

Quantitation

MASCOT

{MATRIX}
{SCIENCE}

Quantitation was first introduced in Mascot 2.2. Our goal is to support all of the popular methodologies.

Quantitation - Overview

Protocol	Basis	Ratios	Examples
reporter	Specific reporter ion peaks within a single MS/MS spectrum	Inter-sample	iTRAQ, ExacTag, TMT
precursor	Extracted ion chromatograms for related precursors within a single dataset	Inter-sample	ICAT, SILAC, ¹⁸ O, ICPL, AQUA, Metabolic
multiplex (Neubert et. al.)	Pairs of sequence ion fragment peaks within a single MS/MS spectrum	Inter-sample	SILAC, ¹⁸ O
replicate	Extracted ion chromatograms for identical precursors across two or more datasets	Inter-sample	Label-free
empai (Ishihama et. al.)	Protein coverage from a database search result	Intra-sample	N/A
average (Silva et. al.)	Extracted ion chromatograms for selected peptides per protein within a single dataset	Intra-sample	N/A

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To make this task manageable, we have classified the various approaches into a limited number of protocols. So far, we have identified 6 distinct protocols.

Reporter is quantitation based on the relative intensities of fragment peaks at fixed m/z values within an MS/MS spectrum. For example, iTRAQ or Tandem Mass Tags

Precursor is quantitation based on the relative intensities of extracted ion chromatograms (XICs) for precursors within a single data set. This is by far the most widely used approach, which can be used with any chemistry that creates a precursor mass shift. For example, ¹⁸O, AQUA, ICAT, ICPL, Metabolic, SILAC, etc., etc.

Multiplex is quantitation based on the relative intensities of sequence ion fragment peaks within an MS/MS spectrum. This is a novel approach, which can be used with any chemistry that labels one peptide terminus, creating a small mass shift, such as ¹⁸O or SILAC under certain conditions.

Replicate is label free quantitation based on the relative intensities of extracted ion chromatograms (XICs) for precursors in multiple data sets aligned using mass and elution time.

All these four methods are used to measure the relative abundance of a protein from sample to sample. For example, whether a particular protein is up or down regulated when an organism is stressed or diseased. The next two methods are used to estimate the relative abundances of different proteins within a single mixture.

emPAI is quantitation for the proteins in a mixture based on protein coverage by the peptide matches in a database search result.

Average is quantitation for the proteins in a mixture based on the application of a rule to the intensities of extracted ion chromatograms (XICs) for the peptide matches in a database search result. For example, the average intensity for the three strongest peptide matches per protein

The rows with a blue background are the protocols that implemented in the search engine, and don't require any additional software.

Quantitation - Overview

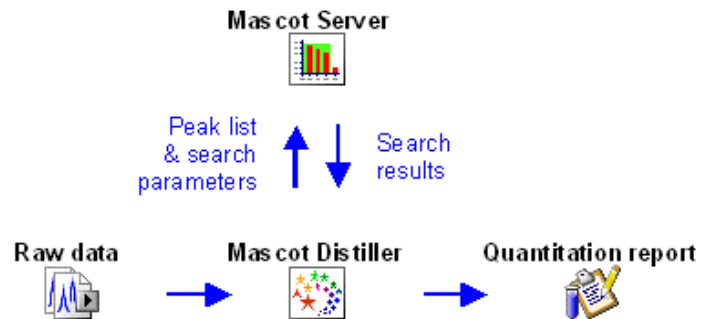
- Quantitation methods that only require information available in the MS/MS peak list are supported in Mascot Server
 - reporter
 - multiplex
 - emPAI
- Methods that require additional information from the raw data file require Mascot Distiller + Quantitation Toolbox
 - precursor
 - replicate
 - average

The common factor for these protocols is that all of the information required for quantitation is contained in the peak list.

The other three methods require additional information from the raw data file, either because it is necessary to integrate the elution profile of each peptide or because information is required for multiple peaks in the survey scan. These methods require that the raw data files are processed using Mascot Distiller.

Quantitation - Overview

Workflow for methods that require additional information from the raw data file, (precursor, replicate, average)



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For methods that require additional information from the raw data file, the workflow looks like this. The raw data file is processed in Distiller and the search submitted to Mascot. When the search is complete, the results are returned to Distiller. The quantitation report can then be generated in Mascot Distiller, which has access to both the Mascot search results and the raw data.

Quantitation

Named
quantitation
methods
keep the
search form
uncluttered

The screenshot shows the Mascot MS/MS Ions Search web interface. The 'Quantitation' section is highlighted, showing a list of quantitation methods: Carbamidomethyl (C), Oxidation (H/W), Phospho (ST), Phospho (TY), Propionamide (C), Pyridylethyl (C), Pyro-carbamidomethyl (N-term C), Sulfo (S), Sulfo (T), Sulfo (Y), TMT (K), and TMT (N-term). The 'Fixed modifications' section is also visible, showing 'Carbamidomethyl (C)' and 'Oxidation (M)'. The 'Variable modifications' section is empty. The 'Peptide tolerance' is set to 0.1 Da, and the 'MS/MS tolerance' is set to 0.1 Da. The 'Peptide charge' is set to 2+, and the 'Monoisotopic' checkbox is checked. The 'Data file' is set to 'Mascot generic', and the 'Instrument' is set to 'MALDI-TOF-TOF'. The 'Precursor' is set to 'm/z', and the 'Error tolerant' checkbox is checked. The 'Report type' is set to 'AUTO', and the 'Report hits' checkbox is checked. The 'Start Search' button is visible at the bottom of the form.

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We wanted to keep the user interface simple. Quantitation adds a huge number of choices and parameters, but there is no point in exposing all of these in the search form.

The approach we have chosen is encapsulate these choices and parameters into named quantitation methods. This means that the search form has just a single new control, which replaces the old ICAT checkbox.

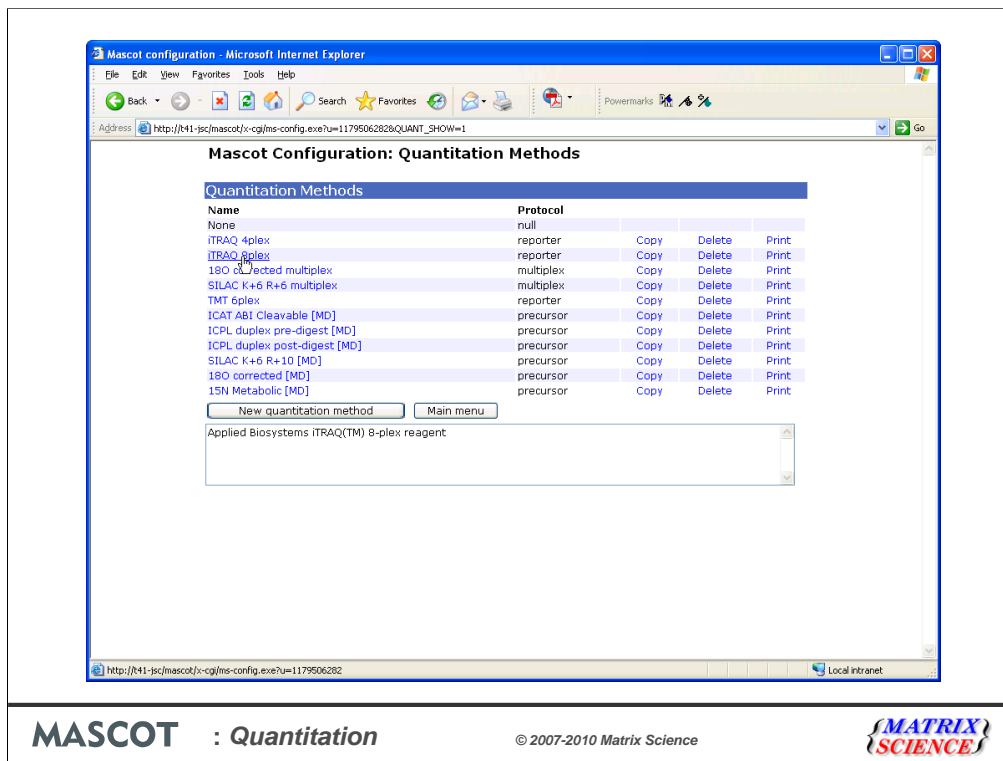
Methods that have [MD] at the end are the ones that require Mascot Distiller

Quantitation

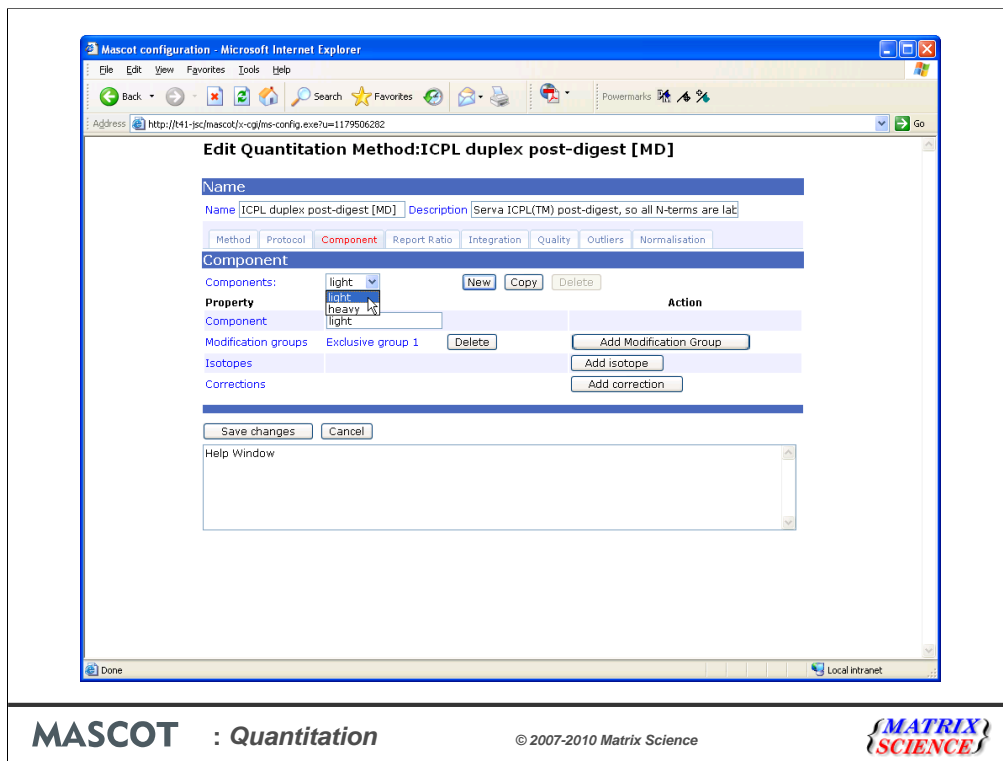
The quantitation methods are defined in a single XML configuration file

- quantitation.xml
- Browser based editor
- Add new methods as required
- Used by Mascot Server and Mascot Distiller

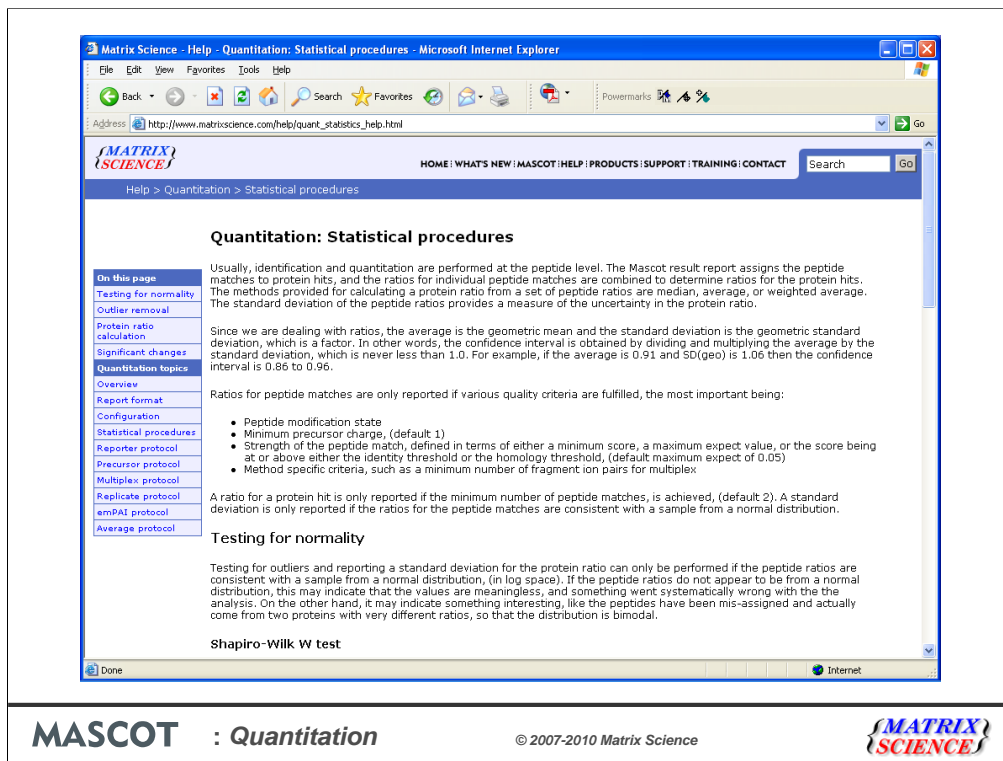
The configuration file that encapsulates the choices and parameters for each quantitation method is called quantitation.xml. This is an XML file, and there is a browser based editor for modifying methods and creating new ones. quantitation.xml lives on the Mascot server and is read by both the search engine and Mascot Distiller



