data csv-files. The name of the data folder is mandatory and must not be altered.

```

parentdirectory/
|-- inputfoldername/
|   |-- data/
|   |   |-- rep1.csv
|   |   '-- rep2.csv
|   |-- input.txt
|   |-- timepoints.txt
|   '-- titration.csv
'-- QPuB-Output/
    |-- OUTPUT_inputfoldername
    |-- OUTPUT_inputfoldername(1)
    '-- OUTPUT_inputfoldername(2)

```

QPuB creates a general output folder **QPuB-Output** on the fly inside the parent directory of the input folder **inputfoldername**. Every time the routine is executed, an individual output subfolder with the name **OUTPUT\_inputfoldername** is created inside **QPuB-Output**. If a subfolder with this name already exists, it will not be overwritten, but a new folder will be created and sequentially numbered, e.g. **OUTPUT\_inputfoldername(1)**. If the user wants to individually name the output folder, it can be done via a flag in the command line (see Chapter 4). All output of the algorithm regarding the current run will be saved inside this subfolder. For monitoring the algorithm run, a progress report will be saved in the file **runQPuB\_ROUT.txt**.

The inputparser reads in **input.txt** and parses the parameters and their values (separated by a colon, see Chapter 2.3.1). If a mandatory parameter is not provided, default values and settings for that parameter will be assigned. All csv-files from the folder **data** are read in as mass spectrometry signal measurements over time.

If the **timepoints.txt** file is provided inside the inputfolder, the parser reads in the time points specified in that file for the calculation of the likelihood. Otherwise, successive time points are taken into account by default.

Finally, the titration data is parsed, if provided. For detailed input specifications, see Section 2.3.1.

### 2.3.3 Data preparation

In this part of QPuB, first, the dimensions of the datasets are read from the data, such as

- number of replicates
- number of time points
- number of time point comparisons
- number of products
- number of amino acids in the substrate sequence

Next, depending on the mechanism of the protease used, the amino acid positions to be considered for mass balance are determined. If we are dealing with an endopeptidase, then the algorithm considers all amino acids in the calculation of the likelihood.

For an exopeptidase, the challenge lies in the systematic mass loss. Since short peptide products often remain undetected by the MS device (the precision varies across the device specifications), the law of mass conservation is harder to satisfy. QPuB takes this shortcoming into account by considering only the amino acid positions contained in the shortest major product observed for the calculation of the likelihood.

#### Filter the data

Upon choosing the filtering option, the products with signal intensities below a threshold are filtered out, because they don't contribute much to the mass balance.



## Plot input signal kinetics

We then visualize the input data by plotting the kinetics of signal intensity over time for all peptide products remaining.

## Assigning cleavage and splice sites of peptide products

To infer where the peptide products originate from in the substrate, we align the product sequence to the substrate sequence, taking nonuniqueness into consideration. We assign cleaved (PCP) and spliced peptides (PSP) according to the following convention (Mishto et al. (2012)): If a product can be created by the process of simple cleavage, then it is assumed to be a PCP.

**Example 1** Assume a substrate with sequence *ABCDEFGHABCD* and the products with sequences *DEFGH* and *FGHABC* respectively. We number the amino acids in the substrate consecutively  $a = 1, \dots, 13$ . We decide peptide 1 to be a PCP with the unique position code *4\_8*, since its sequence is a direct subsequence of the substrate sequence. On the other hand, peptide 2 is a PSP with a nonunique position code of either *6\_8\_1\_3* or *6\_8\_10\_12*. The peptide number, its sequence and its possible positions are saved in a table *identifier.csv*:

<i>number</i>	<i>sequence</i>	<i>position code</i>	<i>position code</i>	<i>...</i>
1	DEFGH	4_8	-	
2	FGHABC	6_8_1_3	6_8_10_12	
...				

## Creation of the position probability matrix

Using the position information, the position probability matrix  $b \in P \times A$  is defined. It contains the probabilities of the amino acid  $a \in [1, A]$  of the substrate being used in the production of peptide  $i \in [1, P]$ . The entry  $b_{ia}$  takes the following form

$$b_{ia} = \frac{1}{N_a} \in [0, 1], \quad (2.3.8)$$

where  $N_a$  is the number of possible origins the amino acid at position  $a$  of product  $i$  has in the substrate. In Example 1 above, the frequencies of the single amino acids in the substrate sequence are  $[2, 2, 2, 2, 1, 1, 1, 1, 1, 2, 2, 2, 2]$ . Now consider the product  $i = 1$ , the cleaved 5mer DEFGH with positions *4\_8*. Following the convention, the positions 4 to 8 get the matrix entries  $b_{14} = b_{15} = b_{16} = b_{17} = b_{18} = \frac{1}{1} = 1$ , all the other positions have probability 0:

$$b_{1:} = [0, 0, 0, 1, 1, 1, 1, 1, 0, 0, 0, 0, 0]. \quad (2.3.9)$$

Product 2, on the other hand, does not have a unique position code assigned. The amino acid A, for example, could stem either from position 1 or 10 in the substrate, making  $N_1 = N_{10} = 2$ . We consider both possibilities equally likely. Hence the probability of A in the peptide 2 stemming from position 1 in the substrate is  $b_{21} = \frac{1}{2}$ . In total, the second row of the position probability matrix reads

$$b_{2:} = [0.5, 0.5, 0.5, 0, 0, 1, 1, 1, 0, 0.5, 0.5, 0.5, 0]. \quad (2.3.10)$$

## Calculation of the change in MS signal intensities between time points

For the calculation of the likelihood, the amount of substrate degraded between two time points is required. By default, consecutive time points are considered. The user can also provide time points to compare in *timepoints.txt* as an input (see Section 2.3.1).

We first subtract the background noise at time 0 from all data points. Then the difference between time points is stored in a variable for the substrate degraded and for all the products respectively.

## Scaling the data

Finally, we scale all signals by the value specified for the parameter `scale_mag` to avoid high orders of magnitude and the product signals by the value specified for the parameter `scale_prod` to match the order of magnitude of the substrate and the products.

### 2.3.4 The adaptive Metropolis-Hastings algorithm

The parameters of interest to be inferred by the algorithm are the conversion factors  $v_i$  of all peptide products. Along with that, the standard deviation  $\sigma$  of the likelihood and the penalty parameter  $\varphi$  for mass gain (description below) are also estimated. Hence, the parameter set becomes  $\Theta = \{v_1, \dots, v_P, \sigma, \varphi\}$  which has a dimension of  $P + 2$ .

#### The prior probability

The prior probability distribution expresses the initial belief for the unknown parameters, before any data is observed. When information about the unknown parameters is available, we can assume certain mathematical form for the prior distribution. It is important to not take this information from the data used in the inference. Previously acquired data can be informative, or the posterior resulting from an inference on that data can be used as an informative prior for the new data. To be unbiased, the QPuB algorithm uses a relatively uninformative flat prior, namely a uniform one:

$$\mathbb{P}(\Theta) = \sum_{i=1}^{P+2} \theta_i, \quad (2.3.11)$$

where

$$\theta_i \sim \begin{cases} \mathcal{U}(10^{-4}, 10^4) & \text{for } i \in [1, P + 1] \text{ (conversion factors, sigma)} \\ \mathcal{U}(0, 1) & \text{for } i = P + 2 \text{ (punishment parameter)} \end{cases}.$$

The range for the conversion factors is chosen like this, because experimental observations suggest a range of the order of magnitude of the conversion factors of around 7 and the factor for the substrate is set to 1 by default. The range for sigma is chosen like this, because... The range for the penalty parameter is set to  $[0, 1]$  to achieve a punishment of mass gain.

#### The likelihood

The likelihood describes the plausibility of a parameter value given new data. Here we make use of the law of mass conservation and define the objective function from Section 2.1 as our likelihood. Moreover, the likelihood function is truncated punishing the mass gain more than mass loss, because amino acids can remain undetected but definitely not created:

$$\mathbb{P}(\Theta|D) = \sum_{t=1}^T \sum_{a=1}^A \left[ \sum_{i=1}^P v_i s_i(t) b_{ia} - \Delta c_0(t) \right], \quad (2.3.12)$$

where

$$\sum_{i=1}^P v_i s_i(t) b_{ia} - \Delta c_0(t) \sim \begin{cases} \mathcal{N}(0, \sigma) & \text{on } [-\infty, 0] \text{ (mass loss)} \\ \mathcal{N}(0, \varphi\sigma) & \text{on } (0, \infty] \text{ (mass gain)} \end{cases}.$$

#### The proposal function

Like in most biological applications, we use a multivariate normal distribution with the current value as the mean. We truncate on the prior interval as follows:

$$g(\theta'|\theta) \sim \mathcal{N}_{tr}(\theta, \sigma_2, a, b) \quad (2.3.13)$$

where

$$\begin{cases} a = 10^{-4}, b = 10^4 & \text{for } \theta_i \in [0, P + 1] \text{ (conversion factors, sigma)} \\ a = 0, b = 1 & \text{for } \theta_i = P + 2 \text{ (punishment parameter)} \end{cases}.$$

Presetting a good scale  $\sigma_2$  for the proposal function is difficult. To overcome this problem, we use adaptive scaling, which learns a good scaling on the fly. See Appendix B for more details. The starting value of the scale parameter is set to  $2.38/\sqrt{P+2}$  for all parameters. The sequence implementing the *vanishing adaptation* strategy has the form  $\Gamma(j) = j^{-\gamma}$  (Haario et al., 2001), where  $j$  is the current iteration number and  $\gamma$  is specified in the input as **GammaExponent** with a default of 0.5. In QPuB, we use the Rao-Blackwellised adaptive Metropolis algorithm. See Appendix C for more details.

### Convergence criterion

For the termination of the QPuB run, a criterion based on the effective sample size (ESS) of the Markov chain is used by default. For large datasets, the ESS tends to be very high, such that QPuB runs for a very long time. In this case, the user may choose to terminate QPuB after a fixed maximum number of iterations. In case the user stops the QPuB routine before termination, the R script **postprocessing.R** (which will be available soon) should be executed to postprocess the current chain and return the final results.

### 2.3.5 Postprocessing

After the termination of the adaptive Metropolis algorithm, the chain needs to be back scaled by  $\text{scale\_prod}^{-1}$ , because we scaled the data by **scale\_prod** during data preparation. The resulting chain is saved in the file **chain\_backscaled.RData**. For further analysis 50% of the chain is removed as burn-in, or according to user input. Summary statistics of the chain is returned in the form of minimum, lower quartile, median, upper quartile, maximum, mean, and standard deviations.

Finally, the absolute concentrations of the peptide products are calculated, saved in csv-files and plotted. If the substrate titration is provided, a linear model is used to fit the mean over the replicates. See figure **substratetitration\_given.png**. The signal intensity for the amount loaded (provided as input parameter **loaded**) in the kinetics is inferred from this first fit and then used to normalize the titration to correspond to the signal intensity at time zero in the kinetics for all replicates. This normalized titration data is again fitted using a linear model, for each replicate separately, see figure **substratetitration\_normalized.png**. The intercept and the slope are then used to determine the absolute amounts via the formula (2.1.7) described above. The substrate concentration is calculated, saved in csv-files and plotted as concentration over time, see figure **substrate.png**.

The substrate degraded is plotted, see figure **substrate\_degraded.png**. For the products, we calculate the 0.05, 0.5 and 0.95 quantiles of the concentrations via formula (2.1.7) using the quantiles of the distributions of the conversion factors respectively. The numeric values are saved in csv-files in the folder **concentrations** and the kinetics are plotted as concentration over time for every peptide product in the folder **plots\_concentrations**. To know which plot belongs to which peptide, use **identifier.csv**. If the titration data is not provided, we use only the correlation (Eq. 2.1.1) to obtain normalized signals. These can be used to qualitatively compare the peptide products but they don't provide absolute amounts.

### 2.3.6 Output

After termination of the algorithm, the sub-folder **OUTPUT\_inputfoldername** contains all the generated output.

