

Statistical analysis of multiple iTRAQ/TMT experiments labeled with variable reporter ion tags using ProteoIQ

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1. Abstract

Isobaric tagging of peptides for reporter ion based quantitation are powerful techniques for mass spectrometry-based quantitative proteomics to analyze differential protein expression [1], [2]. Isobaric reagents are used to label different protein samples with isobaric tags. Samples are then pooled for LC-MS/MS analysis. The majority of the existing bioinformatics tools support statistical analysis of proteins from a single iTRAQ/TMT experiment. However, improved data analysis approaches are required to obtain accurate estimates of biological effects and to increase the power to detect meaningful differences from multiple iTRAQ experiments and large sample sizes [3]. We have developed software modules to perform statistical analysis on iTRAQ data collected from complex proteomics samples across multiple experiments and samples. Different normalization techniques to control for adverse effects of inter- and intra- experimental variability were developed and tested. We demonstrate the utility of the program using differential protein expression analysis of complex myotonic dystrophy in mouse and human patient muscle samples. Data were collected from multiple iTRAQ experiments comparing control and disease muscle samples for both myotonic dystrophy type 1 (DM1) and myotonic dystrophy type 2 diseases. ANOVA was performed to identify proteins that are significantly different across the control and disease groups.

2. Methods

2.1 Sample preparations and design of experiments

Cultured myoblasts (used as control) and skeletal muscle tissues were homogenized in lysis buffer (50mM HEPES, 50% Trifluoroethanol) using ultrasonication. Total protein was quantified using BCA assay (Pierce). Ten µg of protein each from the samples were digested with sequencing grade trypsin (Promega), desalted, labeled with 8plex iTRAQ and pooled according to scheme depicted in figure 1. The description of the samples are as follows.

• All human samples were analyzed by 8plex iTRAQ

• The following codebook explains the naming system of the samples:

- Prefix C: Control
- Prefix DM1: Myotonic dystrophy type 1
- Prefix DM2: Myotonic dystrophy type 2
- The letter F following C, DM1 or DM2: Female
- The letter M following C, DM1 or DM2: Male
- The number following F or M: Patient number

• For example:

- DM1M1- Myotonic dystrophy type 1 patient, male, patient number 1
- DM2F1- Myotonic dystrophy type 1 patient, female, patient number 1
- CM1- Control, male, subject number 1

• There is one sample labeled 'UND'. This sample was from patient suffering from an unrelated neurological disease.

• There are two control channels in DM2 Set1 and DM2 Set2. There is one control channel in DM1

2.2 MudPIT Methods

Pooled iTRAQ labeled samples were analyzed using MudPIT using an Eksigent 2-D nanoLC pump coupled to a nanoESI-LTQ-OrbitrapXL mass spectrometer (Thermo Scientific) as described in Hoek *et al* [5]. The precursor ions were analyzed in the Orbitrap followed by 4 collision induced dissociation (CID) fragment ion scans in the ion trap to identify peptides. The precursor ions were then fragmented by higher-energy collisional dissociation (HCD) to measure reporter ion intensities in the Orbitrap. For each precursor ion, the CID and HCD spectra were merged using Proteome Discoverer v1.3 (Thermo Scientific).

2.3 ProteoIQ software workflows

2.3.1 ProteoIQ schema for combining multiple iTRAQ/TMT experiments

In the iTRAQ/TMT method for relative quantitation of biological samples, each sample is labeled independently with isobaric reporter ion tag and then pooled for MS/MS analysis. In many situations, multiple iTRAQ experiments are combined to obtain accurate estimates of biological effects and to increase the power to detect meaningful differences. Figure 1 shows the schematic representation of ProteoIQ software facilitating combination of multiple iTRAQ/TMT experiments.

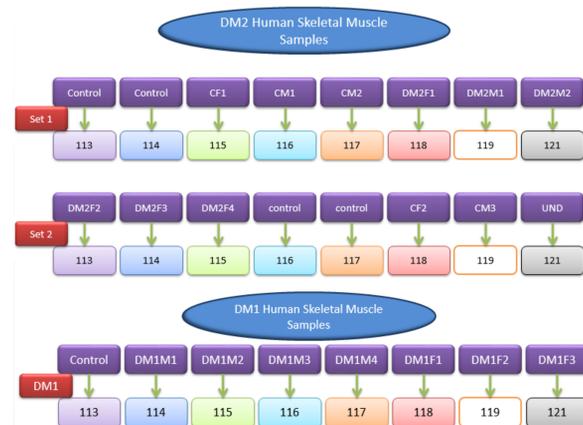


Figure 1: Design of experiments being employed for the 3 iTRAQ experiments.