The browser-based Configuration Editor provides an interface to all the Mascot configuration files. In the case of quantitation, you can edit an existing method or make a copy of it as the basis for a new method

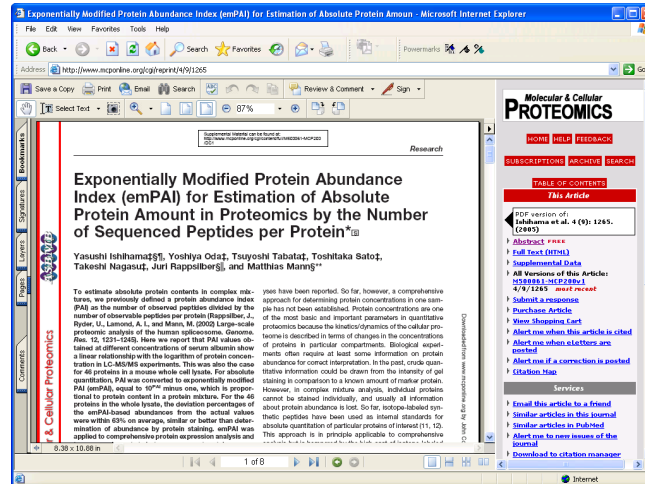


For each method, a tabbed dialog is used to navigate between property pages. In many cases, the property pages correspond to XML elements, but sometimes elements have been combined onto a single page or split across multiple pages so as to give a balanced layout. Here, we can see a duplex ICPL method. The unlabelled and labelled components have been called heavy and light, but you are free to choose your own names so as to make the final report as clear as possible.



We have taken trouble to ensure that appropriate statistical procedures are correctly used. For example, we test that a set of peptide ratios is consistent with a normal distribution before rejecting outliers or reporting a standard deviation. Standard deviations are always geometric, because we are dealing with ratios that conform to a normal distribution in log space.

Quantitation - emPAI



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emPAI quantitation offers approximate, label-free, relative quantitation of the proteins in a mixture based on protein coverage by the peptide matches in a database search result. This approach was developed by Ishihama and colleagues

Quantitation - emPAI

- Very simple

$$emPAI = 10^{\frac{N_{observed}}{N_{observable}}} - 1$$

- Very approximate

- Many assumptions in $N_{observed}$ and $N_{observable}$

- 'Always on'

1. **PPB1_HUMAN** Mass: 58259 Score: 452 Queries matched: 17 emPAI: 1.04
Alkaline phosphatase, placental type precursor (EC 3.1.3.1) (PLAP-1) (Regan isozyme) - Homo sapiens
☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta Miss	Score	Expect	Rank	Peptide	
<input checked="" type="checkbox"/> 27	462.6807	923.3468	923.5116	-0.1649	0	33	0.25	1	R.FPYVALSK.T
<input checked="" type="checkbox"/> 41	517.1760	1032.3375	1032.5604	-0.2229	0	71	6.4e-05	1	R.GSSIFGLAPGK.A
<input checked="" type="checkbox"/> 62	564.6804	1127.3463	1127.5764	-0.2301	0	9	1.2e+02	1	R.GFFLFVEGGK.I

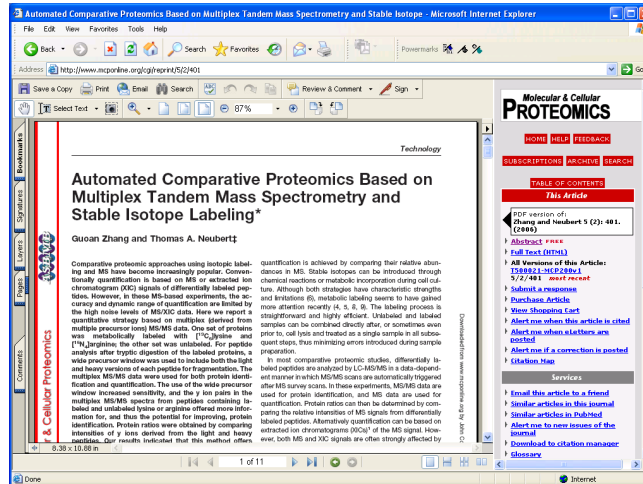
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It is very simple. It is also very approximate, because there are many arbitrary assumptions in the way that the number of observed and observable peptides are calculated. Nevertheless, Ishihama's paper shows that it can be a useful guide to relative amounts. emPAI doesn't require a label or special data processing, so it is always reported in a standard Mascot results report, as long as the number of MS/MS spectra is at least 100

Quantitation - multiplex



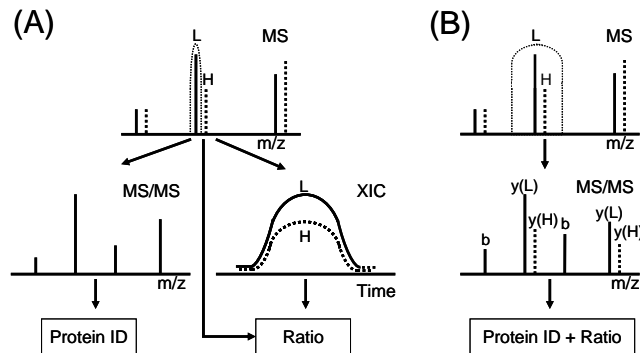
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Multiplex is quantitation based on the relative intensities of sequence ion fragment peaks within an MS/MS spectrum. This approach, developed Zhang and Neubert, can be used with any chemistry that labels one peptide terminus and has a reasonably small mass shift.

Quantitation - multiplex



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This diagram, copied from the MCP paper, illustrates how it works. On the left, we have conventional quantitation; the ‘precursor protocol’ in Mascot terms. This requires the precursor intensity for each component to be integrated across its elution profile. In the case of the multiplex protocol, the MS1 transmission window is set wide enough to allow both components through simultaneously, giving a mixed MS/MS spectrum. The relative amounts can be measured from the sequence ions that include the labelled terminus. If the label is on the carboxy terminus, we see the ratios in the y ions.

Quantitation - multiplex

Requirements:

- Label confined to one peptide terminus
e.g. ^{18}O , or SILAC at K or R with trypsin
- MS1 transmission window must be ~ flat over the label delta
- Heavy and light pair must be 'isolated' in survey scan
- Heavy and light must ~ co-elute
- Label must not affect fragmentation kinetics
- Tough to extend to more than 2 components.

The multiplex method has the potential to give excellent precision, because each ratio is represented by multiple sequence ion pairs. On the other hand, the ratio will only be accurate if several constraints are met.

Quantitation - multiplex

Isobaric Peptide Termini Labeling (IPTL):

- Koehler, C. J., et al., Isobaric Peptide Termini Labeling for MS/MS-Based Quantitative Proteomics, J. Proteome Research 8 4333-4341 (2009)
- Label both termini
- Heavy and light have equal and opposite shifts, e.g.
 - Component 1:
Succinyl d0 at the N-term and IMID d4 at C-term
 - Component 2:
Succinyl d4 at the N-term and IMID d0 at C-term

Isobaric Peptide Termini Labeling (IPTL) is a recent improvement to multiplex. This labels both termini and the difference between the two components is a mass increase at one terminus exactly balanced by a mass decrease at the other. Having isobaric precursors removes the requirement for the transmission window between MS1 and MS2 to be wide enough to accommodate the mass shift introduced by the label.

Peptide Summary Report (SILAC example: NG108-EphB2 from Zhang and Neubert) - Microsoft Internet Explorer

Address: http://www.matrixscience.com/cgi/master_results.pl?file=.../data/F981133.dat

8. [HNRPU_HUMAN](#) Mass: 90423 Score: 130 Queries matched: 4
Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (Scaffold attachment factor A) (SAF-A) (p120) (
☐ Check to include this hit in error tolerant search

Quantitation: Ratio									
	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Heavy/Light
									0.794
									2
									1.021

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Heavy/Light	Peptide
<input checked="" type="checkbox"/> 32	692.2000	1382.3854	1387.7113	-5.3258	0	37	3.1	1	---	K.YNLTNTTIDDK_M + 13C6_NL_K (C-ter
<input checked="" type="checkbox"/> 34	694.6700	1387.3254	1387.7113	-0.3858	0	(17)	3.2e+02	1	---	K.YNLTNTTIDDK_M + 13C6_NL_K (C-ter
<input checked="" type="checkbox"/> 51	824.9751	1647.9357	1652.8577	-4.9220	0	(100)	1.3e-06	1	0.811	R.NFILDQTNVSAQAQR_R + 13C6_NL_R (
<input checked="" type="checkbox"/> 52	827.4146	1652.8147	1652.8577	-0.0431	0	104	5.5e-07	1	0.779	R.NFILDQTNVSAQAQR_R + 13C6_NL_R (

9. [EPHB2_HUMAN](#) Mass: 117417 Score: 130 Queries matched: 4
Ephrin type-B receptor 2 precursor (EC 2.7.10.1) (Tyrosine-protein kinase receptor EPH-3) (DRT) (Re
☐ Check to include this hit in error tolerant search

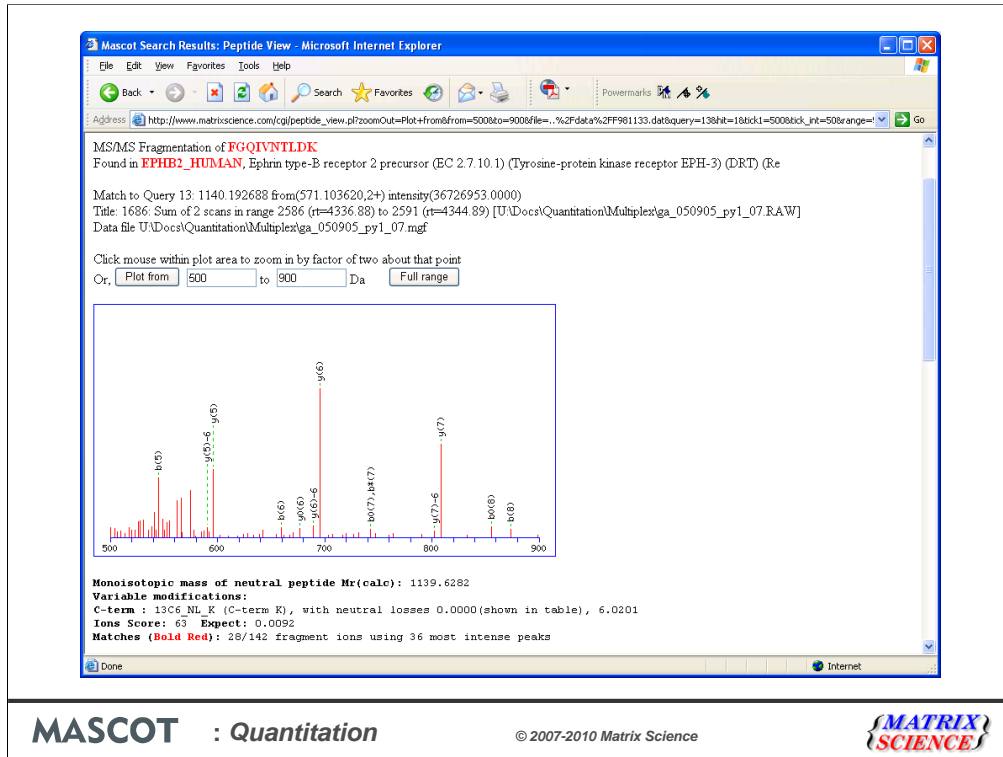
Quantitation: Ratio									
	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Heavy/Light
									10.512
									2
									1.054

