Q4 Your University

Answered: 55 Skipped: 0

#	Responses	Date
1	University of Malta	3/3/2016 12:21 PM
2	University of Malta	3/2/2016 6:59 AM
3	Cambridge	3/1/2016 8:43 AM
4	University of Malta	3/1/2016 8:27 AM
5	University of Malta (previous)	2/29/2016 8:46 PM
6	University of Malta	2/28/2016 3:31 PM
7	University of Malta	2/26/2016 10:35 PM
8	UCL but collaboration with Cambridge	2/26/2016 1:38 PM
9	Cambridge University	2/26/2016 11:50 AM
10	University of Cambridge	2/26/2016 11:41 AM
11	University of Cambridge	2/26/2016 11:10 AM
12	University of Malta	2/25/2016 4:18 PM
13	univeristy of Malta	2/25/2016 1:17 PM
14	University of Malta	2/25/2016 10:04 AM
15	University of Malta	2/25/2016 9:30 AM
16	University of Malta	2/25/2016 6:37 AM
17	University of Malta	2/24/2016 5:21 PM
18	uom	2/24/2016 5:19 PM
19	university of Malta	2/24/2016 5:00 PM
20	University of Malta	2/24/2016 3:30 PM
21	University of Malta	2/24/2016 1:52 PM
22	of Malta	2/24/2016 11:12 AM
23	University of Malta	2/24/2016 6:58 AM
24	University of Malta	2/23/2016 8:54 AM
25	maolta	2/22/2016 2:18 PM
26	KU Leuven	2/22/2016 9:36 AM
27	University of Malta	2/20/2016 3:56 PM
28	University of Malta	2/19/2016 7:39 PM
29	University of Malta	2/19/2016 3:21 PM
30	KULeuven	2/17/2016 12:52 PM
31	University of Malta	2/16/2016 3:53 PM
32	University of Malta	2/16/2016 12:26 PM
33	University of Malta	2/15/2016 2:33 PM
34	University of Malta	2/15/2016 8:59 AM
35	University of Malta	2/11/2016 12:06 PM

36	University of Malta	2/11/2016 9:17 AM
37	University of Malta	2/11/2016 8:59 AM
38	University of Malta	2/11/2016 6:26 AM
39	University of Malta	2/10/2016 12:55 PM
40	University of Malta	2/10/2016 9:17 AM
41	University of Malta	2/10/2016 9:06 AM
42	University of Malta	2/10/2016 8:56 AM
43	University of Malta	2/10/2016 6:02 AM
44	Unversity of Malta	2/9/2016 8:58 PM
45	University of Malta	2/9/2016 7:24 PM
46	University of Malta	2/9/2016 4:58 PM
47	University of Malta	2/9/2016 4:24 PM
48	uoM	2/9/2016 3:51 PM
49	University of Malta	2/9/2016 12:26 PM
50	University of Malta	2/8/2016 9:46 PM
51	University of Malta	2/8/2016 9:23 PM
52	University of Malta	2/8/2016 8:32 PM
53	University of Malta	2/8/2016 6:40 PM
54	KU Leuven	2/8/2016 3:02 PM
55	KU Leuven	2/8/2016 2:59 PM