Reporter Ion Tags								
Experiment No.	113	114	115	116	117	118	119	121
1	Y11	Y12	Y13*	Y14	Y15	Y16	Y17	Y18
2	Y21	Y22	Y23	Y24	Y25	Y26*	Y27	Y28
3	Y31*	Y32	Y33	Y34	Y35	Y36	Y37	Y38
...								
i	Yi1	Yi2*	Yi3	Yi4	Yi5	Yi6	Yi7	Yi8
m	Ym1	Ym2	Ym3	Ym4*	Ym5	Ym6	Ym7	Ym8

Table 1: Typical schematic representation of ProteoIQ software combining multiple iTRAQ/TMT experiments. iTRAQ 8 is used to describe the schema. Yij: Sample labeled with jth reporter ion tag from the experiment number 'i' where i = 1,2,3,...,m and j represents a particular reporter ion tag e.g., 113, 114, 115, 116, etc. Reference sample for each experiment number is represented by Yij with the suffix *.

Figure 2 shows the typical ProteoIQ 3.0 software graphical based user interfaces (user interface hereon) facilitating users to combine 3 experiments that includes DM2 set 1, DM2 set 2 and DM1 set 1.

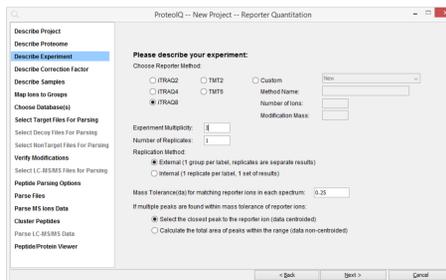


Figure 2(a): Typical ProteoIQ 3.0 user interface allowing users to specify how many experiments need to be combined. Here, we specify the value of Experiment Multiplicity as 3 to combine 2 experiments from DM2 patients and 1 experiment from DM1 patients.

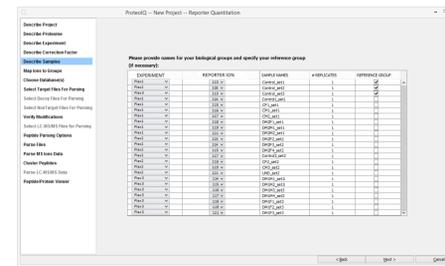


Figure 2(b): Typical ProteoIQ 3.0 user interface allowing users to specify reference samples for each of the experiments labeled with variable reporter ion tags.

2.3.2 Intra-experiment data normalization

Figure 3 shows the schematic representation on how proteins are measured using the ratio to reference sample (removing the variance in the reference channel), log2 normalization (ensuring magnitude independent) values and averaging across replicates (ensuring random observation).

2.3.3 Intra-experiment ANOVA workflow

ProteoIQ generates p-values for proteins based on quantitative information in samples and replicates. In ANOVA the F-statistic tests the significance of quantitation differences between samples against the reproducibility of their replicates. The F-statistic measures the ratio of explained error (difference across samples) to the unexplained error (difference across replicates). Typically p-values < 0.05 lead to the rejection of the null hypothesis and indicate a lower chance of quantitation differences between samples being due to random error.

2.3.4 Inter-experiment ANOVA workflow

Here, ProteoIQ generates p-values for proteins based on quantitative information in biological groups across experiments.

The F-statistic tests the significance of quantitation differences between biological groups. For example, we have 3 types of patients namely control i.e., healthy people, DM1 i.e., patients suffering from DM1 condition and DM2 i.e., patients suffering from DM2 condition. Typically p-value < 0.05 leads to the rejection of the null hypothesis and indicates significant quantitation differences between groups.

Figure 4 shows typical ProteoIQ software user interface that facilitates users to model experimental design i.e., define biological groups and assign samples from experiments as their replicates.

3. Results and Discussion

In this work MS/MS samples are loaded into ProteoIQ 3.0 after database searching is completed using the Sequest database search engine running under Proteome Discoverer [6,7]. To ensure the quality of the results, we select only the proteins and peptides that satisfy the following filters criteria.

- Proteins with at least 3 identified peptides
- 1% FDR threshold for proteins
- Peptides with peptide probability (calculated using Peptide Prophet algorithm) with predicted negatives < predicted positives
- Peptides with iTRAQ modifications
- Proteins with intra experiment ANOVA p-value less than 0.05

Table 2 shows the number of proteins and peptides for each of the experiment (before and after applying the filters).

	Experiment 1		Experiment 2		Experiment 3	
	Before Filter	After Filter	Before Filter	After Filter	Before Filter	After Filter
Total no. of peptides	16687	4562	20545	8393	22517	7116
No. of unique peptides	3022	1130	5184	2580	2378	735
No. of protein groups	449	169	637	252	225	56
No. of proteins	2937	1093	4124	1490	1449	375

Table 2: Experiment wise before- and after- filter statistics of peptides/proteins.