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Heavy/Light	Peptide
<input checked="" type="checkbox"/> 13	571.1036	1140.1927	1139.6282	0.5645	0	63	0.0092	1	10.341	K.FGQIVNTLDK_M + 13C6_NL_K (C-ter
<input checked="" type="checkbox"/> 21	620.9648	1239.9150	1239.6343	0.2807	0	26	45	1	---	R.WTAPEAIQYR_K + 13C6_NL_R (C-ter
<input checked="" type="checkbox"/> 53	837.9240	1673.8335	1672.9277	0.9058	0	43	0.69	1	11.304	K.AHAPLSSGINKPLDRL_T + 13C6_NL_R
<input checked="" type="checkbox"/> 88	1124.9100	2247.8054	2247.1042	0.7012	0	17	1.8e+02	1	---	R.TIPDYTSFNTVDENLEAIK_M + 13C6_NL

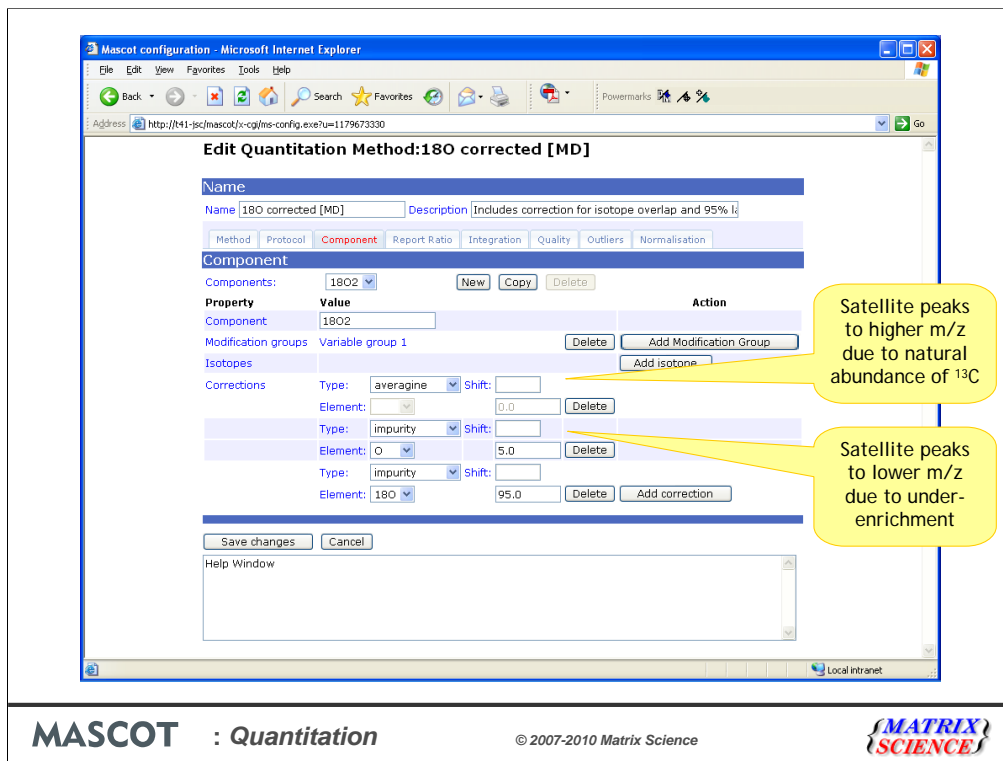
Proteins matching the same set of peptides:
[EPHB2_MOUSE](#) Mass: 110688 Score: 130 Queries matched: 4
Ephrin type-B receptor 2 precursor (EC 2.7.10.1) (Tyrosine-protein kinase receptor EPH-3) (Neural k

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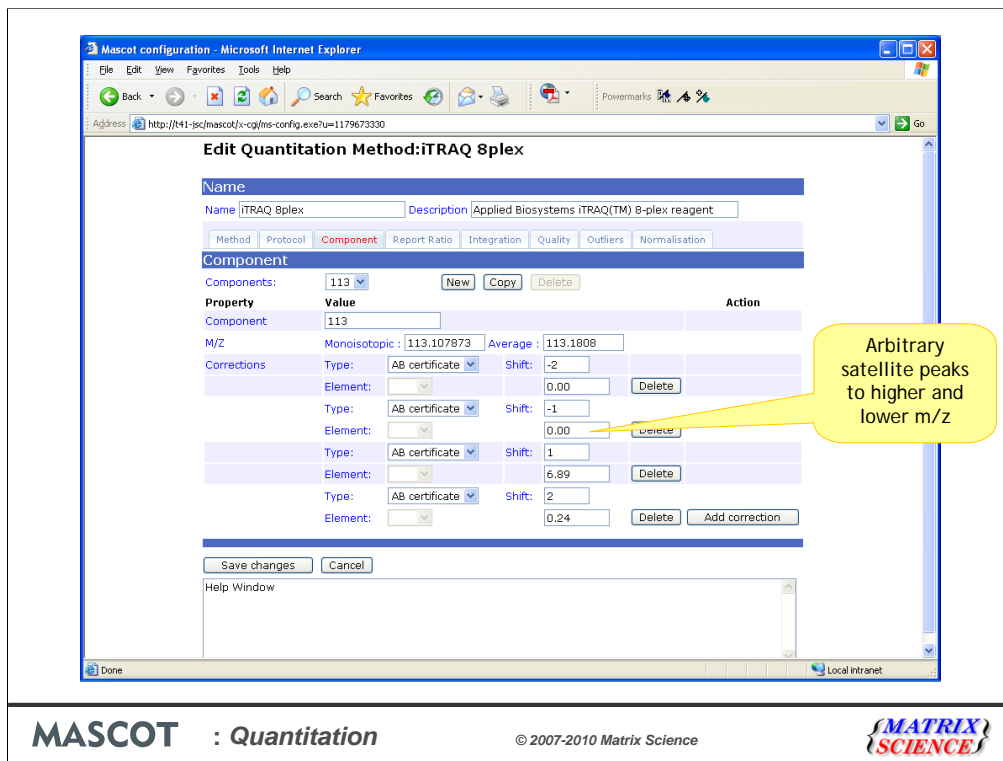
This is an example using a dataset courtesy of Zhang and Neubert. The instrument was an ion trap and the label is 13C(6) SILAC on K and R.



We can see that the heavy component has been strongly up-regulated in this peptide from human ephrin



One of the complications of any type of isotope labelling is isotope impurity. It is rarely possible to get 100% enrichment. In the Mascot quantitation schema, this is described by a correction element. An 'impurity' correction works "downwards". That is, in this 18O method, some of the intensity of peptides labelled with the 18O label will appear at lower mass values because the heavy water is only 95% enriched. A second type of isotope correction, 'averagine', works "upwards". This describes how some of the intensity will be found at higher mass values because of the natural abundances of heavy isotopes. An averagine correction only matters when the mass delta is small, as in the case of 18O labelling.



A third type of isotope correction is used in iTRAQ and TMT, where the correction factors are obtained experimentally, by analysing the isolated reagents. This combines both upward and downward corrections for labels which have complex, multi-isotope compositions

Quantitation - Reporter

TS2Mascot 0.0.90

Spot Sets

- hans
- James
- jmc
- JMCSetup
- Kaajal
- Martin
- New Project
- New Project
- Nick
- NICKM
- New Project
- Spot Set JSC
- New Project
- sarah
- Training

4: Job run 12384; 03/11/2005 18:21:04; MS-MS 2KV Positive

☒ Export all MS/MS spectra in job run
☐ Export selected spectrum only

SPOT LABEL	SPOT NAME	SPOT TYPE	PRECURSOR MASS	OPMODE
1		Unknown	2336.154	MS-MS 2k
1		Unknown	2617.197	MS-MS 2k
1		Unknown	1252.544	MS-MS 2k
1		Unknown	2514.033	MS-MS 2k
1		Unknown	1344.682	MS-MS 2k
1		Unknown	2463.284	MS-MS 2k
1		Unknown	1233.563	MS-MS 2k
1		Unknown	2479.202	MS-MS 2k
1		Unknown	2447.287	MS-MS 2k
3		Unknown	2542.095	MS-MS 2k
4		Unknown	2486.308	MS-MS 2k

Peak Filtering

Mass Range: 60 Da to 20 Da below precursor mass

Minimum S/N: 10 ☒ Monoisotopic peaks only

Mascot Server URL (e.g. <http://localhost/mascot/cgi/>)

<http://koala/mascot/cgi/>

4000 Series Database Connection

Connected to TSQUARED [Change ...](#)

[Exit](#) [Save peak list](#) [Mascot Search](#)

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In data processing terms, the reporter protocol is one of the simplest. However, we did find that the peak list exported from the 4000 series data system or submitted to Mascot from GPS Explorer did not have the correct peak areas for the reporter ions. The numbers are different from those used within GPS Explorer for quantitation. We have had to write our own application to export a suitable peak list from the Oracle database. We've released this utility, called TS2Mascot, as freeware, and you can download it from our web site.

So, for iTRAQ, we could launch TS2Mascot and choose Mascot Search ...

Quantitation - Reporter

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Which brings up the search form. We choose an appropriate quantitation method. We don't need to specify the iTRAQ modifications because these are pre-defined in the quantitation method. Submit the search...

Peptide Summary Report (Time flies like an arrow) - Microsoft Internet Explorer

Address: http://www.matrixscience.com/cgi/master_results.pl?file=../data/F981131.dat

MASCOT Search Results

User : Mel Anogaster
 Email : mel@bioc.cam.ac.uk
 Search title : Time flies like an arrow
 MS data file : U:\Docs\Quantitation\ITRAQ\cantab\denisef28QSTARcor.mgf
 Database : SwissProt 51.6 (257964 sequences; 93947433 residues)
 Quantitation : ITRAQ 4plex [method details](#)
 : Applied Biosystems ITRAQ(TM) reagent
 Timestamp : 19 Feb 2007 at 14:31:55 GMT
 Protein hits : 115/114 116/114 117/114

Protein hits	115/114	116/114	117/114	Protein description
0.914	1.438	1.809	APLP_DROME	Apolipoproteins precursor (Retinoid- and fatty acid-binding glycoprotein)
1.761	2.245	3.225	VIT13_DROME	Vitellogenin-3 precursor (Vitellogenin III) (Yolk protein 3) - Drosophila
1.891	3.221	1.717	PDI_DROME	Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) - Drosophila
1.020	1.191	0.684	UGGG_DROME	UDP-glucose:glycoprotein glucosyltransferase precursor (EC 2.4.1.1)
0.846	1.656	3.233	EF1A_DROME	Elongation factor 1-alpha (EF-1-alpha) (50 kDa female-specific protein)
1.096	4.004	6.741	TOP2_DROME	DNA topoisomerase 2 (EC 5.99.1.3) (DNA topoisomerase II) - Drosophila
0.969	1.221	2.165	RL4_DROME	60S ribosomal protein L4 (L1) - Drosophila melanogaster (Fruit fly)
1.042	2.000	3.426	VDAC_DROME	Voltage-dependent anion-selective channel (Porin) (DmVDAC) - Drosophila
1.422	1.906	1.335	HSP7C_DROME	Heat shock 70 kDa protein cognate 3 precursor (78 kDa glucose-regulated protein)
1.090	1.839	1.182	YL_DROME	Putative vitellogenin receptor precursor (Protein yolkless) (YL) - Drosophila
1.411	2.166	0.928	SPTCA_DROME	Spectrin alpha chain - Drosophila melanogaster (Fruit fly)
0.357	0.831	1.733	ATPB_DROME	ATP synthase subunit beta, mitochondrial precursor (EC 3.6.3.14) - Drosophila
1.051	2.172	2.501	GRLP_DROME	Guanine nucleotide-binding protein subunit beta-like protein (Receptor)
0.747	1.363	2.370	RS3_DROME	40S ribosomal protein S3 - Drosophila melanogaster (Fruit fly)
1.174	1.160	1.554	VIT11_DROME	Vitellogenin-1 precursor (Vitellogenin I) (Yolk protein 1) - Drosophila
1.577	3.060	5.007	RL13_DROME	60S ribosomal protein L13 (BBC1 protein homolog) - Drosophila melanogaster
1.214	1.097	0.717	CALR_DROME	Calreticulin precursor (CRP55) (Calregulin) (HACBP) - Drosophila melanogaster
0.855	1.919	3.548	PKYK_DROME	Pyruvate Kinase (EC 2.7.1.40) (PK) - Drosophila melanogaster (Fruit fly)
0.756	0.752	2.068	PABP_DROME	Polyadenylate-binding protein (Poly(A)-binding protein) (PABP) - Drosophila
1.256	1.958	2.789	RL9_DROME	60S ribosomal protein L9 - Drosophila melanogaster (Fruit fly)
---	---	---	LAMC1_DROME	Laminin subunit gamma-1 precursor (Laminin B2 chain) - Drosophila melanogaster

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And back comes the report. At the top is a summary of the protein ratios. In this example, the method asks for ratios to 114, but you have total flexibility. You can edit the quantitation method to report two pairs, e.g. 115/114 and 117/116, or something more complex, like ratios to the sum of all four channels. Note that you can't do this if you are using our public web site, because this is a shared resource, so you don't have access to the configuration editor.