It has the following structure:

```
OUTPUT_inputfoldername
|-- chain.RData
|-- chain_backscaled.RData
|-- identifier.csv
|-- concentrations
|   |-- conc_five_1.csv
|   |-- conc_five_2.csv
|   |
|   |   :
|   |   :
|   |-- conc_five_R.csv
|   |-- conc_median_1.csv
|   |-- conc_median_2.csv
|   |
|   |   :
|   |   :
|   |-- conc_median_R.csv
|   |-- conc_ninetyfive_1.csv
|   |-- conc_ninetyfive_2.csv
|   |
|   |   :
|   |   :
|   |-- conc_ninetyfive_R.csv
|   |-- substrate_1.csv
|   |
|   |   :
|   |-- substrate_R.csv
|-- plots_concentrations
|   |-- peptide1.png
|   |-- peptide2.png
|   |
|   |   :
|   |   :
|   |-- peptideP.png
|   |-- substrate.png
|   |-- substrate_degraded.png
|-- plots_diagnostics
|   |-- chain_100.pdf
|   |-- chain_200.pdf
|   |
|   |   :
|   |   :
|   |-- chain_Niter.pdf
|   |-- residuals_0.pdf
|   |-- residuals_100.pdf
|   |-- residuals_200.pdf
|   |
|   |   :
|   |   :
|   |-- residuals_Niter.pdf
|-- plots_inputsignals
|   |-- peptide1.png
|   |-- peptide2.png
|   |
|   |   :
|   |   :
|   |-- peptideP.png
|   |-- substrate.png
|   |-- substrate_degraded.png
|-- runQPuB_ROUT.txt
|-- statistics.csv
|-- statistics.pdf
|-- substratetitration_given.png
'-- substratetitration_normalised.png
```

The folder [plots\\_inputsignals](#) is created at the start of the algorithm and contains the kinetics of the signal intensities for every peptide product, the substrate and the substrate degraded. The diagnostic plots (histograms, traces, and residuals) during the run are saved in the folder [plots\\_diagnostics](#) as **chain.pdf** and **residuals.pdf**, respectively. The number denotes the iteration number. The folder [concentrations](#) contains the numeric values of the 0.05, 0.5 and 0.95 quantiles of the absolute amounts in csv-files, one for every replicate respectively. The kinetic plot for every peptide product is contained in the folder [plots\\_concentrations](#). In the plot, the median is depicted by a solid line, the region between 0.05 and 0.95 quantile is the shaded area. Different replicates are denoted by different colors. The concentration of the substrate and the substrate degraded are a single line for every replicate respectively, since the conversion factor is fixed to 1.

Summary of the files and folders produced sequentially as the algorithm proceeds:

<b>runQPuB_ROUT.txt</b>	Progress report of the algorithm. The output of every print command directly goes into this file.
<a href="#">plots_inputsignals</a>	Folder containing the kinetic plots of the input signal intensities for all peptide products
<b>peptide_i.png</b>	Kinetic plot of the input signal intensities for peptide $i$ . In the folder.
<b>identifier.csv</b>	Table of peptide numbers, sequences and position codes
<a href="#">plots_diagnostics</a>	Folder containing the diagnostic plots of the chain and the residuals
<b>chain_j.pdf</b>	Trace plots and distributions of the Markov chain at $j^{th}$ iteration. In the folder.
<b>residuals_j.txt</b>	Residual plots at $j^{th}$ iteration. In the folder.
<b>chain.RData</b>	Markov chain: time series of all parameters
<b>chain_backscaled.RData</b>	Markov chain after backscaling
<b>statistics.csv</b>	Summary statistics of the backscaled Markov chain
<b>statistics.pdf</b>	Graphical summary statistics of the backscaled conversion factors for all peptide products
<b>substratetitration_given.png</b>	Plot of the titration data and the linear fit. Only if titration provided.
<b>substratetitration_normalized.png</b>	Plot of the normalised titration data and the linear fits. Only if titration provided.

### **concentrations**

Folder containing the numerical values of the absolute amounts (if titration provided) or normalised signals (if not provided)

**conc\_five\_rp.csv, conc\_median\_rp.csv,  
conc\_ninetyfive\_rp.csv**

0.05, 0.5 and 0.95 quantiles of concentration kinetics of all products for the  $rp^{th}$  replicate. In the folder.

### **plots\_concentrations**

Folder containing the kinetic plots of the absolute amounts (if titration provided) or normalised signals (if not provided)

**peptide.i.png**

Kinetic plot of the absolute amounts or normalised signal for peptide  $i$ . In the folder.

## 3 | Installation

### 3.1 Installation of the software environment R

QPuB is a software package that runs on the programming language R. To install R on your computer, visit the R webpage [www.r-project.org](http://www.r-project.org). QPuB requires an R version  $\geq 3.5.0$ .

### 3.2 Installation of the required R packages

QPuB requires multiple R packages to be installed. Listed are the required packages and their QPuB specific purpose. Note that some of the packages might require additional packages for internal use.

<b>R.utils</b> (Bengtsson, 2010)	processing of command line arguments
<b>tictoc</b> (Izrailev, 2014)	timing function: CPU time
<b>sys</b> (Stubner et al., 2019)	timing function: system time
<b>tmvtnorm</b> (Wilhelm and Manjunath, 2010)	proposal: truncated multivariate normal distribution
<b>matrixcalc</b> (Novomestky, 2013)	proposal: check whether a matrix is positive definite
<b>corpcor</b> (Schafer et al., 2017)	proposal: make a matrix positive definite
<b>ggdmc</b> (Lin and Heathcote, 2017)	proposal: generate univariate truncated normal distribution
<b>dqrng</b> (Stubner et al., 2019)	acceptance-rejection: generate fast pseudo random numbers
<b>coda</b> (Plummer et al., 2006)	termination: produce an mcmc object for further analysis of the Markov chain
<b>mcmcse</b> (Flegal et al., 2012)	termination: computation of the effective sample size
<b>matrixStats</b> (Bengtsson et al., 2018)	postprocess: computation of standard deviation of columns of a matrix

Packages in R are installed using the command

```
$ R
>> install.packages("packagename")
```

To install all of the required packages at once, type in the command line

```
$ R
>> install.packages(c("R.utils", "tictoc", "sys", "tmvtnorm", "matrixcalc",
  "corpcor", "ggdmc", "dqrng", "coda", "mcmcse", "matrixStats"))
```

### 3.3 Installation of the QPuB routine

QPuB is free available on the software development platform GitHub under the *Quantitative and Systems Biology* profile in the QPuB repository <https://github.com/QuantSysBio/QPuB>. The user requires to download the archive [QPuB-master.zip](https://github.com/QuantSysBio/QPuB/archive/master.zip) and unzip it. Quick link to the zip-file: <https://github.com/QuantSysBio/QPuB/archive/master.zip>.

The unzipped folder **QPuB-master** has the following structure:

```
QPuB-master/
|-- examples/
|   |-- gp100_40-52_proteasome/
|   |   |-- data
|   |   |   |-- k386_1.csv
|   |   |   '-- k386_2.csv
|   |   |-- input.txt
|   |   |-- timepoints.txt
|   |   '-- titration.csv
|   |-- insilico_exopep_noise/
|   |   |-- data
|   |   |   |-- exo_1.csv
|   |   |   '-- exo_2.csv
|   |   '-- input.txt
|   |-- insilico_endopep_noise/
|   |   |-- data
|   |   |   |-- toy_noise_1.csv
|   |   |   '-- toy_noise_2.csv
|   |   '-- input.txt
|   '-- insilico_endopep_nonoise/
|       |-- data
|       |   '-- toy_nonoise.csv
|       '-- input.txt
|-- LICENSE.md
|-- Documentation.pdf
|-- QPuBGit.Rproj
|-- QPuB/
|   |-- additionalfunctions.r
|   |-- datapreparation.r
|   |-- inputparser.r
|   |-- MCMCroutine.r
|   '-- runQPuB.r
|-- logoqpub.png
'-- README.md
```



After unzipping, QPuB is ready to be executed. The folder [QPuB](#) is the heart of the routine, the rest may be deleted by the user. The user may move the [QPuB](#) folder to a desired location.

Details on the general execution are provided in Chapter [4](#). The folder [examples](#) contains four different data sets of varying complexity. We go through them step by step in Chapter [5](#). Note that they already have the folder structure required as stated in Section [2.3.2](#).

## 4 | Usage

### 4.1 Usage of QPuB in the command line

Windows users need to change the delimiting character in the paths accordingly!

In order to run QPuB on your data, follow the steps below. Note that these generic commands are not executable as is, see Chapter 5 for executable commands.

1. Make sure everything is properly installed on your computer (see Chapter 3).
2. Make sure the data files and the inputfolder have the right structure (see Sections 2.3.1 and 2.3.2).
3. Open the terminal/command prompt (How to: [Linux](#), [Mac](#), [Windows](#)).
4. Go to your working directory:

```
$ cd hostname:~\workingdirectory
```

5. The QPuB main script is executed using command line arguments:

```
$ Rscript name_or_path_of_runQPuB.r -infol name_or_path_of_inputfolder  
                                (-outfol outputfoldername -titr titrationfilename)
```

Mandatory arguments:

<b>name_or_path_of_runQPuB.r</b>	name/path of the <b>runQPuB.r</b>
<b>-infol name_or_path_of_inputfolder</b>	name/path of the <b>input folder</b>

Optional arguments:

<b>-outfol outputfoldername</b>	name of the <b>output folder</b> . Do not provide a path!
<b>-titr titrationfilename</b>	name of the <b>titration</b> file. Do not provide a path!

Flags can be specified as `-infol inputfolder` or `--infol=inputfolder`. If an optional input will not be provided, then also omit the flag.

The first argument will always be taken as the name of the R script: `Rscript runQPuB.r`, and does not require a flag. Depending on your working directory, you also have to provide the path to the `runQPuB.r` file:

- a. working directory is QPuB directory: `runQPuB.r`
- b. working directory is somewhere else: `path\QPuB\runQPuB.r`

Depending on the location of the input folder, you also have to provide the path to the folder:

- a. inputfolder is in same parent directory as runQPuB.r: `-infol inputfolder`
- b. inputfolder is somewhere else: `-infol path\inputfolder`

For now, `./` and `../` notation does not work. Please use the full path. Also avoid leading and trailing slashes.

In the following section, we will illustrate the usage of QPuB with some examples.

## 4.2 Usage of QPuB in R user interface

It is highly recommended to run the QPuB routine using Rscript from the terminal to avoid complications. RStudio tends to crash when running QPuB on large data sets.

To run it in the R command line interface or in a graphical user interface such as RGui or RStudio, follow these steps:

1. Open the main Rscript **runQPuB.r** in a text editor or RStudio.
2. Disable/comment lines 34-44. These are for parsing the command line arguments:

```
34 args = commandArgs(trailingOnly=FALSE, asValue=TRUE)
35 keys <- attachLocally(args)
36
37 if (!exists('infol')){
38 stop("This is the QPuB package. \n
39 At least one argument must be supplied: -infol.\n
40 -infol inputfolder (COMPULSORY): ...
41 -outfol outputfolder (OPTIONAL): ...
42 -titr titrationfile (OPTIONAL): ...
43 For documentation see: https://github.com/QuantSysBio/QPuB.\n", call.=FALSE)
44 }
```

3. Enable/uncomment lines 47-49/51 and specify your filenames and paths here:

```
46 # for use in R:
47 setwd("/home/shenze/Downloads/QPuB-master/QPuB")
48 file <- 'runQPuB.r'
49 infol <- 'examples/gp100_40-52_proteasome'
50 outfol <- 'my_fancy_name'
51 titr <- '190423_K386_titration_substrate_charge_3_K386.csv'
```

## 5 | Examples

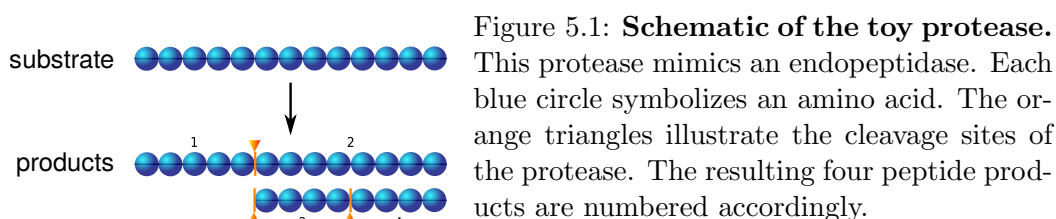
In the following sections, we show a step-by-step execution of the QPuB algorithm on two artificially created data sets with and without noise, and on one experimentally obtained data set.

**Remark:** The units of the quantities in all the examples below are

quantity	unit
signal intensity	XIC
amount	pmol
time	hours
conversion factor	unitless

### 5.1 Example 1: *In silico* endopeptidase data without noise

We first show a trivial example with an exact solution. A toy data set was generated that mimics the digestion by a real protease.



A substrate of length 13 amino acids is digested by an endopeptidase, that can further cleave generated products. It first cleaves the substrate into peptides 1 and 2, and then cleaves peptide 2 resulting in two more products 3 and 4.

The files needed for this example can be found in the folder [examples/insilico\\_endopep\\_noise](#).