Inter-experiment ANOVA report

For further statistical analysis, the three experiments are combined and then modeled the design of experiment by defining three different groups based on the disease conditions namely Patients with DM1, Patients with DM2 and Control and specifying samples as their replicates (Table 3).

# Replicates	Patients with DM1	Patients with DM2	Control
1	DM1M1	DM2F1	Control_114_Exp1
2	DM1M2	DM2M1	CF1
3	DM1M3	DM2M2	CM1
4	DM1M4	DM2F2	CM2
5	DM1F1	DM2F3	CF2
6	DM1F2	DM2F4	CM3
7	DM1F3		Control_117_exp2

Table 3: Design of experiment to test difference in protein quantitation across experiments.

On combining the three experiments, 1803 unique proteins are reported by the software. Out of these proteins, 235 proteins are observed at least in one of the samples of each experiment thereby facilitating the software to calculate inter-experiment ANOVA p-values. Table 5 shows the list of 63 proteins which are observed with p-value < 0.05.

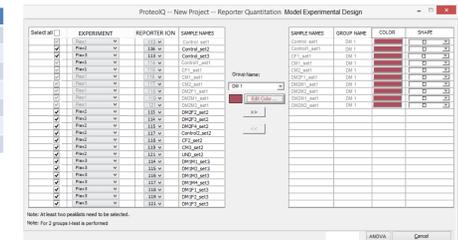


Figure 4: Typical ProteoIQ user interface showing the functionality to define groups and replicates thereby facilitating combination of proteins across multiple iTRAQ samples and perform ANOVA or any other statistical analysis.

Sl. No.	Sequence Id	p-values	Sl. No.	Sequence Id	p-values	Sl. No.	Sequence Id	p-values
1	ENSP00000224237	0.022635	22	ENSP00000366962	0.002606	43	ENSP00000406359	9.72E-05
2	ENSP00000229239	0.003105	23	ENSP00000367008	0.002606	44	ENSP00000407461	0.002606
3	ENSP00000244601	0.002606	24	ENSP00000375391	9.72E-05	45	ENSP00000408907	9.72E-05
4	ENSP00000282050	0.033037	25	ENSP00000375399	9.72E-05	46	ENSP00000419425	0.016946
5	ENSP00000289316	0.002606	26	ENSP00000375736	0.002606	47	ENSP00000422012	0.003143
6	ENSP00000303408	0.002606	27	ENSP00000380065	0.002875	48	ENSP00000427976	0.023446
7	ENSP00000310219	0.00427	28	ENSP00000380067	0.003105	49	ENSP00000430817	0.023446
8	ENSP00000321744	0.002606	29	ENSP00000380068	0.003105	50	ENSP00000431702	0.02777
9	ENSP00000324286	0.002606	30	ENSP00000380070	0.003105	51	ENSP00000435613	0.022626
10	ENSP00000348706	0.002606	31	ENSP00000380100	0.002806	52	ENSP00000445633	0.002606
11	ENSP00000348924	0.002606	32	ENSP00000380177	0.002806	53	ENSP00000445831	0.002606
12	ENSP00000349430	0.002606	33	ENSP00000380180	0.002606	54	ENSP00000446007	0.022635
13	ENSP00000350580	0.002606	34	ENSP00000381736	0.033037	55	ENSP00000446031	0.002606
14	ENSP00000352442	0.002606	35	ENSP00000382915	9.72E-05	56	ENSP00000462132	0.002606
15	ENSP00000353074	0.002606	36	ENSP00000391842	0.026599	57	ENSP00000463319	0.002606
16	ENSP00000358151	0.002606	37	ENSP00000393087	9.72E-05	58	ENSP00000464073	0.002606
17	ENSP00000358164	0.002606	38	ENSP00000394670	0.018477	59	ENSP00000464485	0.002606
18	ENSP00000363071	0.002617	39	ENSP00000401820	0.047961	60	ENSP00000465477	0.033797
19	ENSP00000364801	9.72E-05	40	ENSP00000403530	9.72E-05	61	ENSP00000467037	0.036325
20	ENSP00000364802	9.72E-05	41	ENSP00000404524	9.72E-05	62	ENSP00000475942	0.002606
21	ENSP00000366618	0.002606	42	ENSP00000405975	0.018477	63	ENSP00000476136	0.002606

Table 5: List of proteins with inter-experiment ANOVA p-values < 0.05

The difference in the protein quantitation levels are investigated using mouse models by comparing fold change in protein quantitation levels between HSA-CTG vs HSA-CCTG samples. 139 unique proteins are identified with fold change > 1.5 in Log₂ scale of normalized reporter ion intensity values (Data not shown).

Conclusion

ProteoIQ 3.0 allows users to perform statistical analysis of multiple iTRAQ/TMT experiments labeled with variable reporter ion tags. The above described functionality has also been extended to analyze isotopic label data. A free trial will soon be made available at <http://www.premierbiosoft.com>

Reference

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