Select Summary Report (iTRAQ 8plex) - Microsoft Internet Explorer

Address: http://www.matrixscience.com/cgi/master_results.pl?file=.%2Fdata%2F20080523%2F1guofTST.dat&REPORT=select&sigthreshold=0.05&REPORT=110_server_mudpit_switch

Mascot Search Results

User : johnc
 Email : jcottrell@matrixscience.com
 Search title : iTRAQ 8plex
 MS data file : D:\Distiller_Quant_Test_Data\iTRAQ\4000\merge.txt
 Database : SwissProt 55.3 (366226 sequences; 132054191 residues)
 Quantitation : iTRAQ 8plex [method details](#)
 Applied Biosystems iTRAQ(TM) 8-plex reagent
 Timestamp : 23 May 2008 at 08:51:16 GMT
 Enzyme : Trypsin/P
 Fixed modifications : Methylthio (C), iTRAQ8plex (N-term), iTRAQ8plex (K)
 Variable modifications : Carbamidomethyl (C), Oxidation (M)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 0.3 Da ($H^{13}C = 1$)
 Fragment Mass Tolerance : ± 0.6 Da
 Max Missed Cleavages : 2
 Instrument type : MALDI-TOF-TOF
 Number of queries : 4624
 Protein hits :

114/113	115/113	116/113	117/113	118/113	119/113	121/113	
1.129	1.162	1.222	1.078	1.057	0.977	1.017	TLH2_HUMAN Talin-2 - Homo sapiens
1.007	1.125	1.278	1.113	1.176	1.087	1.029	S41A3_HUMAN Solute carrier family 4
0.947	0.904	0.902	1.289	1.048	1.023	0.860	HDX_HUMAN Highly divergent homeob
1.285	1.189	1.279	1.340	1.093	1.250	0.834	KIF14_HUMAN Kinesin-like protein KI
1.142	1.144	1.306	1.082	1.288	1.039	1.074	AP2M1_HUMAN AP-2 complex subunit mu
1.062	1.275	1.292	1.218	1.200	0.930	0.964	MED17_HUMAN Mediator of RNA polymer
1.054	1.046	1.150	1.142	1.251	1.293	1.170	KCNK5_HUMAN Potassium channel subfa
1.056	0.999	1.211	1.093	1.235	1.041	0.996	EAA1_HUMAN Excitatory amino acid t
---	---	---	---	---	---	---	ODFP1_HUMAN Outer dense fiber prote
1.020	0.856	1.140	0.983	1.155	0.945	0.787	NUCL_HUMAN Nucleolin - Homo sapien
0.903	0.969	1.415	0.914	1.075	0.813	0.808	ZSWH5_HUMAN Zinc finger SWIM domain

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Its very easy to create a new method when a new chemistry becomes available. Here, for example, is the iTRAQ 8plex

Select Summary Report (John Rogers TMT PQD extract_msn.exe) - Microsoft Internet Explorer

Address: [http://localhost:8080/mascot/quant_report_detail=18_quant_outliers_method=autob_quant_min_num_peptides=20_min_precursor_charge=16_quant_pep_threshold_type=at-least+homology](#)

MASCOT Search Results

User :
 Email :
 Search title : 6plex TMT data from a collaborative demonstration by Proteome Sciences and Thermo Scientific, (PQD on LTQ XL).
 MS data file :
 Database : SwissProt 30.1 (39992 sequences, 1213333 residues)
 Quantitation : TMT 6plex [Method details](#)
 : Proteome Sciences sixplex Tandem Mass Tag
 Timestamp : 4 Apr 2008 at 12:45:45 GMT
 Enzyme : Trypsin/P
 Fixed modifications : Carbamidomethyl (C), TMT6plex (N-term), TMT6plex (K)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 2.5 Da
 Fragment Mass Tolerance : ± 0.35 Da
 Max Missed Cleavages : 2
 Instrument type : ESI-TRAP
 Number of queries : 8131
 Protein hits :

	127/126	128/126	129/126	130/126	131/126	
1.880	2.576	4.305	1.958	0.679	OVAL_CHICK	Ovalbumin - Gallus gallus (Chicken)
1.877	2.754	3.881	1.908	0.512	ALBU_BOVIN	Serum albumin precursor - Bos taurus
2.027	3.339	4.409	2.621	0.793	TRY1_BOVIN	Cationic trypsin precursor - Bos taurus
2.227	3.030	4.318	2.291	0.619	LYSC_CHICK	Lysozyme C precursor - Gallus gallus
2.082	2.965	4.078	2.022	0.735	MYG_EQUUS	Myoglobin - Equus burchelli (Plains Zebu)
2.213	3.186	4.211	2.276	0.779	CAH2_BOVIN	Carbonic anhydrase 2 - Bos taurus
1.708	2.693	3.259	2.481	0.626	G3P_FIG	Glyceraldehyde-3-phosphate dehydrogenase

Select Summary Report

Format As: Select Summary (protein hits) [Help](#)

MASCOT : Quantitation

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And the TMT tags now marketed by Thermo

Peak picking

Reporter ions are not peptides!

Cannot use conventional de-isotoping

- If using mascot.dll, get 1.6b23 or later
- If using Mascot Distiller, get 2.2.0 or later
- Unless your peak picking software has support for a “reporter ion window”, turn off de-isotoping

For the reporter protocol, i.e. iTRAQ or TMT, you have to be very careful with peak detection. Reporter ions do not have natural isotope distributions, so anything that assumes this will not be reliable. Whatever peak picking software you use, you'll probably need to experiment with the settings. For wiff files, the latest version of mascot.dll has a window around the reporter ion region where it does not perform de-isotoping. You can download this from the Analyst help page on our web site.

Normalisation

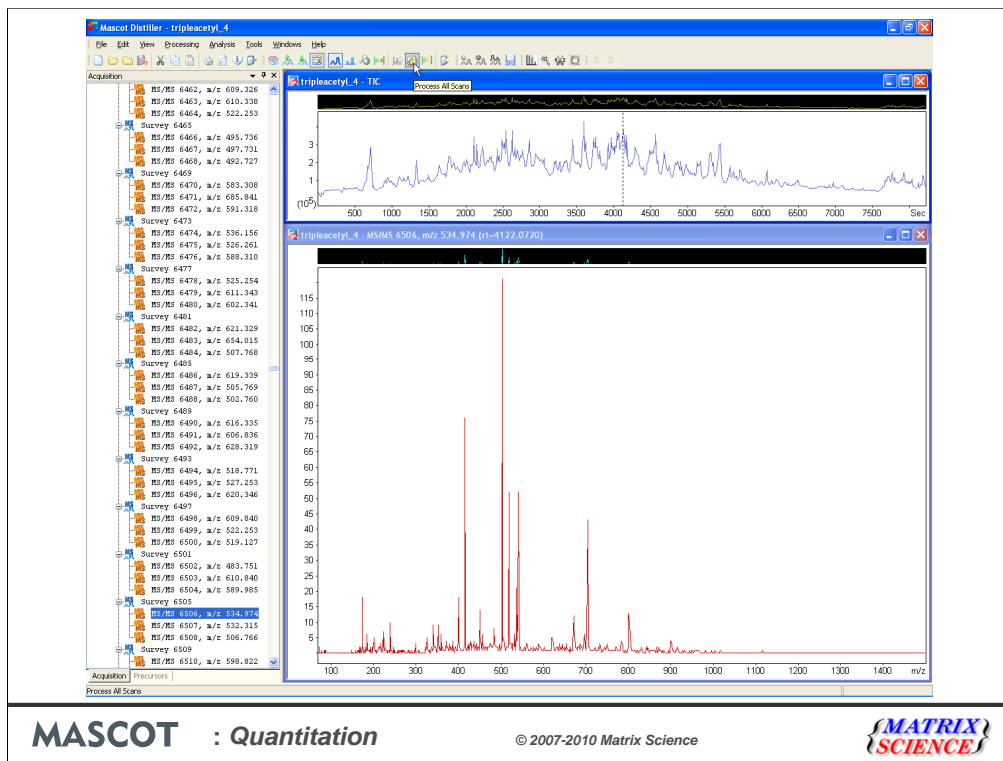
When to use normalisation

- Analysing equal total weights of protein from a complex mixture, e.g. cell lysate - YES
- Starting with equal numbers of cells - NO
- Isolating a sub-set of proteins by affinity methods - NO
- Looking at a synthetic dilution series - NO

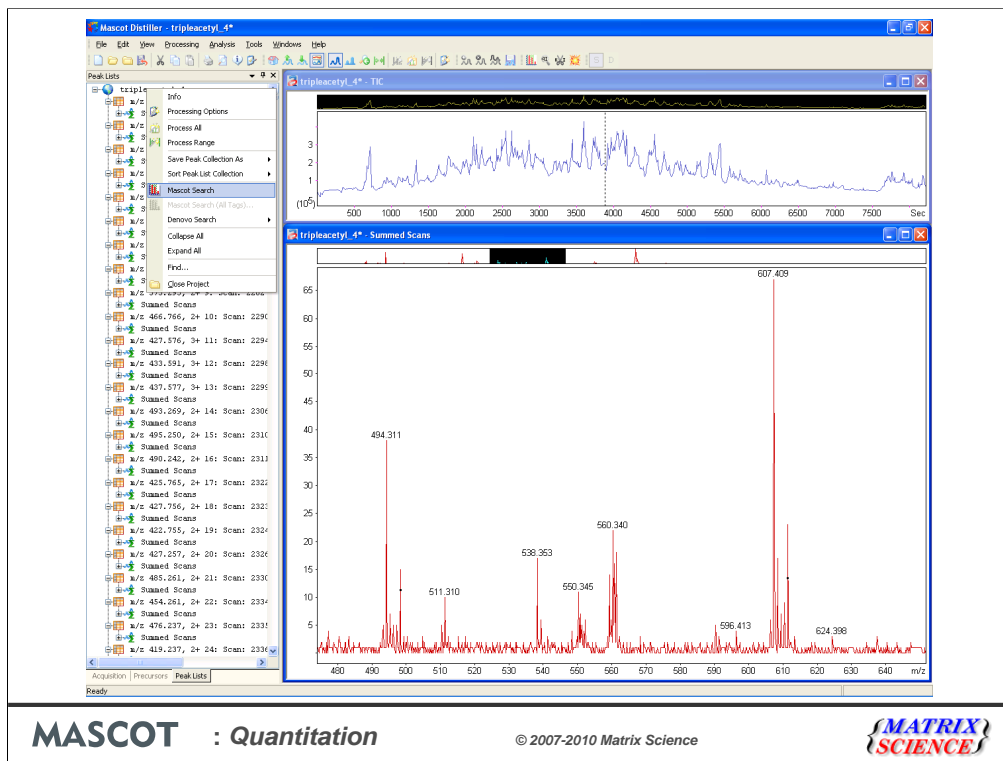
We've had a number of technical support questions about normalisation. What does it do and when should it be used?