#### 5.1.1 Construction of the data

To create the numeric data, we assume that all products of the digestion are detected. We simulate the concentrations of the substrate and the four products over time according to the rules, i.e. the sum of the amounts of amino acids at a given time must sum up to the amount of substrate in the beginning. We divided the concentrations by preset conversion factors:

reagent	factor
substrate	1
peptide 1	0.01
peptide 2	0.1
peptide 3	0.5
peptide 4	0.99

The resulting signal intensities (see formula (2.1.1)) were multiplied by  $10^7$  to get to a more realistic order of magnitude. This data is saved in the file **endo3\_nonoise.csv**:

```
"sequence",0,1,2,3,4
"ABCDEFGHJKLM",1000000000,800000000,700000000,650000000,600000000
"ABCDE",0,2000000000,3000000000,3500000000,4000000000
"FGHIJKLM",0,400000000,200000000,150000000,150000000
"FGHI",0,320000000,200000000,400000000,500000000
"JKLM",0,161616161.616162,101010101.010101,202020202.020202,252525252.525253
```

Note that it has the format required, see Section 2.3.1. The header specifies the time points in hours in an increasing order i.e. left to right is from time 0 to time  $t > 0$ . The first column contains the sequences of the substrate and all the peptide products. Subsequent columns show the mass spectrometry intensities for each sequence over time.

### 5.1.2 Input

For this simple example, we use all default settings in the input.txt (see Section 2.3.1). The only mandatory input without default is the mechanism of the protease, which in this case is an endopeptidase. Since no titration is provided, we don't need to specify how much substrate was loaded. This input is ignored by the parser.

```
##### MANDATORY INPUT

# mechanism of the underlying enzyme: 'endopep', 'exopep'
enzyme: endopep

# amount of substrate loaded for kinetics (if titration provided)
loaded: 100
```

We want to compare successive time points (default), so the file timepoints.txt does not need to be provided. For this artificial example we don't have any titration data.

### 5.1.3 Execution

Let's go through the steps of Chapter 4.

1. If you haven't done that already, install R and the required R packages now (see Chapter 3).
2. The examples in the [QPuB-master](#) folder are already in the right format.
3. Open the terminal.
4. In the following, it is assumed that the folder [QPuB-master](#) is allocated in your [Downloads](#) folder. If not, please change the paths in the commands accordingly. We choose the working directory to be the [QPuB](#) folder:

```
$ cd Downloads/QPuB-master/QPuB
```

5. Execute the runQPuB.r script with the desired input folder:

```
$ Rscript runQPuB.r -infol examples/insilico_endopep_nonoise
```

If you want the output folder to have a specific name, add the flag `-outfol my_fancy_name`.

### 5.1.4 Output

Once executed, information on the QPuB directory and the input folder used is prompted in the command window:

```

Path of QPuB: /home/shenze/Downloads/QPuB-master/QPuB
Path of input folder: /home/shenze/Downloads/QPuB-master/insilico_endopep_nonoise

CREATING OUTPUT DIRECTORY...
Path of output folder: /home/shenze/Downloads/QPuB-master/QPuB-Output/OUT_insilico_endopep_nonoise
Note: Do not change folder name during run!

Terminal output redirected to runQPuB_ROUT.txt.
RUNNING...

```

A general output folder [QPuB-Output](#) will now be created in the [examples](#) folder. Here you can find all the outputs of all the runs we will execute in the following. By default, the output folder [OUT\\_insilico\\_endopep\\_nonoise](#) is created (or the folder with the user defined name [my\\_fancy\\_name](#)). All output regarding this run can be found [here](#).

## The ROUT-file

The progress report can be inspected in `runQPuB_ROUT.txt`. First the input parameters, signal intensity data, timepoints and titration used are printed and information about the data manipulation is given:

```

READING INPUT PARAMETERS...
      V1      V2
1      enzyme endopep
2      loaded    100
3      plot_chain TRUE
4      plot_residuals TRUE
5      freq_plot 10000
6      plotdet    TRUE
7      vecplot    FALSE
8      freq_save 10000
9      scaleprod  TRUE
10     filterprod FALSE
11     threshold 1e6
12     conv_lower 1e-4
13     conv_upper 1e4
14     sigma_lower 1e-4
15     sigma_upper 1e4
16     conv_start 1
17     sigma_start 10
18     pun_start 0.1
19     OptAccRate 0.234
20     Track      TRUE
21     GammaExponent 0.5
22     burnFrac    0.5
23     burnGibbs 1000
24     thinGibbs   20
25 TerminationCriterion TRUE
26     MaxIter    10000
27     ESSiter    10000
28     ConfLevel  0.05
29     Tolerance  0.05

READING INPUT DATA...
[[1]]
[[1]][[1]]
      sequence      0      1      2      3      4
1 ABCDEFGHIJKLM 1000000000 8000000000 7000000000 6500000000 6000000000
2      ABCDE      0 20000000000 30000000000 35000000000 40000000000

```

3	FGHIJKLM	0	400000000	2000000000	1500000000	1500000000
4	FGHI	0	320000000	200000000	400000000	500000000
5	JKLM	0	161616162	101010101	202020202	252525253

SETTING TIMEPOINTS FOR COMPARISON...

Setting timepoints to default: comparing successive timepoints.

	[,1]	[,2]
[1,]	0	1
[2,]	1	2
[3,]	2	3
[4,]	3	4

READING INPUT TITRATION...

No titration file given.

PREPARING DATA...

Data scaled by 1e-08 to avoid large orders of magnitude.

Products scaled by 0.0209415394228141 to match order of magnitude of the substrate.

Note that the data is rounded for the print command, but the exact values are used in the algorithm!  
As the simulation progresses the ROUT-file is constantly being updated:

Convergence achieved when effective sample size > 8708

RUNNING INFERENCE...

Starting time: 2019-07-25 17:01:00

Iteration: 1000

Acceptance rate: 0.235

Iteration: 2000

Acceptance rate: 0.244

Iteration: 3000

Acceptance rate: 0.237

Iteration: 4000

Acceptance rate: 0.23875

Iteration: 5000

Acceptance rate: 0.2338

Iteration: 6000

Acceptance rate: 0.2318333333333333

Iteration: 7000

Acceptance rate: 0.231285714285714

Iteration: 8000

Acceptance rate: 0.230625

Iteration: 9000

Acceptance rate: 0.23

Iteration: 10000

Acceptance rate: 0.2305

Effective sample size: 603.08807349756

:

Iteration: 26000

Acceptance rate: 0.231192307692308

Effective sample size: 8334.19764449216

Iteration: 27000

Acceptance rate: 0.231592592592593

Effective sample size: 9827.97921636141

Stop run: Chain converged.

```
Finishing time: 2019-07-25 17:01:35
Total running time: 35.535 sec elapsed
```

After 10000 iterations, the algorithm starts checking for convergence every 1000 iterations. The simulation terminates once the effective sample size reaches the minimum value which here is 8708. In this run, it took 27000 iterations or 35 seconds to converge. Remark: The timekeeping strongly depends on the hardware configurations used. The user is referred to Section 5.5.

```
PRODUCING SUMMARY OF RESULTS...
  Statistical summary in statistics.csv
  Distributions of conversion factors in summary.pdf

CALCULATING ABSOLUTE CONCENTRATIONS...
WARNING: No substrate titration provided. Only calculating normalized signals!
  Numeric values in folder 'concentrations'.
  Kinetic plots in folder 'plots_concentrations'.

THE END.
```

After termination, the summary of parameters and the absolute concentrations are produced. Note that in this simple example, only normalized signals are returned, since we did not provide titration data.

### The diagnostic plots

The performance of the algorithm can be checked in the diagnostic plots. The mass deviation of the QPuB solution to the real solution can be investigated in the residuals. Note the improvement of the residuals from before starting QPuB just using the startvalues 1:

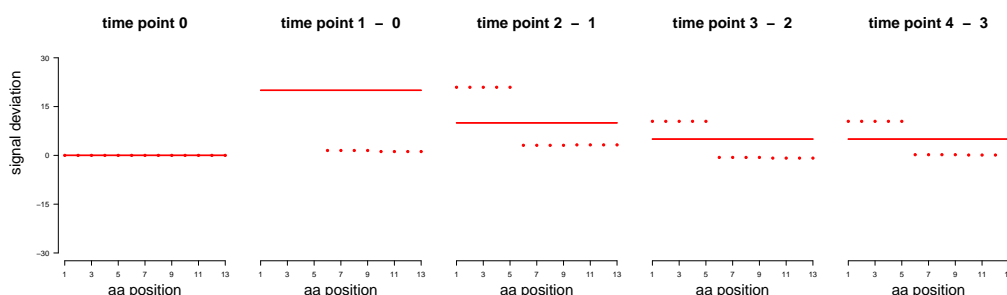


Figure 5.2: Residuals using startvalues (residuals\_0.pdf)

to the residuals after termination of QPuB using the estimated values:

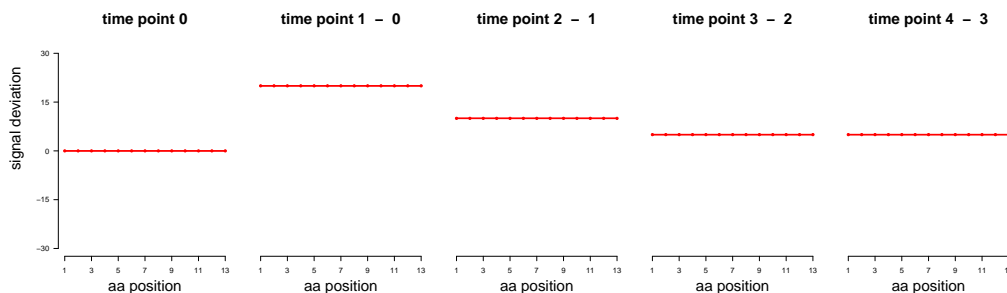


Figure 5.3: Residuals using estimated values (residuals\_27000.pdf)



The horizontal line is the amount of substrate degraded between one time point and the preceeding and represents the real solution. This should coincide with the amount of each amino acid in the products, depicted as boxplots which are returned from QPuB. Here they are very narrow and coincide exactly with the real solution. We don't have any mass gain or mass loss.

In the chain-plots we see the distribution of the parameter values in the first column and the trace of the Marcov chain in the second column:

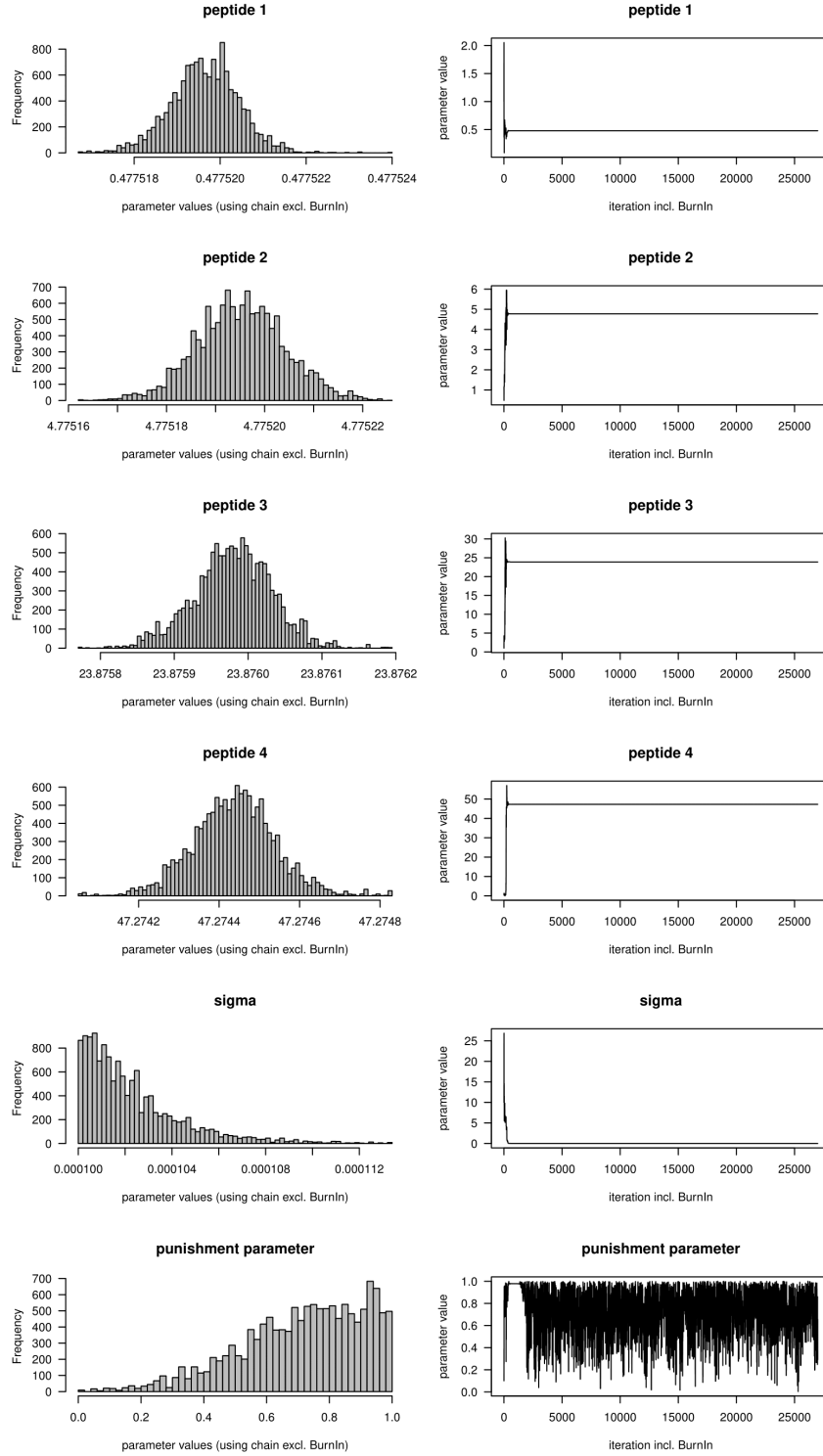


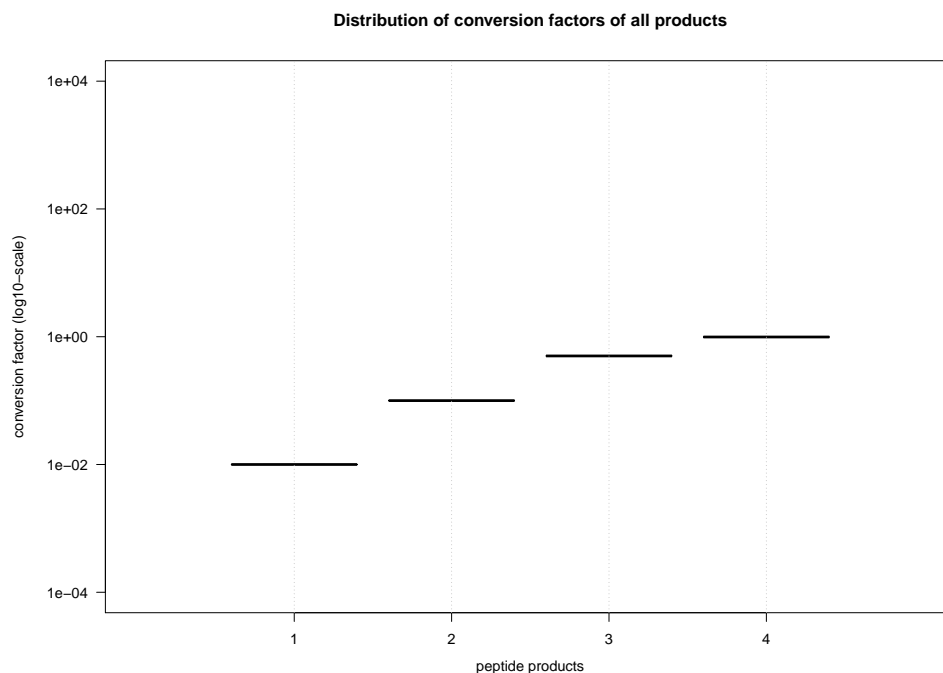
Figure 5.4: Distribution and trace of the Marcov chain after termination (chain\_27000.pdf)

## The conversion factors

By the way the data was constructed, it is easy to control, if the algorithm achieves to correctly infer the “unknown” conversion factors, which here are (0.01, 0.1, 0.5, 0.99). Since there is no noise, with the help of QPuB, these conversion factors should be retained almost exactly from the intensity measurements. Note that the chain-plots are created using the scaled chain. Therefore here the values are not correct yet. For the file statistics.csv the chain has been backscaled. We see that the distributions have a very narrow spread and the medians equal the exact values almost perfectly:

parameter	min	0.05-quart.	median	0.95-quart.	max	mean	std
ABCDE	1.00E-02	1.00E-02	1.00E-02	1.00E-02	1.00E-02	1.00E-02	1.66E-08
FGHIJKLM	1.00E-01	1.00E-01	1.00E-01	1.00E-01	1.00E-01	1.00E-01	1.88E-07
FGHI	5.00E-01	5.00E-01	5.00E-01	5.00E-01	5.00E-01	5.00E-01	1.10E-06
JKLM	9.90E-01	9.90E-01	9.90E-01	9.90E-01	9.90E-01	9.90E-01	2.16E-06
sigma	1.00E-04	1.01E-04	1.02E-04	1.03E-04	1.07E-04	1.02E-04	2.11E-06
pun	1.70E-01	5.90E-01	7.43E-01	8.73E-01	1.00E+00	7.15E-01	1.96E-01

Note that the numeric values in the file are given with all digits and not rounded as shown here. The same is observed graphically in statistics.pdf, which contains the distributions of the conversion factor estimates (y-axis in log-scale):



## Comparing the input signals and the output normalized signals:

The folder [plots\\_inputsignals](#) contains the signal intensity kinetics and the folder [plots\\_concentrations](#) contains the resulting concentration kinetics, or normalized signal kinetics, when no titration is provided.

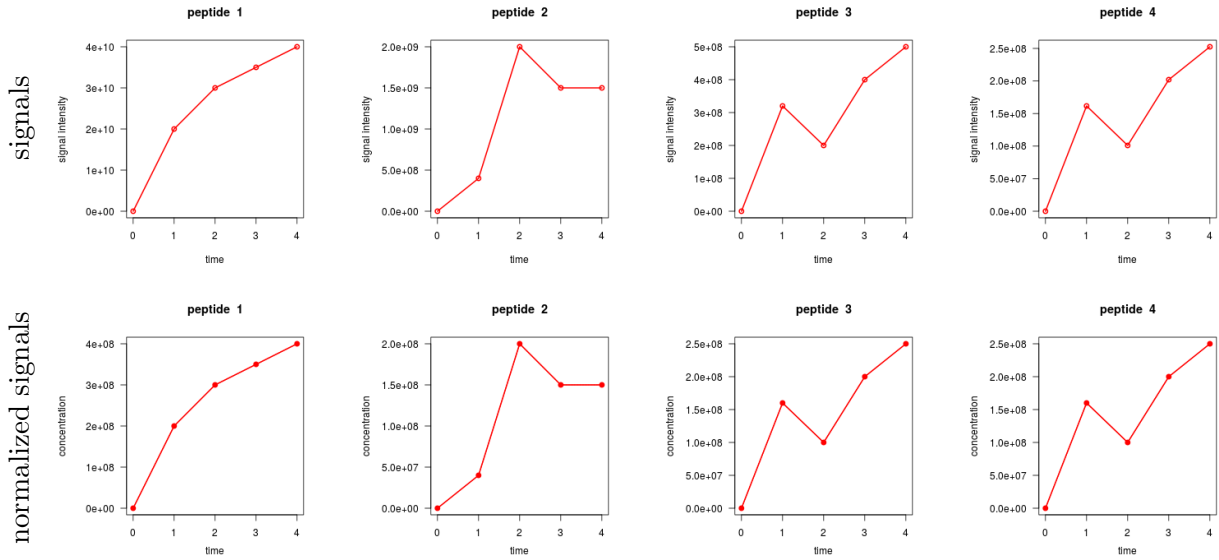


Figure 5.5: Kinetics of the input signal intensities and the output normalized signal intensities.

Because the conversion factor distributions have such a very narrow spread, the normalized signals seem to be single lines instead of shaded areas.

Note that when comparing the peptides based on their signal intensities, peptide 2 is more abundant than peptide 3 and 4. When comparing them based on their normalized signal intensities on the other hand, peptide 3 and 4 are more abundant.

## 5.2 Example 2: *In silico* endopeptidase data with noise

In reality, MS data is noisy. In the next example, we use the same toy endopeptidase as in Example 1 but a different set of conversion factors to create the data. In addition, we add multiplicative noise.

The files needed for this example can be found in the folder [examples/insilico\\_endopep\\_noise](#).

### 5.2.1 Description of the data

The set of conversion factors used has a larger range  $[0,100]$ , which corresponds better to the new Orbitrap data:

reagent	factor
substrate	1
peptide 1	0.01
peptide 2	1
peptide 3	10
peptide 4	100

To the resulting signal intensities, we added multiplicative noise with a standard deviation of 0.2:

$$s_i = \frac{c_i}{v_i} * 10^7 * \nu \quad \text{where } \nu \sim \mathcal{N}(1, 0.2) \quad (5.2.1)$$

MS data usually comes in at least duplicates of biological and/or technical replicates. In this example, we have two replicates saved as **insilico\_endopep\_noise\_1.csv** and **insilico\_endopep\_noise\_2.csv**:

```
"sequence",0,1,2,3,4
"ABCDEFGHIJKLM",1329645593.90514,568892651.666362,739675212.686849,540034688.5801,...
"ABCDE",0,19550437927.5625,35093569014.2052,26785506340.1762,39645400838.1994
"FGHIJKLM",0,50803398.6346583,175111773.541086,129201866.259695,171923799.737804
"FGHI",0,19107329.1597266,11876738.232878,18509229.8771212,27264645.4799232
"JKLM",0,1516140.01373127,528357.666760176,1486536.72037556,2002493.27216031
```

```
"sequence",0,1,2,3,4
"ABCDEFGHIJKLM",819141294.60402,760543309.443102,768562309.0676,751308648.361924,...
"ABCDE",0,24837882034.8424,18057674163.491,48865876487.9947,27284340396.4229
"FGHIJKLM",0,35746926.3663144,200506865.840624,156332268.517916,135109719.872524
"FGHI",0,15846649.3284839,9457129.03488233,21181638.8346666,31924244.7741753
"JKLM",0,1315410.61255498,713261.520152447,2069670.89032181,1297700.25667272
```

## 5.2.2 Input

The input specification is kept the same as that of the previous example without noise.

## 5.2.3 Execution

The steps are analogous to Example 1 following the general usage routine as described in Chapter 4. For the execution we use the input folder `insilico_endopep_noise` and the output folder `OUT_insilico_endopep_noise` inside the general output folder is created:

```
$ Rscript runQPuB.r -infol examples/insilico_endopep_noise

Path of QPuB: /home/shenze/Downloads/QPuB-master/QPuB
Path of input folder: /home/shenze/Downloads/QPuB-master/insilico_endopep_noise

CREATING OUTPUT DIRECTORY...
Path of output folder: /home/shenze/Downloads/QPuB-master/QPuB-Output/OUT_insilico_endopep_noise
Note: Do not change folder name during run!

Terminal output redirected to runQPuB_ROUT.txt.
RUNNING...
```

## 5.2.4 Output

In this run, convergence was achieved after 284000 iterations, which took roughly 20 minutes (see Section 5.5).

Again, QPuB achieved an improvement in mass conservation when comparing the residuals using the startvalues 1:

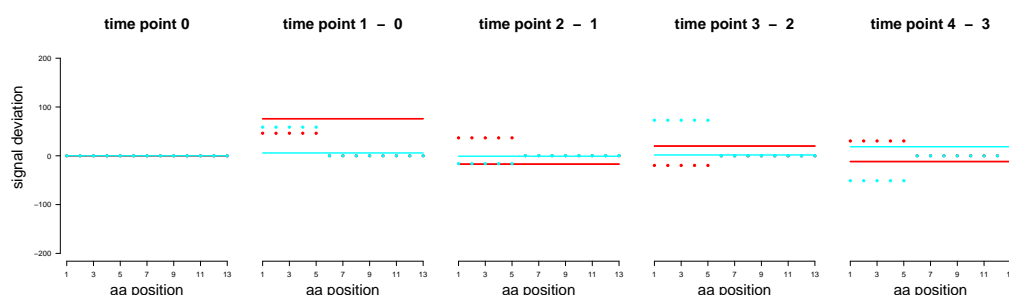


Figure 5.6: Residuals using startvalues (residuals\_0.pdf)

to the residuals after termination of QPuB using the estimated values:

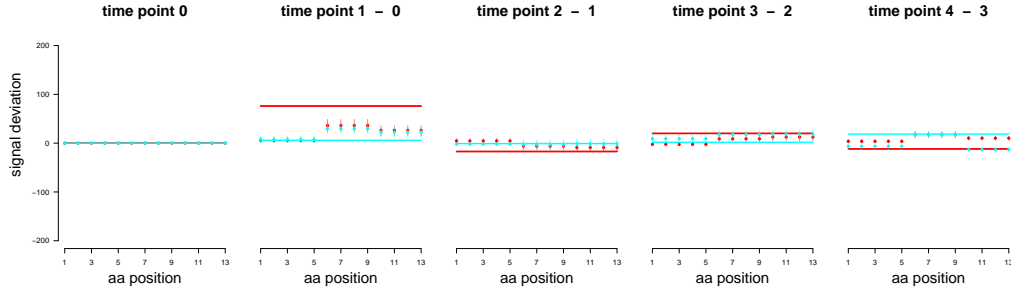


Figure 5.7: Residuals using estimated values (residuals\_284000.pdf)

The two colors represent the two replicates. Again, the horizontal line is the signal of substrate degraded. The dot depicts the median of the distribution of the QPuB solution and the vertical line stretches from 5% to 95% quantile. During the QPuB run, the boxplots approach the vertical lines to minimize the mass deviation.