Q5 Your Department/Institute

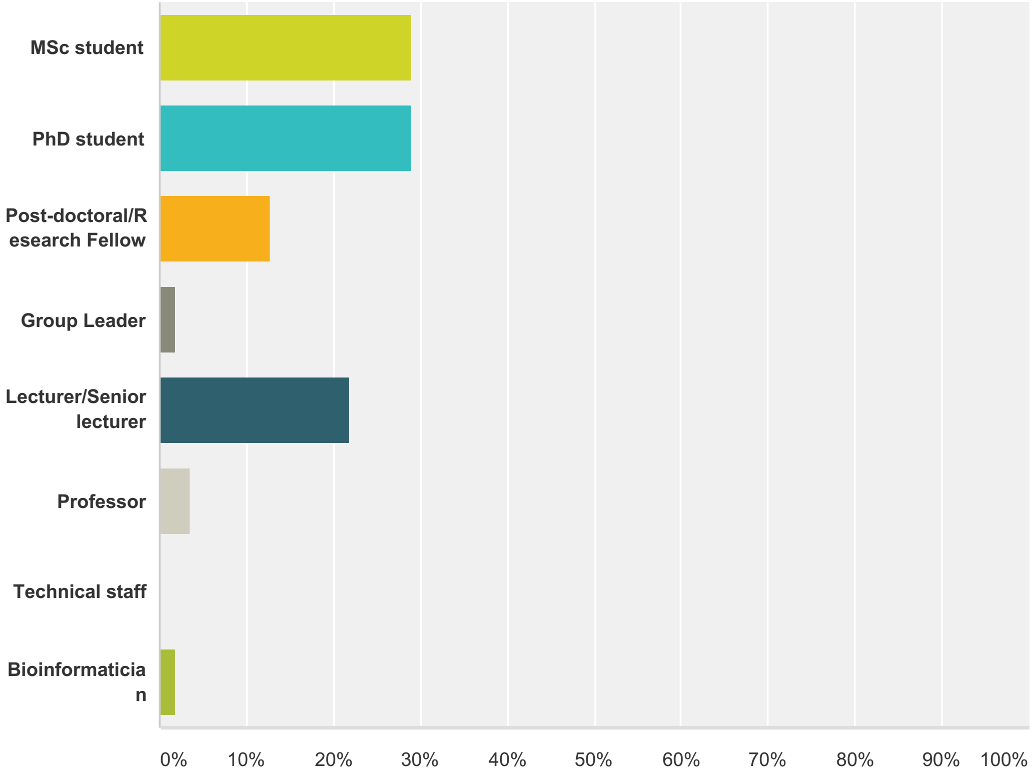
Answered: 55 Skipped: 0

#	Responses	Date
1	Earth Systems	3/3/2016 12:21 PM
2	Department of Pathology	3/2/2016 6:59 AM
3	Haematology	3/1/2016 8:43 AM
4	Department of Applied Biomedical Science	3/1/2016 8:27 AM
5	Department of Applied Biomedical Science (previous)	2/29/2016 8:46 PM
6	Department of Applied Biomedical Science	2/28/2016 3:31 PM
7	Department of Anatomy	2/26/2016 10:35 PM
8	Haematology	2/26/2016 1:38 PM
9	Haematology	2/26/2016 11:50 AM
10	Department of Haematology	2/26/2016 11:41 AM
11	Haematology	2/26/2016 11:10 AM
12	Communications and Computer Engineering	2/25/2016 4:18 PM
13	molecular biology and genetics	2/25/2016 1:17 PM
14	Faculty of Health Sciences	2/25/2016 10:04 AM
15	Centre of Molecular Medicine	2/25/2016 9:30 AM
16	Faculty of Medicine	2/25/2016 6:37 AM
17	Department of Applied Biomedical Science, Faculty of Health Sciences	2/24/2016 5:21 PM
18	biology	2/24/2016 5:19 PM
19	molecular genetics	2/24/2016 5:00 PM
20	Physiology and Biochemistry	2/24/2016 3:30 PM
21	Pathology/Biomedical Sciences	2/24/2016 1:52 PM
22	Applied Biomedical Science	2/24/2016 11:12 AM
23	Dept. of Physiology and Biochemistry	2/24/2016 6:58 AM
24	Department of Physiology and Biochemistry	2/23/2016 8:54 AM
25	science	2/22/2016 2:18 PM
26	Department of Cardiovascular Sciences	2/22/2016 9:36 AM
27	Department of Pharmacy	2/20/2016 3:56 PM
28	Institute of Earth Systems	2/19/2016 7:39 PM
29	Applied Biomedical Science	2/19/2016 3:21 PM
30	Center for Molecular and Vascular Biology	2/17/2016 12:52 PM
31	Department of Physiology & Biochemistry	2/16/2016 3:53 PM
32	Centre for Molecular Medicine and Biobanking	2/16/2016 12:26 PM
33	Faculty of Medicine & Surgery, Department of Clinical Pharmacology and Therapeutics	2/15/2016 2:33 PM
34	Department of Physiology and Biochemistry	2/15/2016 8:59 AM
35	Medicine	2/11/2016 12:06 PM

36	Physiology and Biochemistry	2/11/2016 9:17 AM
37	Physiology and Biochemistry	2/11/2016 8:59 AM
38	Department of Applied Biomedical Science	2/11/2016 6:26 AM
39	Faculty of Health Sciences	2/10/2016 12:55 PM
40	Centre for Molecular Medicine and Biobanking	2/10/2016 9:17 AM
41	Molecular Diagnostics Pathology Department MDH	2/10/2016 9:06 AM
42	Department of Physiology & Biochemistry	2/10/2016 8:56 AM
43	Faculty of Health Sciences	2/10/2016 6:02 AM
44	Centre for Molecular Medicine and Biobanking	2/9/2016 8:58 PM
45	Applied Biomedical Science	2/9/2016 7:24 PM
46	Institute of Earth Systems, Division of Rural Science and Food Systems	2/9/2016 4:58 PM
47	Department of Applied Biomedical Science	2/9/2016 4:24 PM
48	physiology	2/9/2016 3:51 PM
49	Physiology & Biochemistry	2/9/2016 12:26 PM
50	Computer Science	2/8/2016 9:46 PM
51	Computer Science and AI	2/8/2016 9:23 PM
52	Computer Information Systems	2/8/2016 8:32 PM
53	Department of Physiology & Biochemistry	2/8/2016 6:40 PM
54	Department of Cardiovascular Sciences	2/8/2016 3:02 PM
55	Cardiovascular Sciences	2/8/2016 2:59 PM

Q6 Which is your position/job title?