First, you have to make an intelligent decision whether normalisation is appropriate. It depends entirely on the experiment. Normalisation forces the average or median ratio to be 1. If the average or median ratio is supposed to be 1, this is the smart thing to do, and eliminates systematic errors. In other cases, it is the wrong thing to do. For example, if you are analysing a standard, where the ratio is supposed to be (say) 3:1, you wouldn't want to force it to be 1:1

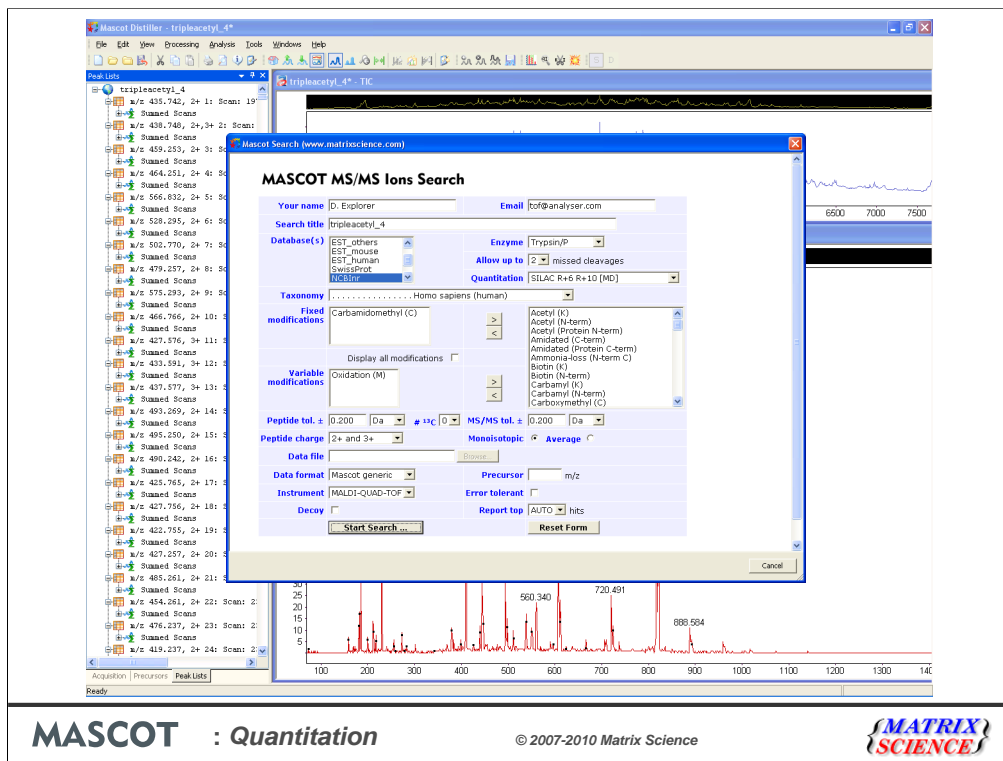
Whether to use sum, median or weighted, is best decided by running some standards (e.g. a cell lysate spiked with varying amounts of a known protein) and seeing which gives the best accuracy and precision.



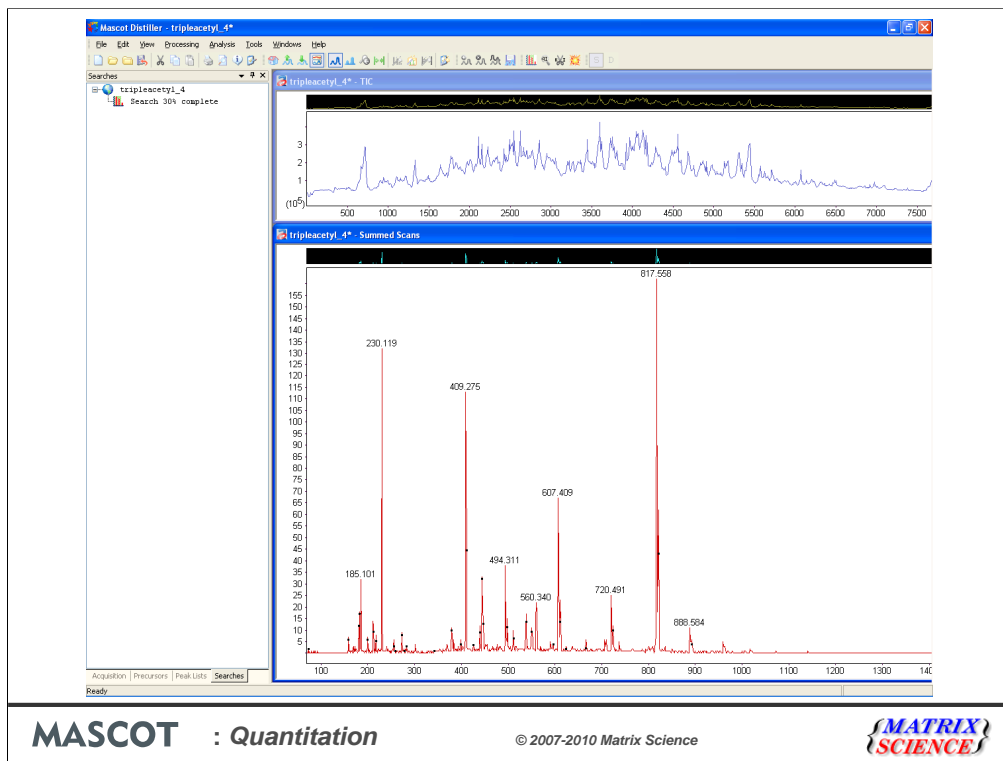
Lets turn to the precursor protocol. This is where we have to use the Mascot Distiller Quantitation Toolbox. I'm going to illustrate the workflow using one of the QStar sample data sets that can be downloaded from the MSQuant home page. This is a SILAC sample with three components: unlabelled, Arg labelled with $^{13}\text{C}(6)$, and Arg labelled with $^{13}\text{C}(6)^{15}\text{N}(4)$. First, we open the Wiff file in Mascot Distiller, and process it into peak lists



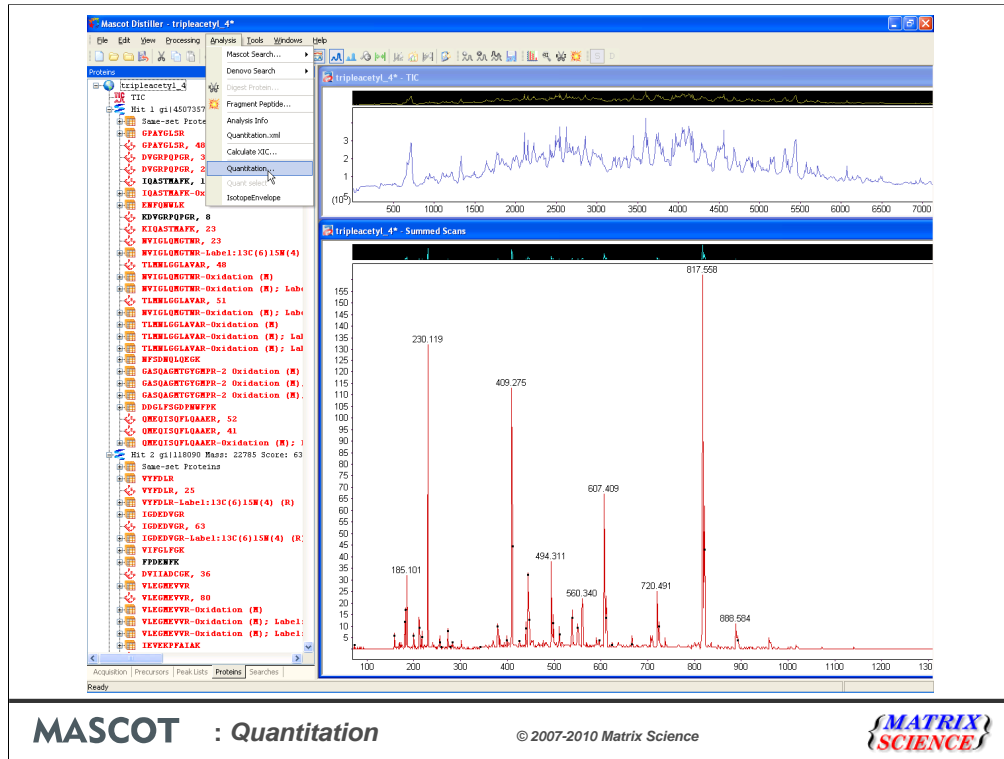
The peak lists are submitted to a Mascot Server to be searched



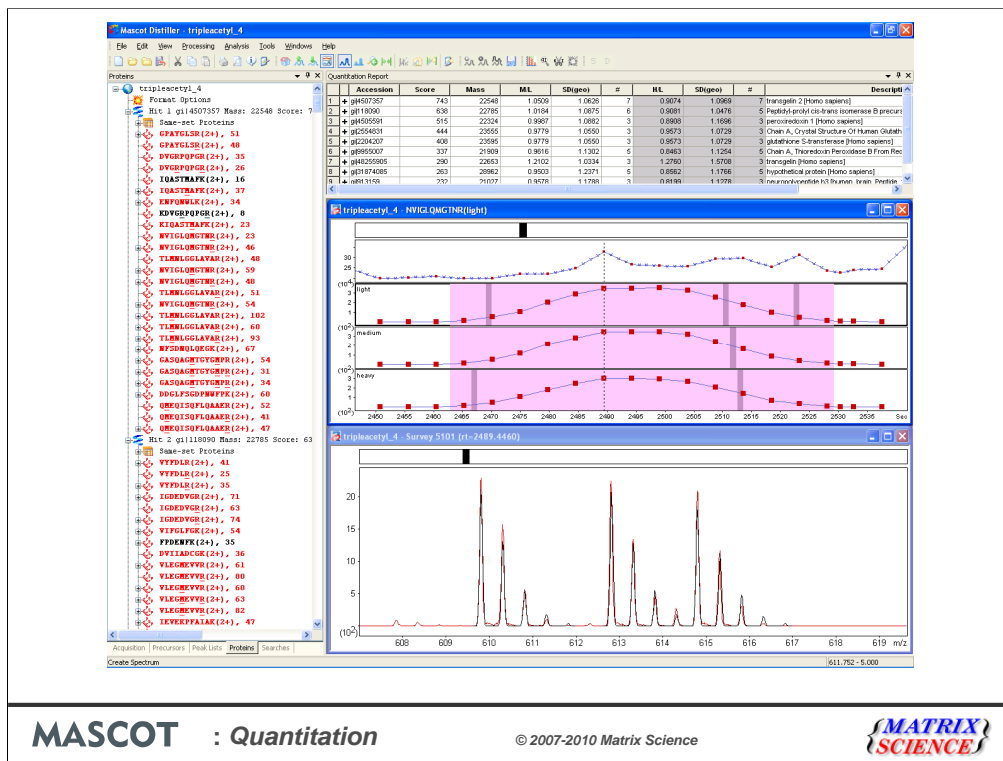
There's an opportunity to tweak the search conditions, but most of the important settings, including the modifications, are embedded in the selected quantitation method



We get progress reports while the search is running



When the search is complete, the results are imported into Distiller. All the required information is now available, so Distiller is in a position to generate a quantitation report



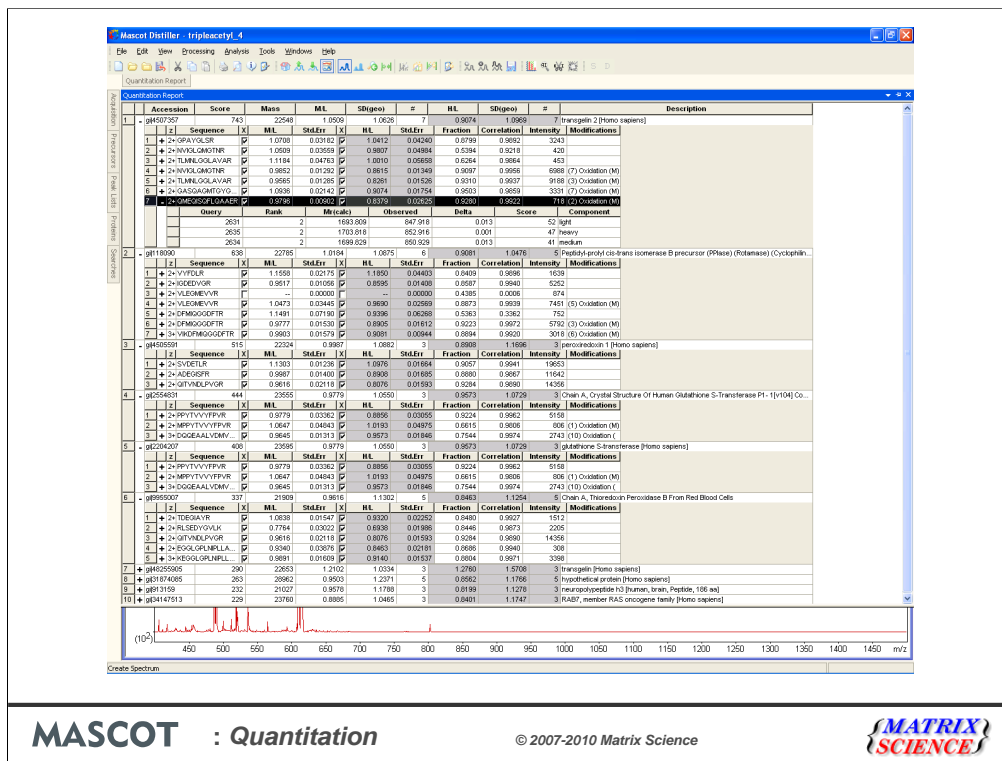
The quantitation results are displayed in a grid control, spreadsheet-style. More about this on the next slide

Below the grid is a chromatogram window. This is displaying the TIC plus extracted ion chromatograms for the three components, light, medium, and heavy.