Note that for the noisy data, the distributions now are broader than in the case without noise:

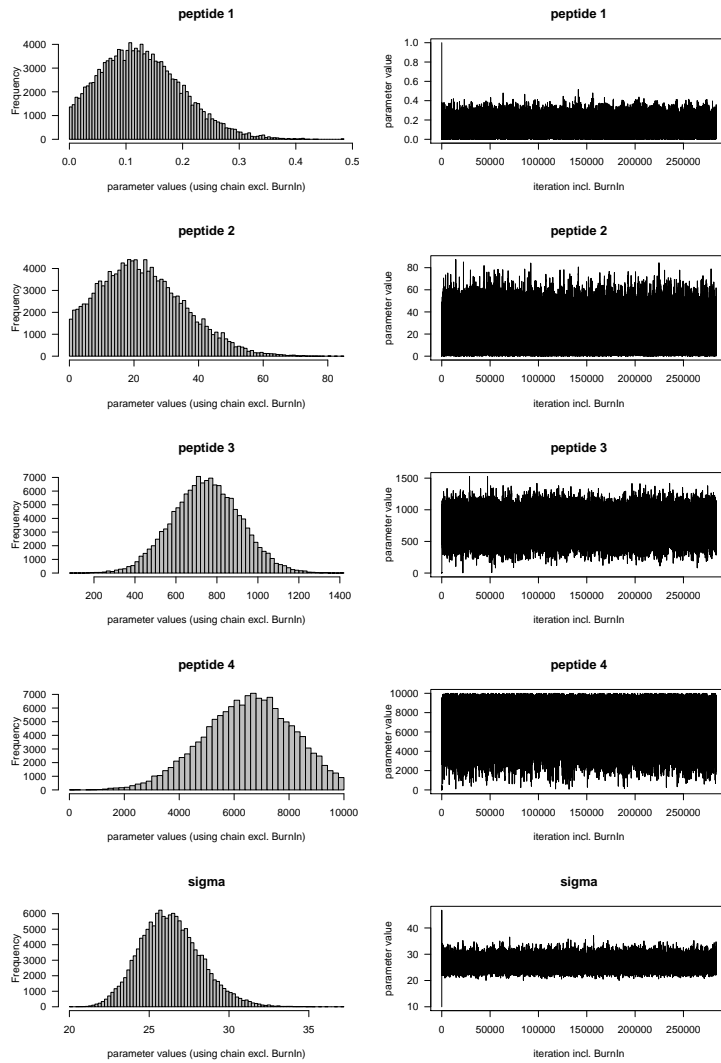
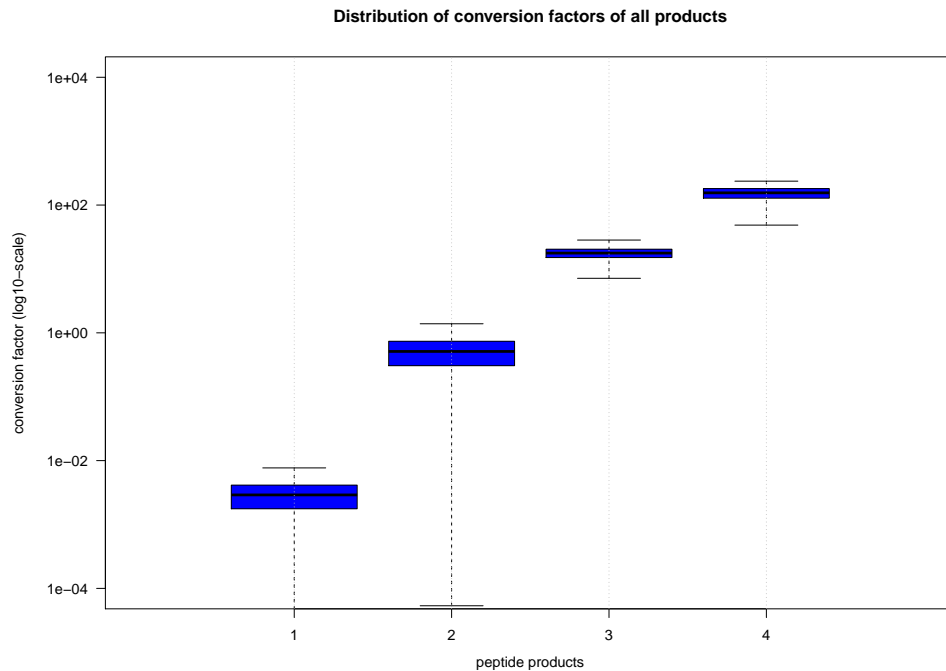


Figure 5.8: Distribution and trace of the Markov chain after termination (chain\_284000.pdf)

Again, the chain has to be backscaled before being able to validate the values with the preset values (0.01, 1, 10, 100):



The noise in the data is now reflected in the kinetics of the amounts. We now clearly see the uncertainty in the form of shaded areas. We plot the region between 5% and 95% quantile surrounding the medians (solid line). Different colors represent the two replicates matching for the input and the output figures. Note again, that the output is only normalised signals and not absolute amounts.

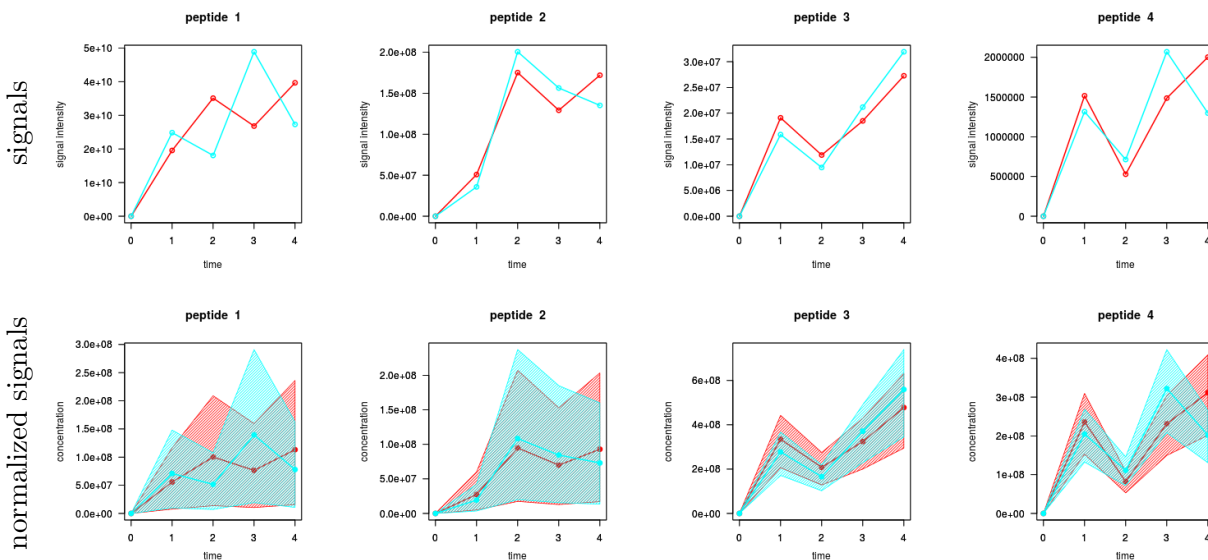


Figure 5.9: Kinetics of the input signal intensities and the output normalized signal intensities.

### 5.3 Example 3: *In silico* exopeptidase data with noise

In this example we have a brief look at an exopeptidase digestion with a simulated data set with noise. A substrate of length 13 amino acids is digested by an exopeptidase, that cleaves the N-terminal peptide bond and releases one amino acid at a time. The resulting major peptide products stagger in length from 12 to 9 amino acids.

The files needed for this example can be found in the folder [examples/insilico\\_exopep\\_noise](#).

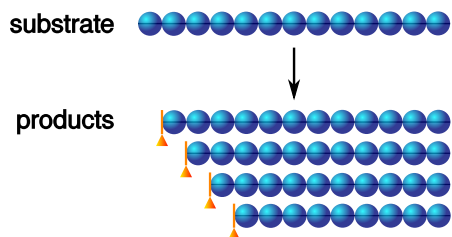


Figure 5.10: **Schematic of the toy protease.** This protease mimics an exopeptidase. Each blue circle symbolizes an amino acid. The orange triangles illustrate the cleavage sites of the protease. The resulting four peptide products are numbered accordingly.

### 5.3.1 Description of the data

We use conversion factors on a large range  $[0,100]$ :

reagent	factor
substrate	1
peptide 1	0.01
peptide 2	1
peptide 3	10
peptide 4	100

The numeric values of the two replicates are

```
"sequence",0,1,2,3,4
"ABCDEFGHIJKLM",1039479599.37841,767583534.613125,445122260.342802,781309553.513323,...
"BCDEFGHIJKLM",0,9517944742.56169,14727672946.9299,14837983979.8048,16951130395.6594
"CDEFGHIJKLM",0,68867333.0735263,53196387.08569,104221859.395179,43924437.9600196
"DEFGHIJKLM",0,2440697.92744741,3980110.04521406,4240804.94109268,5082210.92993794
"EFGHIJKLM",0,99905.7955368122,236836.013256818,269650.335610024,652694.26679792
```

and

```
"sequence",0,1,2,3,4
"ABCDEFGHIJKLM",957707814.037546,667923672.65818,708443560.478777,583433264.674484,...
"BCDEFGHIJKLM",0,11017982507.9007,23445919239.8043,17943464692.4523,24054930628.215
"CDEFGHIJKLM",0,78780822.2186872,95858343.225741,109776164.612945,97446705.5030333
"DEFGHIJKLM",0,2051008.73597168,4154573.06877254,3917755.87933799,5854462.93908368
"EFGHIJKLM",0,61543.8852615179,241326.899572676,288915.74507079,442516.312112294
```

Note, that the sequences of the peptide products are consecutive subsequences of each other.

### 5.3.2 Input

The mechanism of the protease must be specified:

```
##### MANDATORY INPUT

# mechanism of the underlying enzyme: 'endopep', 'exopep'
enzyme: exopep

# amount of substrate loaded for kinetics (if titration provided)
loaded: 100
```

All other input is kept to default.

### 5.3.3 Execution

The steps are analogous to the previous examples following the general usage routine as described in Chapter 4. For the execution we use the input folder [insilico\\_exopep\\_noise](#). This time, we specify a user-defined output folder name adding the flag `-outfol`:

```
$ Rscript runQPuB.r -infol examples/insilico_exopep_noise -outfol OUTPUT_example3_exopeptida
```

Observe, that the output folder with the user defined name `OUTPUT_example3_exopeptidase` inside the general output folder is created.

### 5.3.4 Output

The algorithm terminated after 322000 iterations in 25min (see Section 5.5).

In exopeptidases, the first few amino acids are not considered for the mass balance. In this example, where the shortest major product has a length of 9 amino acids, the first four amino acids are ignored for the calculation of the likelihood. This can be observed in the residual plots, where the mass deviation of the first four amino acids from the substrate degraded is not minimised.

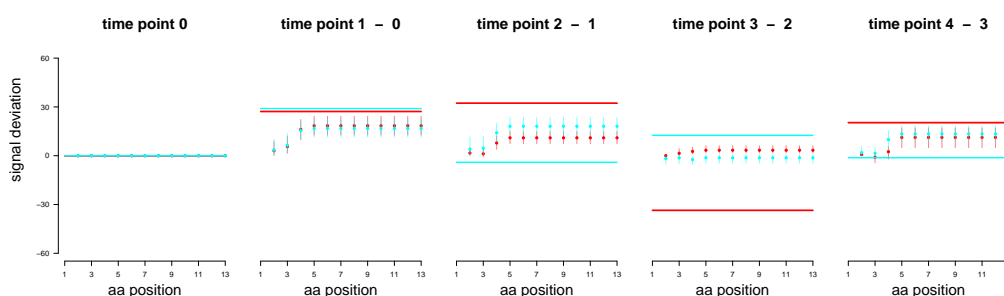


Figure 5.11: Residuals using estimated values (residuals\_322000.pdf)

## 5.4 Example 4: *gp100*<sub>40–52</sub> digestion by the 26S proteasome

In this last example, we run QPuB on real data. We consider a proteasome digestion of the polypeptide *gp100*<sub>40–52</sub>. This data set is more complex than the toy data, with 22 products. Naturally, the conversion factors are unknown. Due to data for more time points being available, we hope for good accuracy. Additionally, titration data is provided in the file `190423_K386_titration_substrate_charge_3.csv`. With this, QPuB will be able to return estimates of the absolute concentrations instead of only normalized signal intensities.