Answered: 55 Skipped: 0



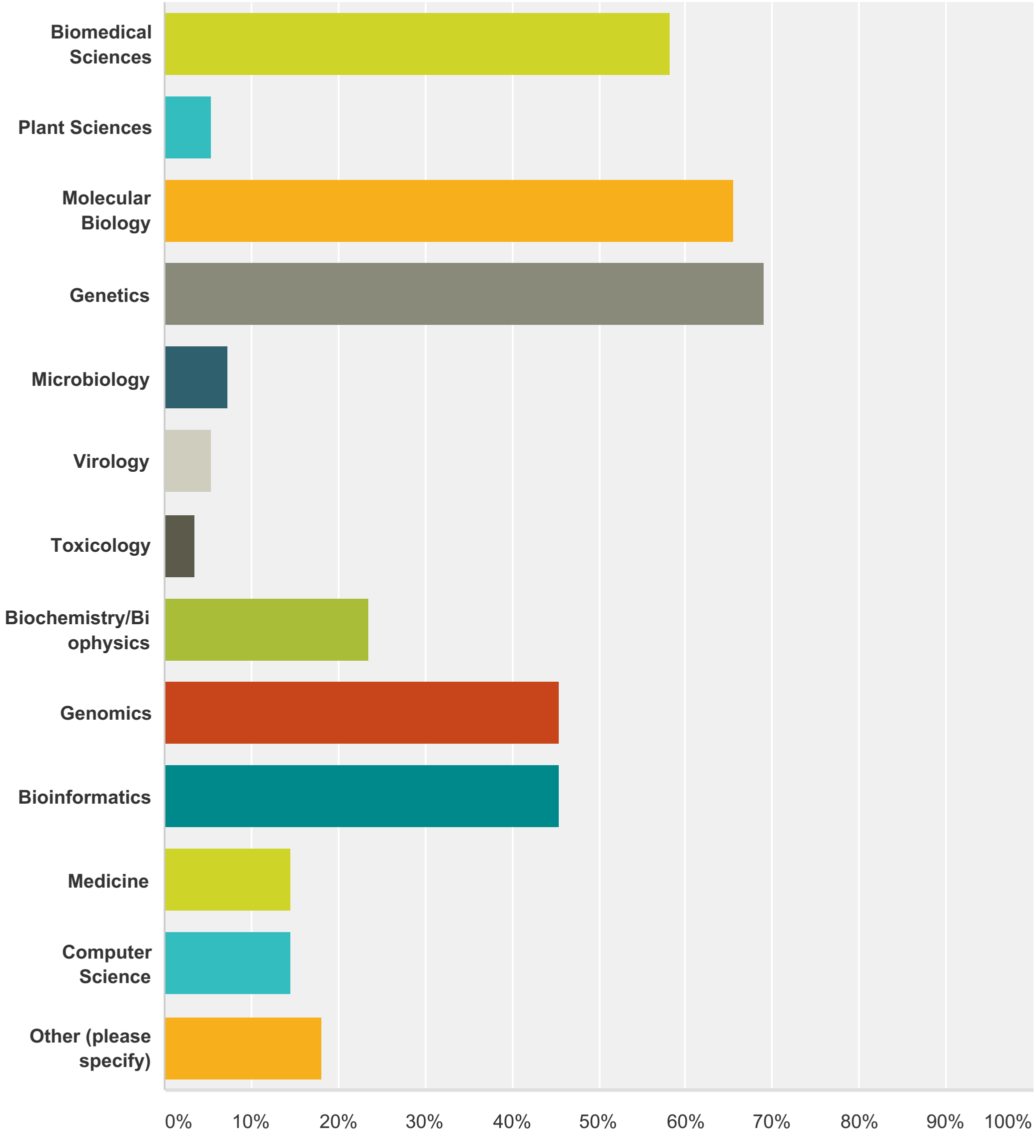
Answer Choices	Responses	
MSc student	**29.09%**	16
PhD student	**29.09%**	16
Post-doctoral/Research Fellow	**12.73%**	7
Group Leader	**1.82%**	1
Lecturer/Senior lecturer	**21.82%**	12
Professor	**3.64%**	2
Technical staff	**0.00%**	0
Bioinformatician	**1.82%**	1
Total		**55**

#	Other (please specify)	Date
1	Works at Mater Dei hospital as a Medical Lab Scientist	2/29/2016 8:46 PM
2	part-time Biomedical Scientist	2/24/2016 1:52 PM
3	student	2/22/2016 2:18 PM
4	Undergraduate student	2/20/2016 3:56 PM
5	Research Support Officer	2/16/2016 3:53 PM

6	Allied Health Pratitioner	2/10/2016 9:06 AM
7	Research Support Officer	2/10/2016 8:56 AM
8	Researcher	2/9/2016 12:26 PM
9	Visiting Lecturer / PhD Graduate	2/8/2016 9:46 PM
10	Research Support Officer	2/8/2016 6:40 PM

Q7 What is your discipline of interest?