When you click on an XIC, the scan window at the bottom shows the precursor region of the survey scan. The observed spectrum is in red. This is overlaid with black traces showing the isotope distributions calculated for the ratio being reported. You can make a visual judgement about the quality of the fit. The overlay can be turned on and off using a context menu.

To the left is an explorer tree showing the search results. If you are familiar with the explorer trees in Distiller, you might notice that this tree is a new one, which shows the peptide matches grouped into proteins, like the standard Mascot Peptide Summary report

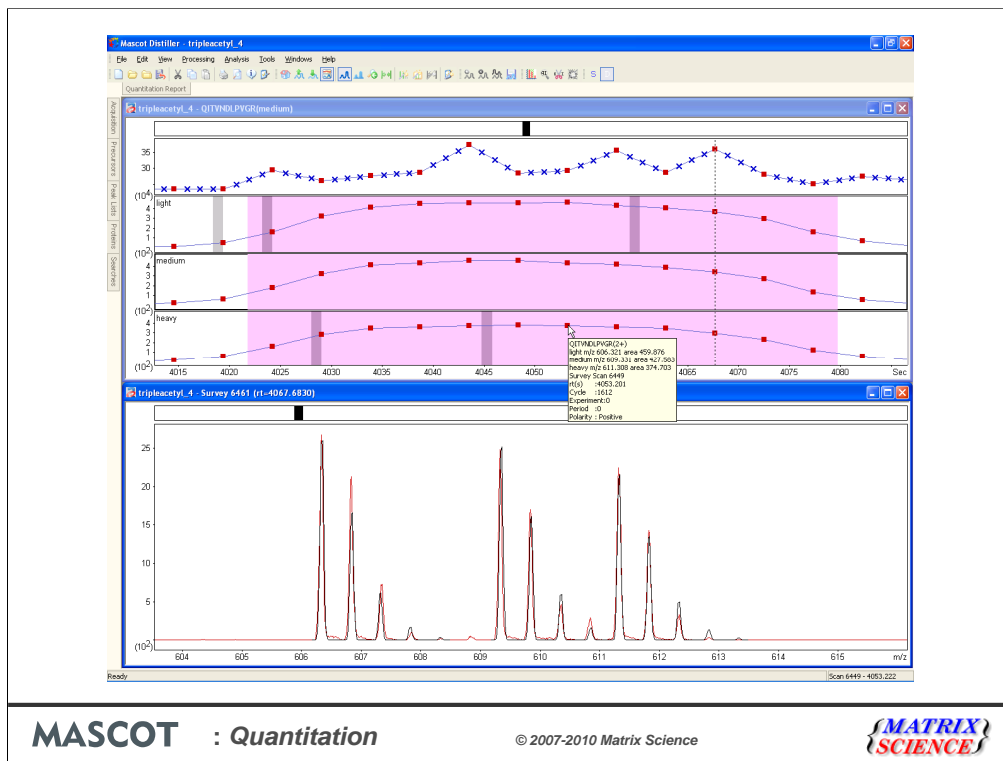
However big your screen, its always difficult to find enough room to display everything. To try and make best use of limited space, the grid and tree can be unpinned, so that they fly out when required and disappear when you move the mouse away.



Here, the grid has been unpinned and is being displayed over the top of the other windows. Some protein hits have been expanded to show individual peptides. One peptide has been expanded to show the corresponding Mascot matches. There's a lot going on here. If you want to study the numbers, this is the place to look. If you don't, then you can hide many of the columns to make the display simpler.

Because this is a three component experiment, two ratios are reported: M/L and H/L. These labels come from the method, and could equally well use sample IDs or whatever you prefer.

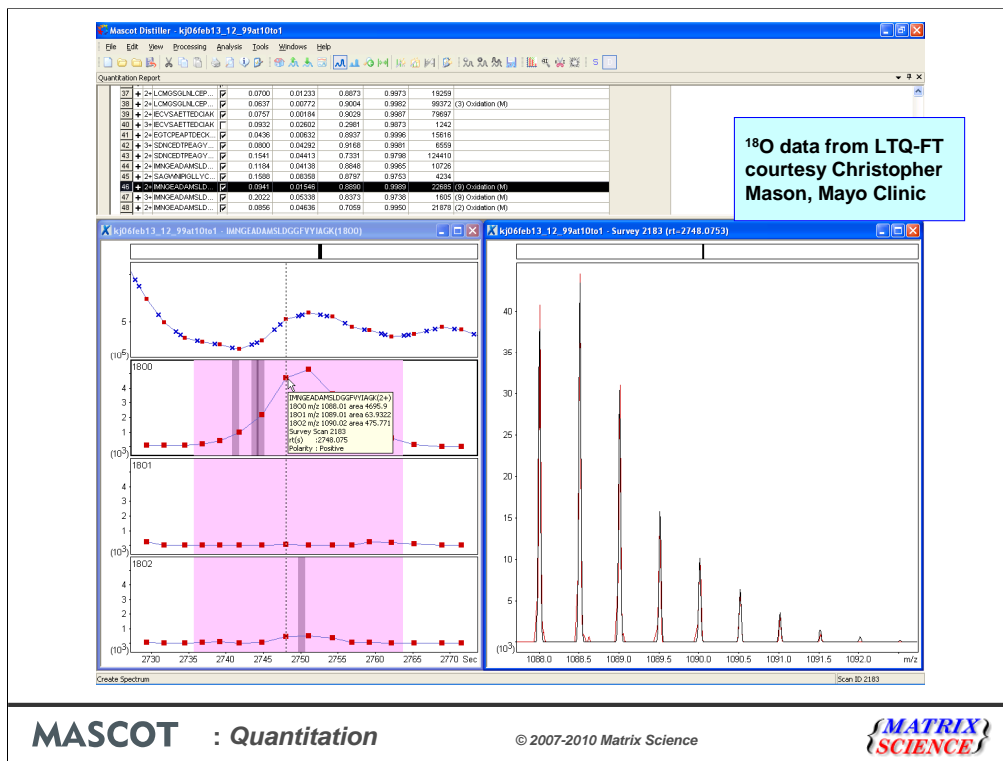
The checkboxes allow you to over-ride the decisions made by the software. If a checkbox is cleared, the peptide ratio is rejected and does not contribute to the protein ratio



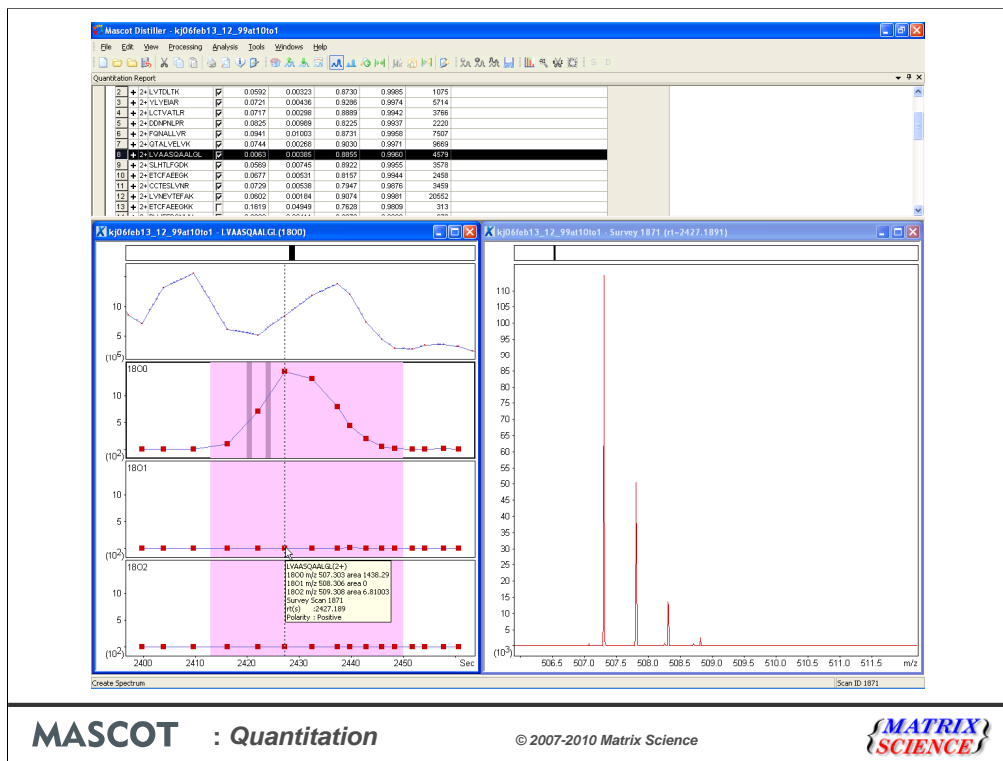
You can spend many happy hours devising different ways to arrange the Windows. With the tree and quant grid unpinned, we can see the chromatogram and scan windows more clearly. A tooltip for each scan provides mass and charge information.

The light purple region is the XIC peak. These are the scans that have been integrated to determine the ratios. The grey bands, which look dark purple when within the XIC peak, are the scans for which we have Mascot matches. In this particular case, there is no match for the medium. The precursor is inferred from its mass and co-elution.

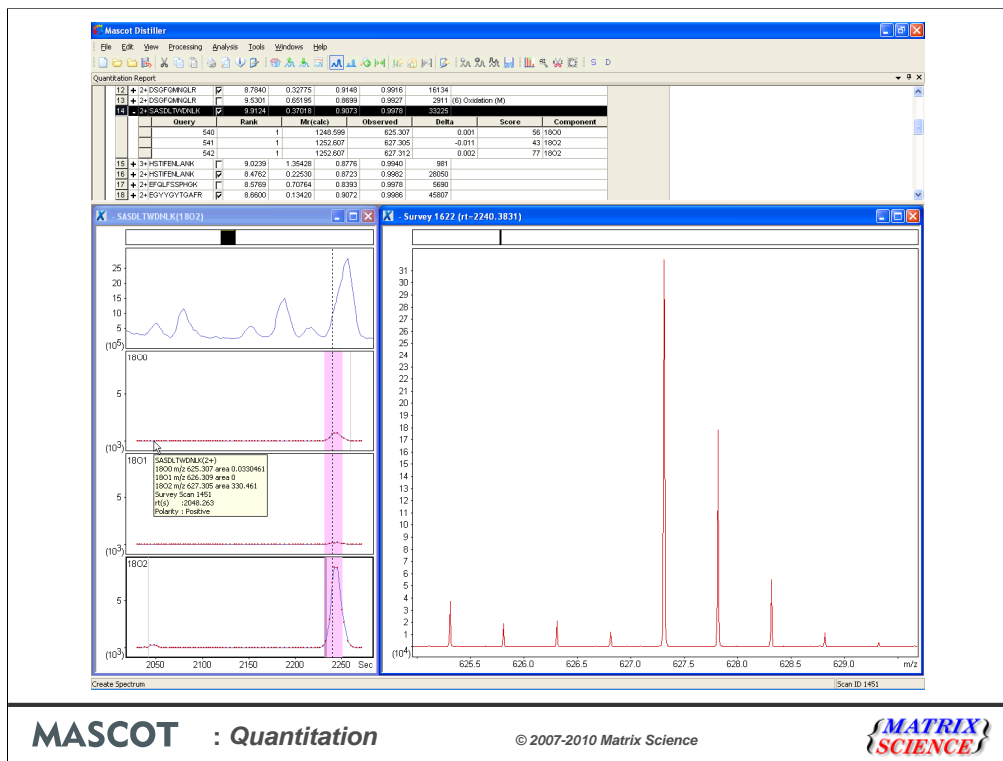
Whenever isotope distributions overlap, as happens here for the medium and heavy, this is accounted for in all calculations, as is incomplete enrichment. Obviously, in an individual scan, the fit is unlikely to be perfect. However, I hope you'll agree that we can immediately judge that the ratio isn't too bad and we can see there are no serious interferences or other problems in this particular scan