The files needed for this example can be found in the folder `examples/Prot_K386`.

### 5.4.1 Description of the data

We performed measurements in two biological replicates with two technical replicates each. The data Here we show an extract of the data of replicate 1 (file `MB_rep1.csv`) representatively:

```
"sequence",0,0.5,1,1.5,2,3,4
"RTKAWNRQLYPEW",889000000000,555000000000,275000000000,138000000000,...
"RTKAWNR",602223570.8,26815376683,36730723646,39209161583,...
"RTKAWNRQ",55800309.63,640192510.2,925034589.8,887510434.5,...
"QLYPEW",11376959737,287000000000,430000000000,494000000000,...
"RTKAWNRQL",10556780,243434100,390208800,423406200,...
"AWNRQLYPEW",70264400,559101900,465079500,326049100,...
"WNRQLYPEW",292355200,2026874000,1553277000,1063177000,...
"NRQLYPEW",36468690,289681600,312958600,232331900,...
...
```



### 5.4.2 Input

As mandatory input, we provide the mechanism of the protease: The proteasome is an endopeptidase. Since we provide a titration file, the amount of substrate loaded for the kinetics must be specified - In our case that was 200 pmol. The unit has to match the units in the titration file.

```
##### MANDATORY INPUT

# mechanism of the underlying enzyme: 'endopep', 'exoep'
enzyme: endopep

# amount of substrate loaded for kinetics (if titration provided)
loaded: 200
```

For a data set with this complexity, termination using the ESS criterion takes several days. We use a maximum iteration number of  $10^5$  instead, because the chains look already pretty converged:

```
### TERMINATION CRITERION
# TRUE: termination via effective sample size calculation.
# FALSE: enables the MaxIter variable, which is the maximum number of
# iterations the MCMC will run
TerminationCriterion: FALSE
MaxIter: 1e5
```

All other input stays as default for now. We will test different settings later (Section 5.4.5).

### 5.4.3 Execution

The steps are analogous to Example 1 and 2 following the general usage routine as described in Chapter 4. Since we want to use the titration data, we have to add another flag with the name of the file to the command line:

```
$ Rscript runQPuB.r -infol gp100_40-52_proteasome -titr 190423_K386_titration_substrate_charge_3.csv

Path of QPuB: /Users/shenze/Downloads/QPuB-master/QPuB
Path of input folder: /Users/shenze/Downloads/QPuB-master/gp100_40-52_proteasome

CREATING OUTPUT DIRECTORY...
Path of output folder: /Users/shenze/Downloads/QPuB-master/QPuB-Output/OUT_gp100_40-52_proteasome
NOTE: Do not change folder name during run!

Terminal output redirected to runQPuB_ROUT.txt.
RUNNING...
```

### 5.4.4 Output

#### The ROUT-file

Although we have half time points (0.5h, 1.5h) in the data set, the time points will be treated by their integer counts, numbering the six time points in the kinetics consecutively. For starters, we use the default of comparing successive time points. Later we will check, what changes when providing a userdefined file timepoints.txt omitting certain time point comparisons, see Section 5.4.5.

```

SETTING TIMEPOINTS FOR COMPARISON...
Setting timepoints to default: comparing successive timepoints.
      [,1] [,2]
[1,]    0    1
[2,]    1    2
[3,]    2    3
[4,]    3    4
[5,]    4    5
[6,]    5    6

```

Since we provided titration data using the flag `-titr`, it will be used for the calculation of the absolute amounts in the end:

```

READING INPUT TITRATION...
...from file 190423_K386_titration_substrate_charge_3.csv
      pmol      rep1      rep2
1    0.0 8.738783e+06 3.385014e+07
2    6.5 1.258559e+11 1.260661e+11
3   12.5 2.282229e+11 2.521959e+11
4   25.0 5.184945e+11 5.131968e+11
5   50.0 1.029977e+12 1.004578e+12
6   75.0 1.323855e+12 1.263028e+12
7  100.0 1.654654e+12 1.751555e+12

PREPARING DATA...
Data scaled by 1e-10 to avoid large orders of magnitude.
Products scaled by 1.67036496314502 to match order of magnitude of the substrate.

```

## Termination

As preset, the run stops after  $10^5$  iterations, which took roughly 18 minutes (see Section 5.5):

```

Iteration: 1e+05
Acceptance rate: 0.23377

Stop run: Maximum number of iterations reached.

Finishing time: 2019-08-01 12:23:21
Total running time: 1102.109 sec elapsed

```

## Diagnostic plots

Again, QPuB achieved an improvement in mass conservation when comparing the residuals using the startvalues 1:

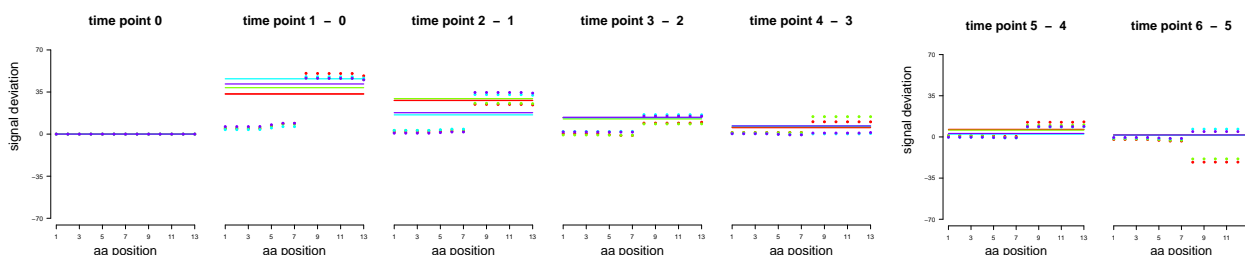


Figure 5.12: Residuals using startvalues (residuals\_0.pdf)

to the residuals after termination of QPuB using the estimated values:

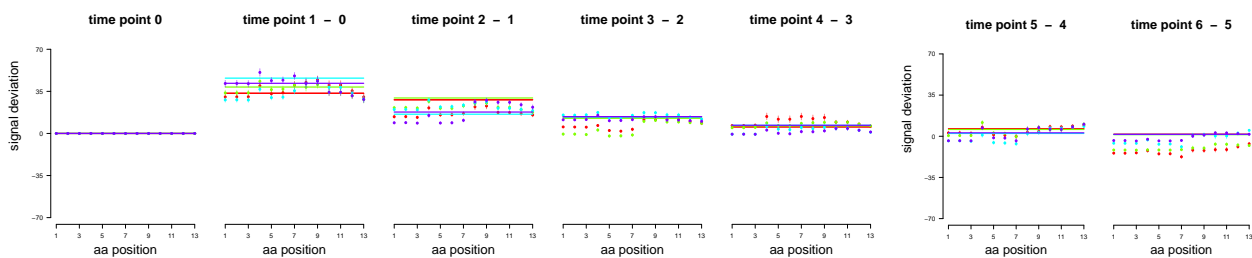


Figure 5.13: Residuals using estimated values (residuals\_100000.pdf)

Here is a choice of parameter distributions:

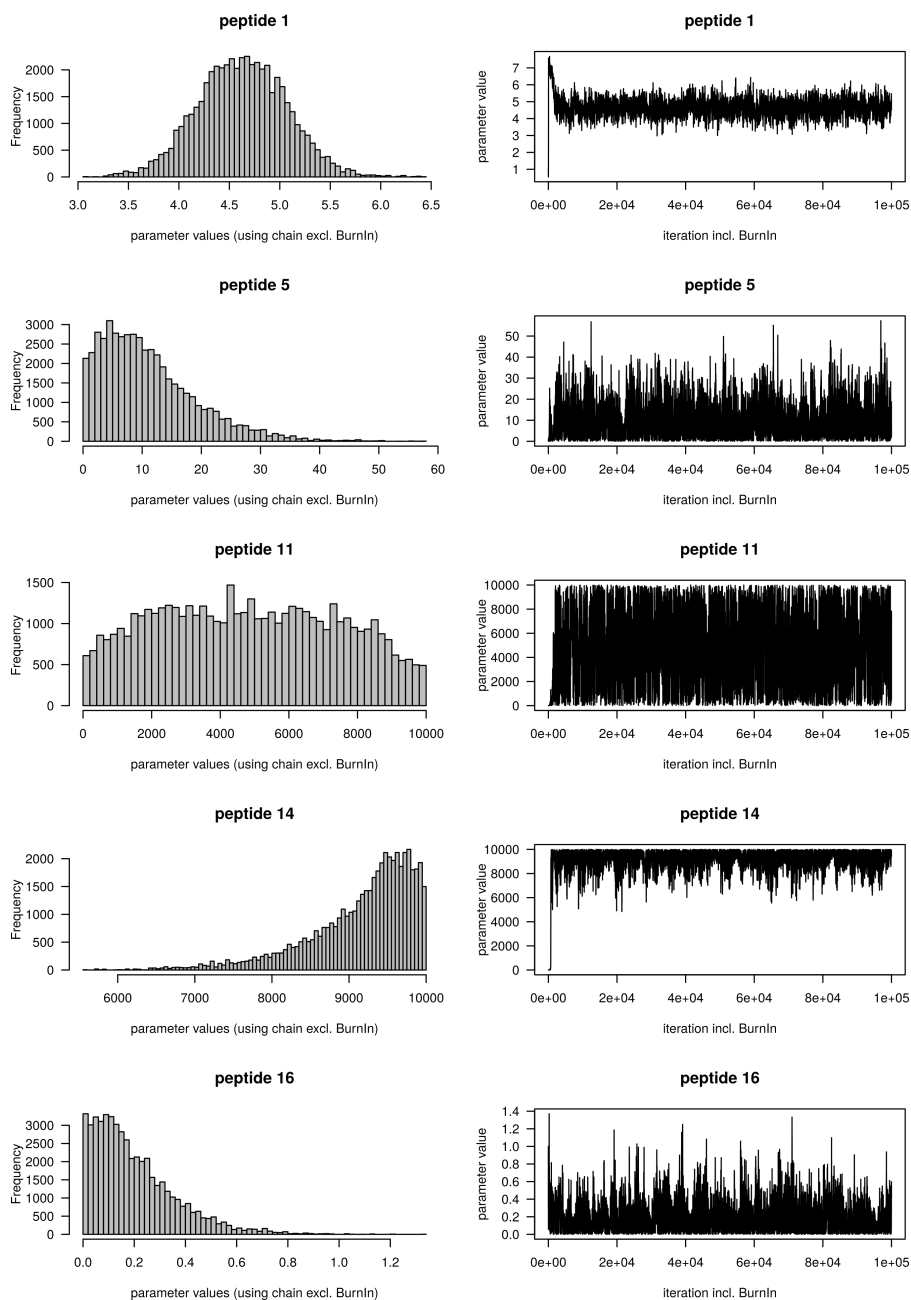
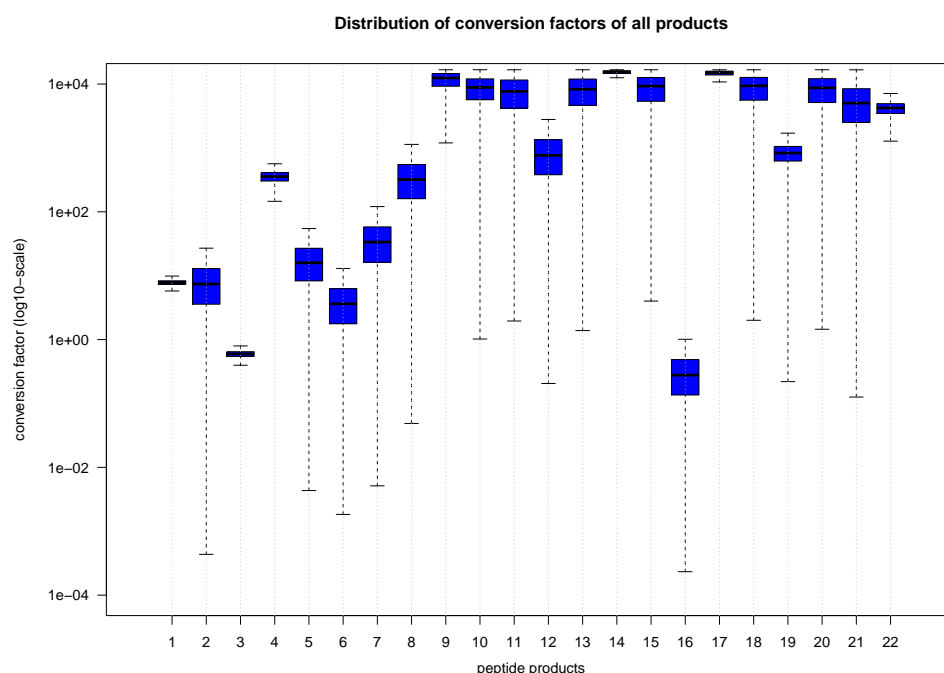


Figure 5.14: Distribution and trace of the Markov chain of selected peptides after termination (chain\_100000.pdf)

## Final results

Again, the chain has to be backscaled before being able to calculate the concentrations. The conversion factors that QPuB infers from the data are graphically shown in the file **statistics.pdf** with numeric values saved in **statistics.csv**:



Since we provided the titration data of the substrate, the absolute concentrations can be calculated from the input signals and not only the normalized signals are returned.