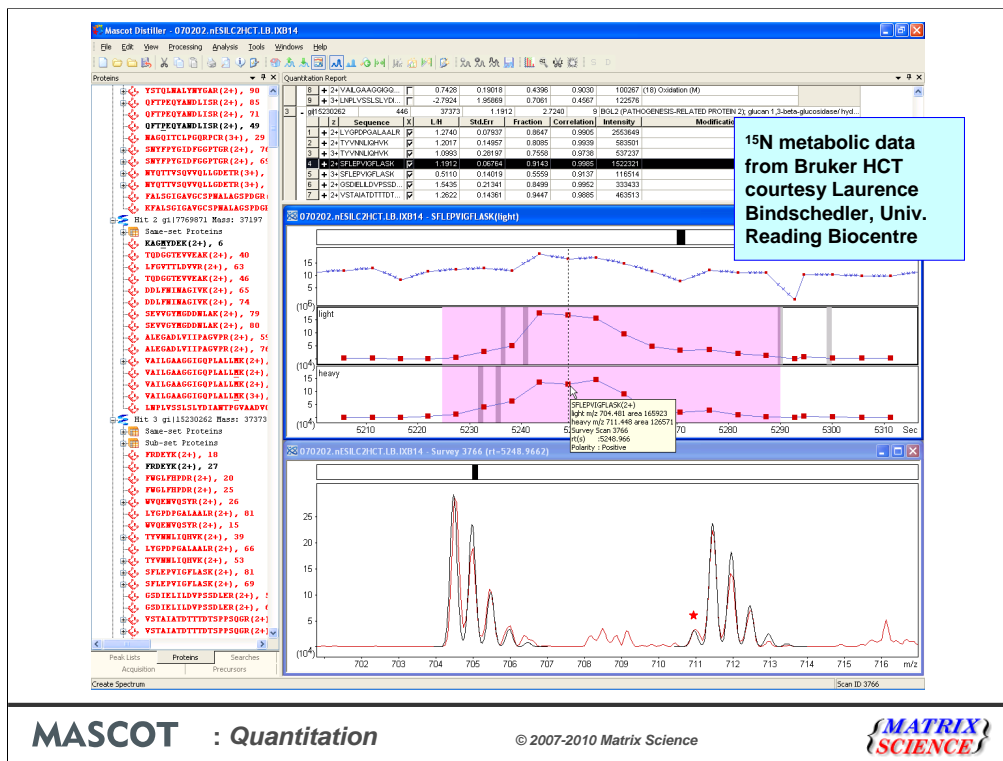
This is O-18 data from an LTQ-FT, courtesy Christopher Mason, Mayo Clinic. The sample is part of a dilution series and this one is particularly tricky because the ratio is 10:1, light to heavy. Obviously, with only a 4 Da separation, the isotope distribution for the heavy is smoothly overlapped by the tail of the light distribution, particularly for larger peptides. At the protein level, the ratios come out around 0.08, which we think isn't too bad.



This is the C-terminal peptide of BSA, which should be unlabelled, so reassuring to see the ratio is indeed close to zero

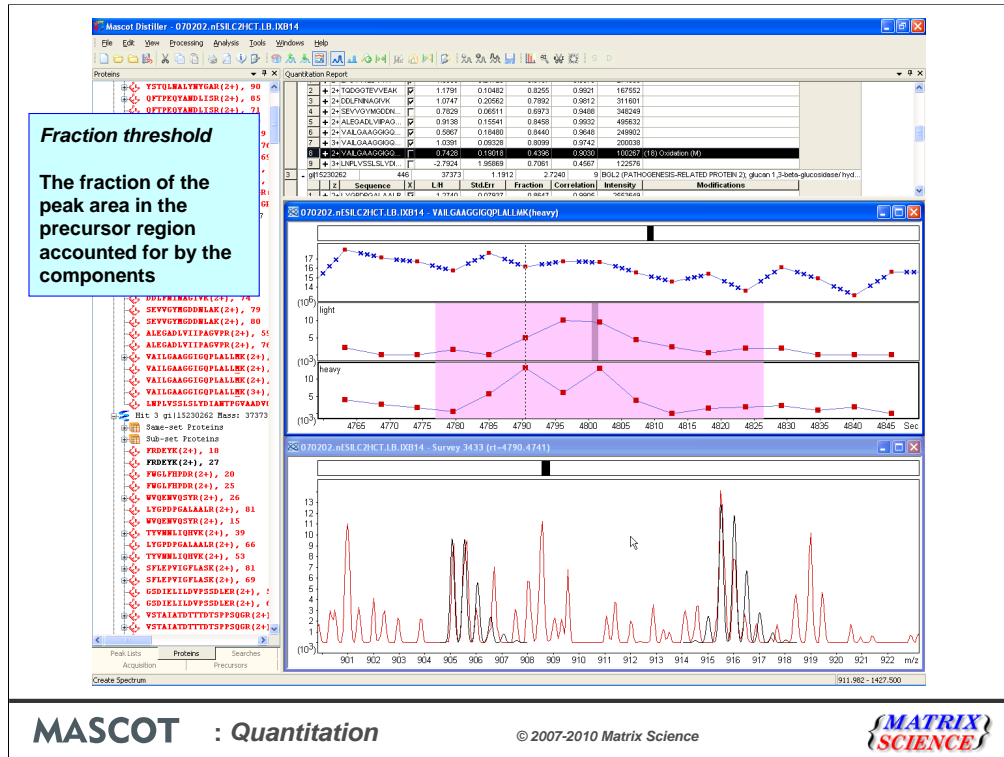


Sometimes, XIC peak detection is a challenge. The starting point is set of scans for which we have Mascot matches. You can hardly see, but in this case, there is a grey band way out here for a match obtained some 3 minutes before the main peak came through. The XIC peak detection algorithm has decided that the bulk of the signal is within the much narrower region to the right, as shown by the purple highlight. This, by the way, is still O-18, but the sample is now 1:10 light to heavy.

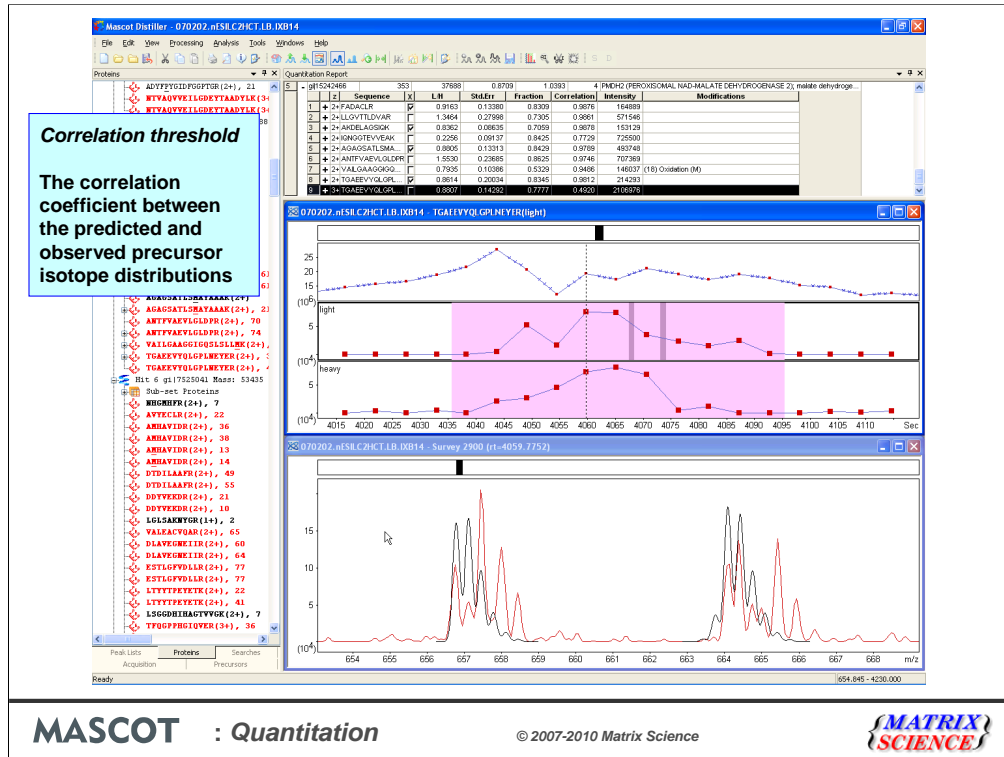


Now some metabolic data, courtesy of Rainer Cramer's group at the Reading Biocentre. In the heavy component, all the nitrogens in the proteins have been replaced by N-15. The calculated distributions (black) fit reasonably well to the observed peaks (red). Notice the peak marked with a red star. This is due to the 1% isotope impurity.

For this particular ratio, there is evidence for some interference between the light and heavy precursors, and also something happening off to the right, but in general, this is a clean spectrum and can be expected to give a good ratio. We expect that most people will want the software to make this judgement, most of the time. In the quantitation grid, the figures in the columns headed standard error, fraction, and correlation are measures of the quality of the spectrum in the precursor region. The software compares these numbers with thresholds to decide whether to accept or reject a ratio. If you want, you can over-ride these decisions using the checkboxes. I'll describe briefly how each of these criteria work

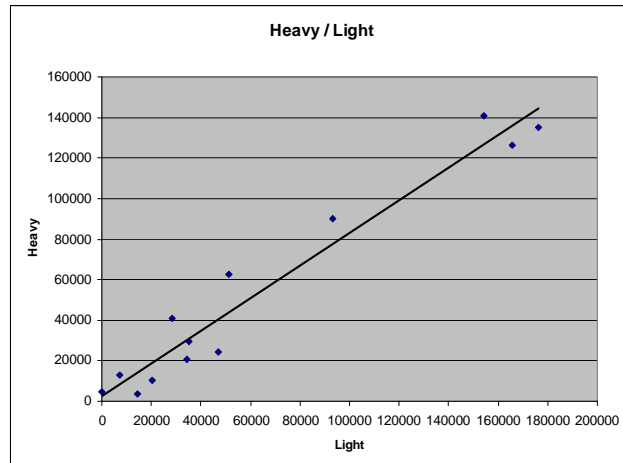


Fraction is the fraction of the peak area in the precursor region accounted for by the components. Here is a spectrum where there are a lot of interfering peaks. When we add up the areas, the expected precursors only account for 44% of the area, so the ratio is rejected. This threshold, like the others, is set as part of the quantitation method.



What about a case where the interfering peaks come right on top of the precursor peaks? A test on the matched fraction won't help. This is why we have a second test on the shape of the distribution. This uses the correlation coefficient between the predicted and observed precursor isotope distributions. Here is a case where a ratio fails the test, because the correlation coefficient is only 0.49

Quantitation - Precursor



Each point represents the heavy and light intensities in a scan from the XIC peak. The straight line is a least squares fit

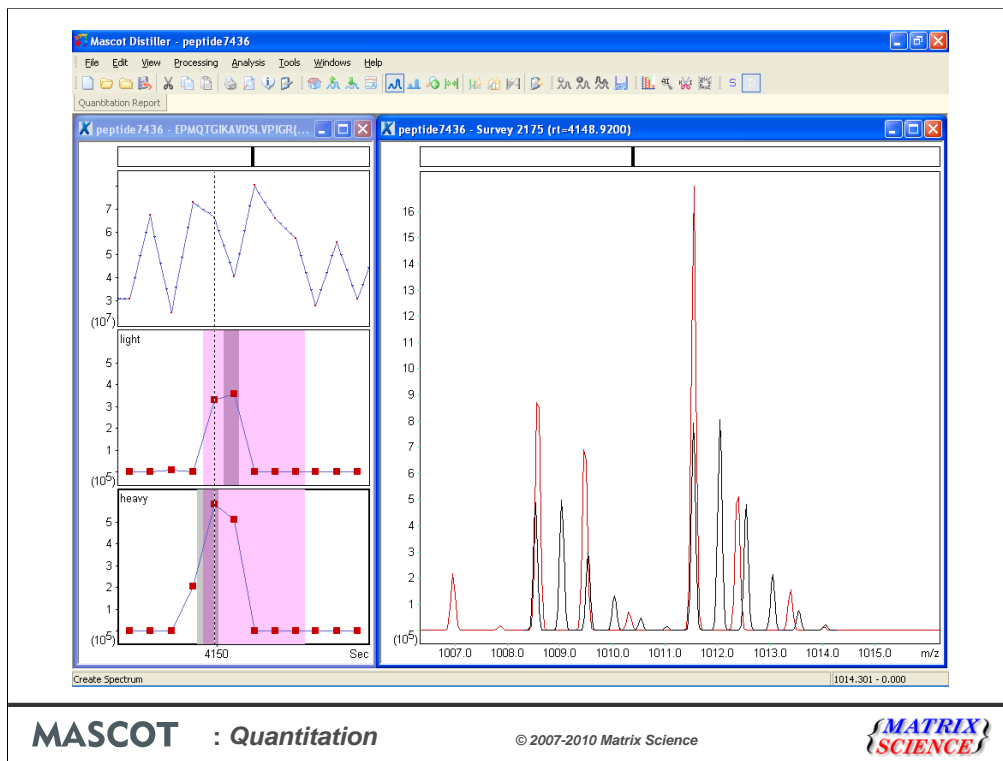
- The gradient is the best estimate of the ratio.
- Any background is corrected
- The standard error for the fit is a good measure of the reliability of the ratio