### CALCULATING ABSOLUTE CONCENTRATIONS...

... using substrate titration from file 190423\_K386\_titration\_substrate\_charge\_3\_K386.csv

Linear fit of the substrate titration before normalization:

intercept: 44479107527.5953, slope: 17042776518.3551

Using this fit, the signal for amount loaded 200 is 3453034411198.62

Linear fit of the substrate titration after normalization, mean over replicates:

intercept: 11451356077.9449, slope: 4387743219.61028

Substrate and product amounts:

Numeric values in folder 'concentrations'.

Kinetic plots in folder 'plots\_concentrations'.

Plots of the linear fits of the substrate titration before and after normalization are created. (Reminder: Normalization means modifying the titration data such that the signal of the amount of substrate loaded to the kinetics equals the signal at the beginning of the substrate signal kinetics.)

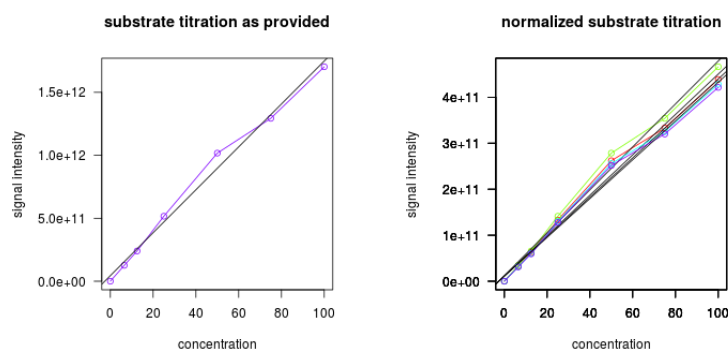


Figure 5.15: The files substratetitration\_given.png and substratetitration\_normalized.png.

For numeric values of the amounts of the substrate and the products, see folder [concentrations](#). For graphical output see folder [plots.concentrations](#). Here we only show 4 of the 23 products.

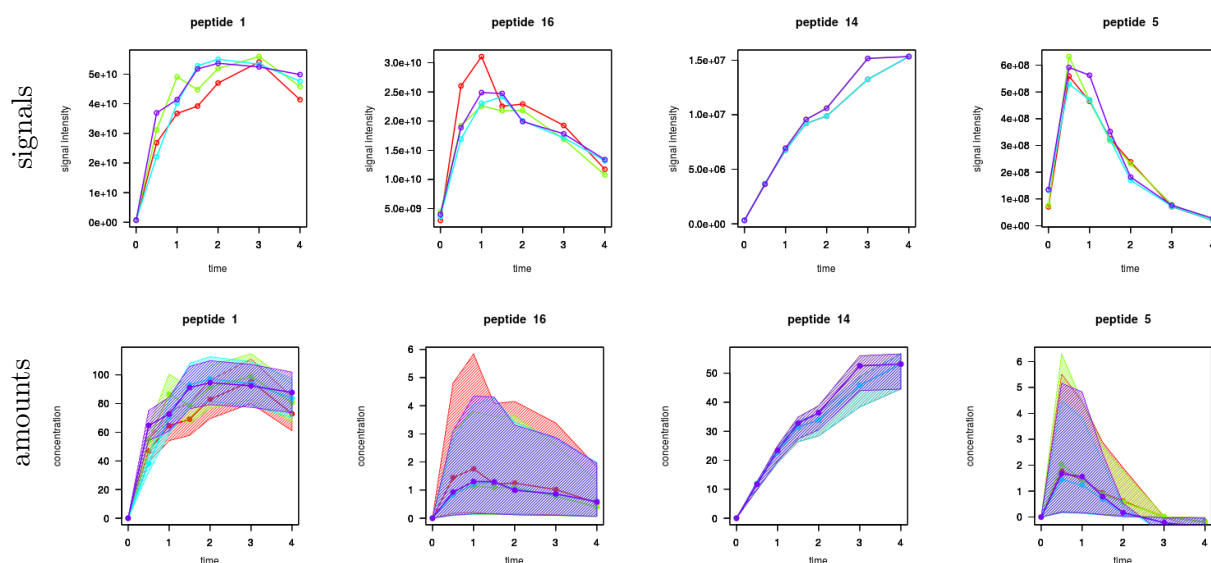


Figure 5.16: Kinetics of the input signal intensities and the output concentrations.

Peptide 1 is an example of a product with a high signal intensity and a resulting high concentration. Peptide 17 also has a high signal intensity but actually has quite a low abundance. Peptide 15 on the other hand has a very low signal intensity but a reasonably high amount. Note that if the signal at some time point  $t > 0$  drops below the signal intensity of time  $t = 0$ , then the concentrations may become negative like for peptide 5.

#### 5.4.5 Changing some of the Options

The above examples were executed making use of the many default settings. This section is dedicated to testing some of the options provided on the data of this particular example.

##### Remove last time point

Since in the last time point (after 4h) the substrate is almost completely degraded and the difference between 3h and 4h is so small, that the effect size is too small compared to the level of noise in the data, we decide to remove the last time point from the calculation of the likelihood. This can be done by providing the file **timepoints.txt**:

```
0 1
1 2
2 3
4 5
```

Note that in the residual figure, the plot for this pair of time points is created nevertheless.

##### Filter products

When inspecting the chain plots, note that some peptides can have a very broad distribution. As an example see peptide 11 in Fig. 5.14. Their signal intensity is so small that they don't contribute much to the mass balance and their conversion factors are hard to infer, since the level of noise in the data is bigger. Those peptides are very low abundant with a concentration below 1 pmol.

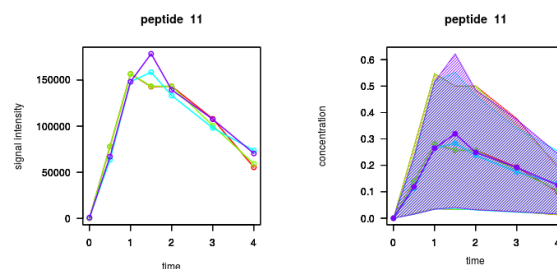


Figure 5.17: Signal intensities and absolute amount of peptide 11.

By activating the filtering option in the input.txt, these products are removed from the data set. We use the default threshold of  $10^6$  as the minimum signal intensity - all peptide products with a signal intensity below this threshold will be removed. This setting reduces the complexity of the data set by decreasing the number of products:

```
### DATA MANIPULATION
# Scale products to match order of magnitude of substrate
scaleprod: TRUE
# Filter out products which have a signal intensity below the threshold.
# If TRUE then threshold must be set.
filterprod: TRUE
threshold: 1e6
```

In this example, the dimension is reduced from 22 peptides to 16 peptides. Note that the number of a peptide in identifier.txt in the filtered case does not correspond to the number of the peptide in the unfiltered case!

### Not scaling products

By default, QPuB scales the signal intensities of all peptide products to match the order of magnitude of the substrate. In this way the prior ranges are less dependent on the specific data set and therefore can be set to  $[10^{-4}, 10^4]$  by default. This range was chosen because the conversion factor of the substrate is fixed to 1 and the experimentally observed order of magnitude of the conversion factor range is approximately 7. If the user does not want to make use of this, the prior range and the starting values have to be adjusted in the file input.txt. To illustrate the effect of this scaling option, we execute QPuB without scaling:

```
### DATA MANIPULATION
# Scale products to match order of magnitude of substrate
scaleprod: FALSE
# Filter out products which have a signal intensity below the threshold.
# If TRUE then threshold must be set.
filterprod: FALSE
threshold: 1e6
```

### Different Gamma exponent

For high dimensional data, we recommend adjusting the Gamma exponent used in the function to achieve vanishing adaptation. With a lower exponent, the adaptation vanishes later:

```
### ADVANCED ALGORITHM PARAMETERS
# optimal acceptance rate
OptAccRate: 0.234
# track performance of the run: print acceptance rate and effective sample size
Track: TRUE
# Exponent for the sequence to realize vanishing adaptation.
# Choose a value between 0 and 1.
GammaExponent: 0.01
# Fraction of the Markov chain to consider as burn-in, 0.25 means 25% burn-in
burnFrac: 0.5
```

## 5.5 System specifications

The timekeeping in the example runs is system and hardware dependent.

### Linux

We used a Linux machine with the following specifications:

```
Machine: Dell Precision Tower 3420
OS: Linux Ubuntu 16.04 xenial (64bit)
CPU: Intel(R) Core(TM) i7-7700 CPU @ 3.60GHz (8 cores)
RAM: 32GB
```

Running Example 1 on this Linux machine took roughly 35 sec.

Running Example 4 on this Linux machine took roughly 18 min.

### Apple

We used an Apple machine with the following specifications:

```
Machine: Apple MacBook Pro
OC: macOS High Sierra 10.13.6
CPU: Intel Core i7 @ 2.5 GHz (1 cores)
RAM: 8GB
```

Running Example 1 on this Apple machine took roughly 59 sec.

Running Example 4 on this Apple machine took roughly 24 min.

### Windows

We used a Windows machine with the following specifications:

```
Machine: Acer Aspire V3
OS: Windows 8.1 (64 bit)
CPU: Intel(R) Core(TM) i5-4210U CPU @ 1.7 GHz 2.4 GHz
RAM: 8GB
```

Running Example 1 on this Windows machine took roughly 85 sec.

Running Example 4 on this Windows machine took roughly 45 min.

## 6 | Troubleshooting

In this chapter, we listed a non-exhaustive list of issues that the user might run into while running QPuB. However, users are **strongly recommended** to keep track of the **runQPuB.ROUT.txt** from **the very beginning of the run**, as all the outputs including the warnings that might be generated for providing an out-of-range value for a particular input parameter, are printed.

### 6.1 Multiple installation of R

The user must make sure that the version of the R is 3.5.0 or above. In case, the user has multiple installation of R, the path to the R executable corresponding to the version specified for the QPuB should be provided. For Windows, please click [here](#) for more details on how to include the desired R executable in the PATH variable.

### 6.2 Command line execution

Care must be taken while writing the command line to run QPuB. For example, the following type of command will generate an error:

```
$ Rscript path_to_runQPuB.r -infol ../examples/example_folder
```

Instead, the **right** command type is

```
$ Rscript path_to_runQPuB.r -infol examples/example_folder
```

The same rules applies while including the titration file, for example, assuming the name of the example folder as **P** and the corresponding titration file name is **titration\_P**, the following command

```
$ Rscript path_to_runQPuB.r -infol examples/P -titr examples/P/titration_P.csv
```

will generate an error, while the command

```
$ Rscript path_to_runQPuB.r -infol examples/P -titr titration_P.csv
```

will work nicely. The folder does not have to be specified, the titration data file must be located in the input folder **P**.

### 6.3 MCMC chains

It may happen that the Markov chain is not exploring the parameter space. There might be several reasons for that. For example, the value of **sigma\_start** is so low that the chain stops exploring the parameter space. At the same time if the value of the **GammaExponent** is higher, due to vanishing nature of the adaptation, the covariance matrix will remain stationary leaving the chain stuck in an undesired region. Therefore, one solution to this is to stop the adaptation at the beginning for



sufficient exploration and then resume the adaptation again after visually inspecting the chain. This may take several trial runs to know the number of iterations needed before starting the adaptation. Remember that this problem is different than the one where the chain needs to be adapted at the beginning to reach the target covariance matrix. But, it may take over millions of iterations before reaching the target region. This is especially the case for higher dimensions (Rosenthal et al., 2011). Overall, depending upon the problem, users are recommended to experiment with the parameters controlling the adaptation scheme and the Markov chain. In Rosenthal et al. (2011), the authors provide an excellent summary of various pathological cases regarding adaptive scheme and optimal scaling for MCMC.

# Appendix

## A Bayesian statistical inference

Bayesian statistical inference deduces properties of an underlying probability distribution following the Bayes' rule, which tells us the formal way to update the probabilities based on new information. For a typical parameter estimation problem, assuming  $\theta$  is the set of parameters,  $M$  denotes the model, and  $d$  denotes the data set, the Bayes' rule states that

$$\mathbb{P}(\theta|d, M) = \frac{\mathbb{P}(d|\theta, M)\mathbb{P}(\theta|M)}{\mathbb{P}(d|M)}, \quad (\text{A.1})$$

where

- $\mathbb{P}(\theta) := \mathbb{P}(\theta|d, M)$  is called the **posterior probability**.
- $\mathcal{L}(\theta) := \mathbb{P}(d|\theta, M)$  is called the **likelihood**.
- $\pi(\theta) := \mathbb{P}(\theta|M)$  is called the **prior probability**.
- $z := \mathbb{P}(d|M)$  is called the **marginal likelihood probability** and expressed as

$$z = \int \mathcal{L}(\theta)\pi(\theta)d\theta. \quad (\text{A.2})$$

The normalisation constant  $z$  makes the  $\mathbb{P}(\theta)$  a genuine probability density for  $\theta$ . For model comparison, this constant is immensely important as for example, the relative posterior probability between two models  $M_1$  and  $M_2$  is expressed as

$$\frac{\mathbb{P}(M_1|d)}{\mathbb{P}(M_2|d)} = \frac{\pi(M_1)\mathbb{P}(d|M_1)}{\pi(M_2)\mathbb{P}(d|M_2)} = \frac{\pi(M_1)z_{M_1}}{\pi(M_2)z_{M_2}}. \quad (\text{A.3})$$

Unfortunately, for a high-dimensional problem, the integral Eq. (A.2) is difficult to solve analytically and can even become computationally intractable. In such scenarios, we rely on Markov chain Monte Carlo (MCMC) methods.

## B Markov chain Monte Carlo

The basic idea of an MCMC algorithm is to learn the posterior distribution  $\mathbb{P}(\theta)$  by first initiating a Markov chain of parameters whose equilibrium distribution corresponds to  $\mathbb{P}(\theta)$ , and then approximating the desired distribution by producing enough samples of  $\theta$  using Monte Carlo sampling techniques.

Among various MCMC algorithms, two extremely popular ones include the Metropolis-Hastings (M-H) algorithm (Metropolis et al., 1953; Hastings, 1970) and the Gibbs sampler (Geman and Geman, 1987).

## Metropolis-Hastings algorithm

Assuming  $\mathbb{P}(\theta)$  is defined on a state space  $\mathcal{X}_\theta$ , the M-H algorithm proposes a geometric way to construct a Markov chain  $\{X_n\}_{n \in \mathbb{N}}$  on  $\mathcal{X}_\theta$  that is ergodic (statistical property can be deduced from a single and sufficiently long random sample) and stationary (irreducible) with respect to  $\mathbb{P}(\theta)$ , which means if  $X_n \sim \mathbb{P}(\theta)$ , then  $X_{n+1} \sim \mathbb{P}(\theta)$ . Algorithmically, the M-H sampler can be written in the following way (Robert and Casella, 1999):

```

Given  $X_0, n = 0$ ;
while  $X_n \not\sim \mathbb{P}(\theta)$  do
    Propose a candidate  $Y_n \sim q(y|X_n)$ ;

    
$$X_{n+1} = \begin{cases} Y_n & \text{with probability } \rho(X_n, Y_n) \\ X_n & \text{with probability } 1 - \rho(X_n, Y_n) \end{cases}$$


    where,
    
$$\rho(x, y) = \min \left\{ \frac{\mathbb{P}(y)q(y|x)}{\mathbb{P}(x)q(x|y)}, 1 \right\}$$


     $n = n + 1$ 
end

```

**Algorithm 1:** The Metropolis-Hastings algorithm

In QPuB, we assumed a symmetric proposal distribution i.e.  $q(y|x) = q(x|y)$ , and therefore used the Metropolis algorithm (Metropolis and Ulam, 1949; Metropolis et al., 1953). For example, one typical choice of a symmetric  $q$  is the normal distribution

$$q_\sigma(x|y) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{1}{2\sigma^2}(y-x)^2\right),$$

where  $\sigma^2$  is the variance of the proposed increments and defines the Markov transition probability. It has to be noted, that for an optimal performance of an MCMC algorithm involving such variance parameter  $\sigma^2$  associated with the Markov transition probability has to be tuned, which leads to a class of adaptive version of MCMC algorithms (Andrieu and Thoms, 2008).

## C Adaptive Markov chain Monte Carlo

The goal of adaptive Markov chain Monte Carlo (MCMC) methods is to fine-tune the proposal distribution for a specific target distribution. The adaptation step proceeds following a Robbins-Monro recursion (Robbins and Monro, 1951), which is a stochastic approximation algorithm to find the root of a function whose values are not available directly. To put mathematically, assume  $N(\theta)$  is a random variable whose measurement is available, and  $\mathbb{E}[N(\theta)] = M(\theta)$ , whose measurement is not available, then for a constant  $\alpha$  the recursion will find the root of the equation  $M(\theta) = \alpha$  using the following recursion

$$\theta_{n+1} = \theta_n - a_n(N(\theta_n) - \alpha), \tag{C.4}$$

where  $\{a_n\}_{n=1,2,\dots}$  is the sequence of positive step sizes satisfying the following conditions

$$\sum_{n=0}^{\infty} a_n = \infty \quad \text{and} \quad \sum_{n=0}^{\infty} a_n^2 < \infty.$$

A suitable choice for  $a_n$  satisfying the above two conditions is the quantity  $\frac{a}{n}$ , for  $a > 0$  as suggested by Robbins-Monro. Now, consider the observed random variable as  $N(\theta, X)$ , where  $X$  is some random

effect. Then if we consider  $M(\theta^*) = \min_{\theta} \mathbb{E}[N(\theta, X)]$ , this is equivalent to find the root of the gradient of the  $M(\theta) = 0$ . Denoting  $\nabla M(\theta)$  as  $Q(\theta, X)$ , we have to redefine the recursion Eq. (C.4) as:

$$\theta_{n+1} = \theta_n - a_{n+1}Q(\theta_n, X_{n+1}). \quad (\text{C.5})$$

This is equivalent to the attempt to find a root to the mean field equation

$$h(\theta) = \int_{\mathbb{R}^d} Q(\theta, X) \mathbb{P}(X) dX.$$

In the adaptive Metropolis (AM) setting,  $\theta_n = (\mu_n, \sigma_n^2)$ , and considering  $\mathbb{P}(X)$  has a second moment,  $h(\theta)$  has the unique root in  $(\mu_{\mathbb{P}(X)}, \sigma_{\mathbb{P}(X)}^2)$ . For the multivariate case, the variance will be translated to the covariance matrix  $\Sigma$ .

By construction, the adaptive version of MCMC is not Markovian unless the stepsize  $a_{n+1}$  is a monotonically decreasing sequence as shown in [Andrieu and Thoms \(2008\)](#). In addition, the authors provide an adaptive strategy for the scaling factor for  $\Sigma$ , based on the same Robbins-Monro recursion. Assuming AM in a multivariate setting, updating steps for  $\mu, \Sigma$ , and the scaling factor  $r$  after acceptance/rejection of a sample are as follows

$$\begin{aligned} \log(r_{n+1}) &= \log(r_n) + a_{n+1} \left( \rho(X_{n+1}, X_n), \rho^* \right) \\ \mu_{n+1} &= \mu_n + a_{n+1} \left( X_{n+1} - \mu_n \right) \\ \Sigma_{n+1} &= \Sigma_n + a_{n+1} \left( (X_{n+1} - \mu_n)(X_{n+1} - \mu_n)^T - \Sigma_n \right) \end{aligned}$$

### Rao-Blackwellization of AM algorithm

Rao-Blackwellization of M-H algorithm facilitates the finding of the unique unbiased estimators for  $\mu$  and  $\Sigma$  with minimum most variance ([Casella and Robert, 1996](#)). Before the Rao-Blackwellization of the M-H algorithm, let us briefly review the Rao-Blackwell Theorem and its significance to further motivate this improvement.

Consider  $X$  is a random vector representing the data and  $\theta$  is the set of parameters defining the distribution of  $X$ . A statistics  $S(X)$  is said to be *sufficient* if the conditional distribution of  $X$  given  $S$  i.e,  $\mathbb{P}(X|S)$  is independent of  $\theta$ . Furthermore, a statistic  $T(X)$  is an unbiased estimator of  $g(\theta)$ , a function of  $\theta$ , if  $\mathbb{E}_{\theta}[T(X)] = g(\theta)$ , then the Rao-Blackwell Theorem states:

**Theorem 1** *The variance of the conditional expectation  $\mathbb{E}[T(X)|S(X)]$  i.e.  $\text{Var}[\mathbb{E}[T(X)|S(X)]]$  is upper bounded by the variance of the unbiased estimator  $T(X)$  i.e.  $\text{Var}[\mathbb{E}[T(X)|S(X)]] \leq \text{Var}[T(X)]$ , and  $\mathbb{E}[T(X)|S(X)]$  is unbiased.*

In the M-H algorithm, the acceptance-rejection step of the proposal  $Y_n$  can be rewritten as

$$\text{if } (\mathcal{U}_n[0, 1] \leq \rho(X_n, Y_n)) \{ \text{then accept } Y_n \}.$$

Now, using the indicator variable  $\mathbb{I}$ , the above condition can be reformulated as the following:

$$X_{n+1} := \mathbb{I}\{\mathcal{U}_n \leq \rho(X_n, Y_n)\}Y_n + \mathbb{I}\{\mathcal{U}_n > \rho(X_n, Y_n)\}X_n.$$

The expectation of  $X_{n+1}$  with respect to  $\mathcal{U}_n$  conditional upon  $X_n$  and the proposed transition  $Y_n$  leads to

$$\mathbb{E}_{\mathcal{U}_n}[X_{n+1}|X_n, Y_n] := \overline{X_{n+1}} = \rho(X_n, Y_n)Y_n + (1 - \rho(X_n, Y_n))X_n. \quad (\text{C.6})$$

Furthermore, if we consider the statistic  $S(X_n)$  as  $X_n$ , then  $S(X_n)$  is *linearly sufficient* (Witting, 1987). Moreover,  $T_n(X) = X_n$  is unbiased (for large  $n$ ) since  $\mathbb{E}_\theta[T_n(X)] = E(X)$  (ignores all the points except the last one for any  $n$ ). Therefore, according to Theorem 1, we have

$$\text{Var}[\mathbb{E}_{\mathcal{U}_n}[X_{n+1}|X_n, Y_n]] \leq \text{Var}[\mathbb{E}_{\mathcal{U}_n}[X_{n+1}]].$$

Applying the Rao-Blackwellised updates for  $\mu$  and  $\Sigma$  we have

$$\begin{aligned} \mu_{n+1} &= \mu_n + \gamma_{n+1}(\bar{X}_{n+1} - \mu_n) \\ \Sigma_{n+1} &= \Sigma_n + \gamma_{n+1}[(X_{n+1} - \mu_n)(X_{n+1} - \mu_n)^T - \Sigma_n] \end{aligned} \quad (\text{C.7})$$

## D Truncated multivariate normal distribution

In many real life scenarios, support for the proposed samples are constrained. In that case, instead of the full distribution, we have to consider the *truncated* version of the distribution and draw samples from the same. Mathematically, this means we have to sample from the following probability distribution function (Wilhelm and Manjunath, 2010):

$$f(X, \mu, \Sigma, A, B) = \begin{cases} \frac{\exp\left\{\frac{1}{2}(X - \mu)^T \Sigma^{-1}(\mathbf{x} - \mu)\right\}}{\int_A^B \exp\left\{\frac{1}{2}(x - \mu)^T \Sigma^{-1}(X - \mu)\right\} dX} & \text{for } A \leq X \leq B \\ 0 & \text{otherwise,} \end{cases} \quad (\text{D.8})$$

where  $\mu$  is the mean vector, and  $\Sigma$  is the covariance matrix. In QPuB, we used the R routine *rtmvnorm* from the package *tmvtnorm* (Wilhelm and Manjunath, 2010) to generate proposals from a truncated multivariate normal distribution.

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