MASCOT : Quantitation

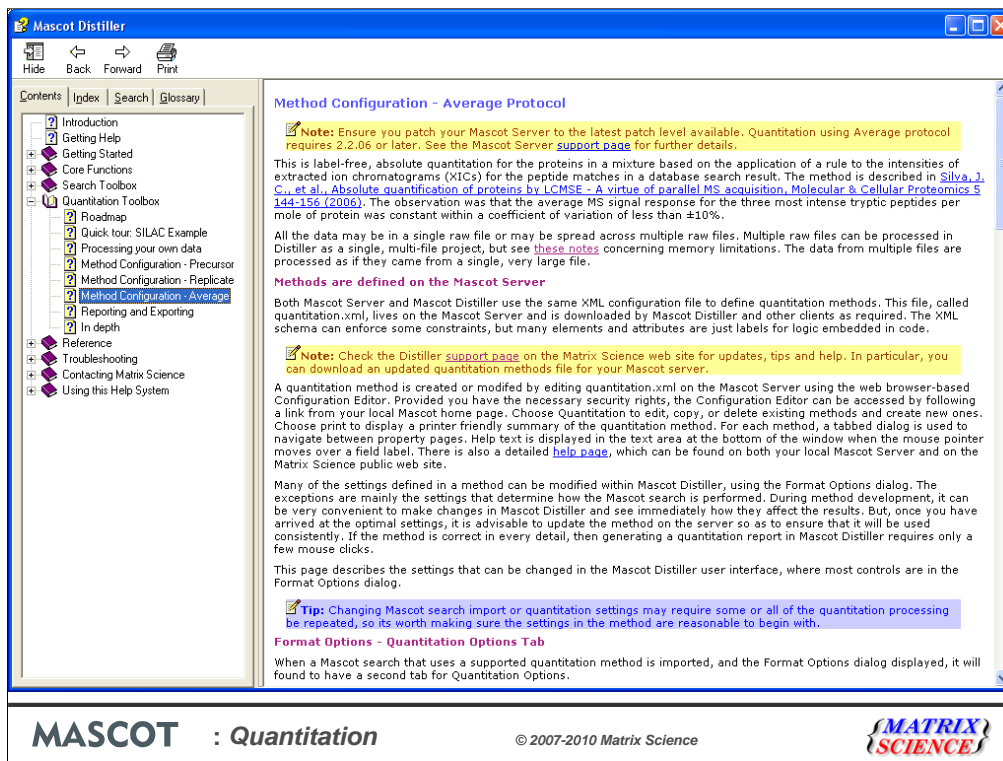
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Another column reports the estimated standard error for the calculated ratio. Each ratio comes from making a least squares fit to the component intensities from the scans in the XIC peak. Here, for example, each point represents the heavy and light intensities in one scan. The gradient of the fitted line is the best estimate of the ratio. The standard error for the fit is a good measure of the reliability of the ratio, and can simply be tested against another threshold.

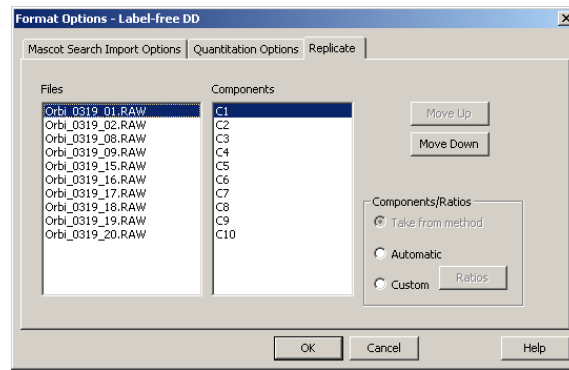


Of course, as always, garbage in means garbage out. Here is a case where the raw data are centroids, not profiles. Although we have good strong MS/MS, when you look at the survey scans, there are no proper isotope distributions. The monoisotopic peaks are approximately in the right place, but the spacings to the isotope peaks are almost random. The charge state is 2+, and the calculated overlay shows what the distributions should look like. Presumably, there was something seriously wrong with the original peak picking. We simply cannot expect to get decent quantitative information out of data like this.



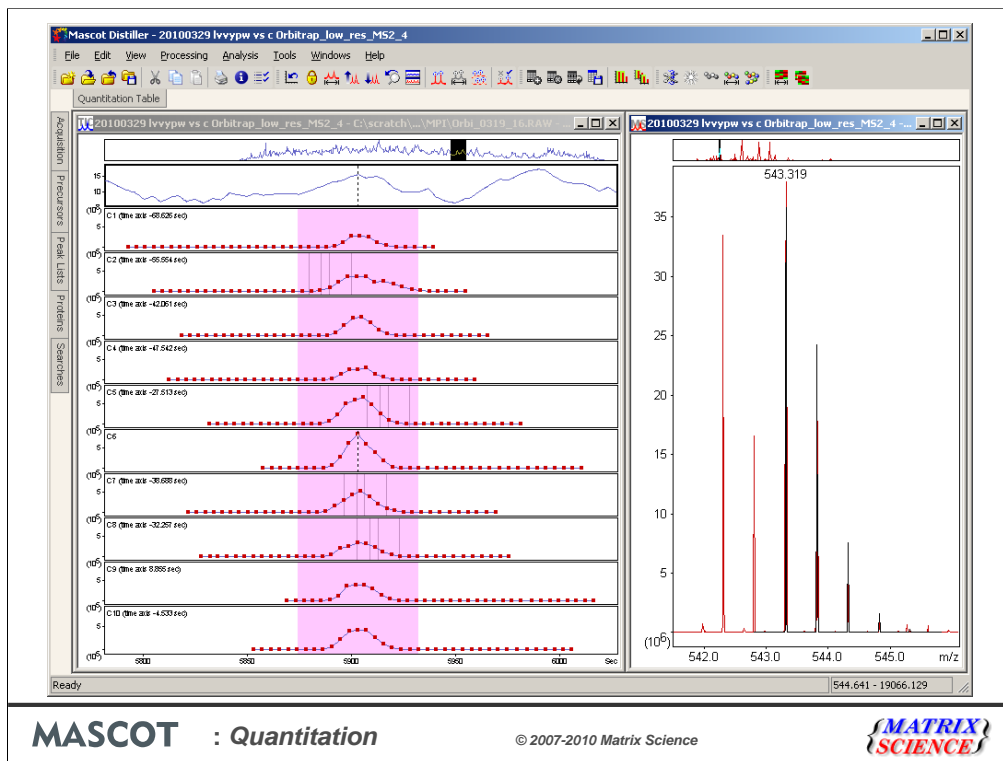
In the interests of time, we'll skip over the Average protocol, but use this opportunity to point out that Distiller comes with comprehensive help. This page gives an overview of how Average works and details of all the configuration settings. There are similar pages for precursor and replicate.

Replicate

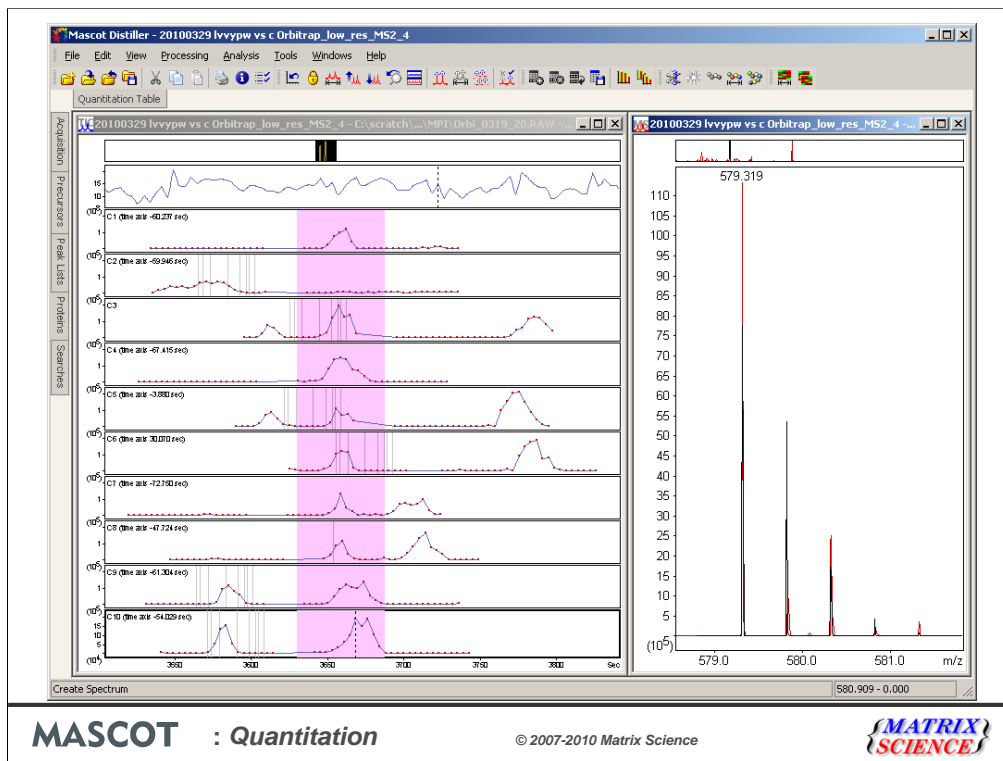


Replicate, you may remember, is 'label free'. Our implementation is identification driven, not feature driven. Distiller starts from the MS/MS data, imports the peptide matches from a Mascot search, then looks in the MS data for the precursors. As with precursor, you don't need MS/MS in every file. You could have one file containing MS/MS and 9 files containing just MS and all identifications would be based on the first file.

A replicate project is always a multi-file project, with one file for each component. You can define ratios or have them auto-generated, with one file selected as reference and all the others reported relative to it.



The tricky part of label free is time alignment of the chromatograms. Distiller does its best, and here is an example where things are working, even though the precursor region is heavily overlapped



But, here it fails. Distiller can manage small misalignments OK, but not severe misalignments or multiple XIC peaks. If alignment fails for a particular peptide, then the ratio is meaningless.

Miscellaneous

- Arg-Pro Conversion of SILAC label is supported
- Quantitation can be limited to 'unique' peptides
- Quantitation results, including all intermediate values, can be exported as XML
- XSLT style sheets can transform this XML into browser based HTML reports with SVG graphics
- Copying and pasting these reports is best route to Excel
- All steps from peak picking to quantitation can be automated using Mascot Daemon

Some final points

Selected Literature

- Ross, P. L., et al., *Multiplexed protein quantitation in Saccharomyces cerevisiae using amine-reactive isobaric tagging reagents*, Molecular & Cellular Proteomics 3 1154-1169 (2004) - [iTRAQ](#)
- Zhang, G. A. and Neubert, T. A., *Automated comparative proteomics based on multiplex tandem mass spectrometry and stable isotope labeling*, Molecular & Cellular Proteomics 5 401-411 (2006) - [Multiplex](#)
- Beynon, R. J. and Pratt, J. M., *Metabolic labeling of proteins for proteomics*, Molecular & Cellular Proteomics 4 857-872 (2005) - [Metabolic](#)
- Ong, S. E. and Mann, M., *Mass spectrometry-based proteomics turns quantitative*, Nature Chemical Biology 1 252-262 (2005) - [General review](#)
- Lill, J., *Proteomic tools for quantitation by mass spectrometry*, Mass Spectrometry Reviews 22 182-194 (2003) - [General review](#)
- Julka, S. and Regnier, F., *Quantification in proteomics through stable isotope coding: A review*, Journal of Proteome Research 3 350-363 (2004) - [General review](#)
- Bantscheff, M., et al., *Quantitative mass spectrometry in proteomics: a critical review*, Analytical and Bioanalytical Chemistry 389 1017-1031 (2007) - [General review](#)