Answered: 55 Skipped: 0



Answer Choices	Responses	
Biomedical Sciences	**58.18%**	32
Plant Sciences	**5.45%**	3
Molecular Biology	**65.45%**	36
Genetics	**69.09%**	38
Microbiology	**7.27%**	4
Virology	**5.45%**	3
Toxicology	**3.64%**	2
Biochemistry/Biophysics	**23.64%**	13

Genomics	**45.45%**	25
Bioinformatics	**45.45%**	25
Medicine	**14.55%**	8
Computer Science	**14.55%**	8
Other (please specify)	**18.18%**	10
Total Respondents: 55		

#	Other (please specify)	Date
1	Entomologist	3/3/2016 12:21 PM
2	Embryology	2/26/2016 10:35 PM
3	Signal Processing, Machine Learning	2/25/2016 4:18 PM
4	Cancer genetics	2/24/2016 1:52 PM
5	Epigenetics	2/22/2016 9:36 AM
6	Orthodontics	2/11/2016 9:17 AM
7	Proteomics	2/9/2016 8:58 PM
8	Forensic Genetics	2/9/2016 12:26 PM
9	Machine Learning, Grammatical Inference	2/8/2016 9:46 PM
10	Chemistry	2/8/2016 6:40 PM

Q8 What is your main research topic? Please briefly outline your research project.Here is an example: "I work on the analysis of differential exon usage in cancer samples using RNA-seq"

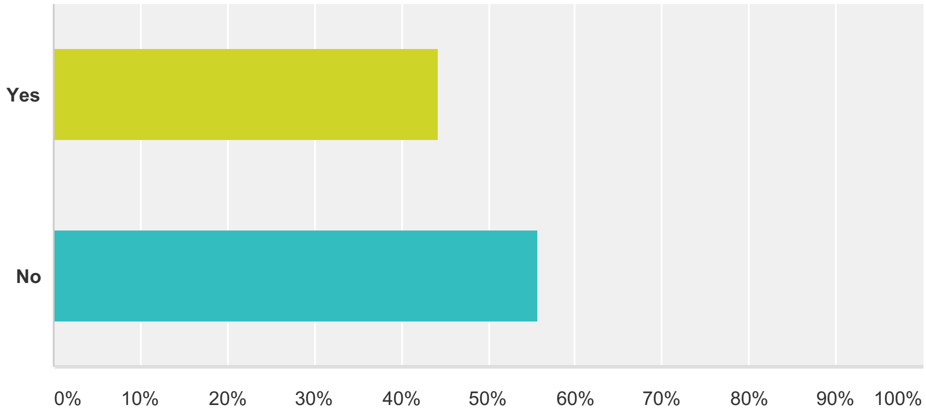
Answered: 43 Skipped: 12

#	Responses	Date
1	Taxonomy but I am now also working with identification of cryptic species using genetics.	3/3/2016 12:25 PM
2	Working on a 40-gene panel for RNA expression in Breast cancer FFPE samples.	3/2/2016 7:07 AM
3	My project involves sequencing the genome and potentially identifying the causative mutations for a specified rare genetic condition by using Next Generation Sequencing technology.	3/1/2016 8:34 AM
4	My research topic for my Masters degree was NGS of targeted genes on Parkinsons (and Parkinsonism) samples.	2/29/2016 8:58 PM
5	My research project involves the study of the underlying genetic causes of the two neurodevelopmental conditions autism spectrum disorder and specific language impairment through the application of SNP arrays for linkage analysis and exome sequencing.	2/28/2016 11:20 PM
6	I work in the field of embryology and reproducitve immunology	2/26/2016 10:54 PM
7	I work on the discovery and proof of causal genes in bleeding and platelet disorders. I am currently focussing on the molecular biology side including CRISPR and forward programming of cell lines to megakaryocytes	2/26/2016 1:43 PM
8	The aim of the project is the molecular characterisation of SMIM1, a gene recently identified which underlies the VEL-antigen, and is a novel regulator of erythropoiesis and megakaryopoiesis. SMIM1 seems to be involved in iron uptake and it is likely part of a membrane multi-protein complex. Observations in Zebrafish knock down for SMIM1 and blood donors carriers of the mutation in VEL antigen (1/5000) pinpointed that SMIM1 not only is important in red blood cell biology but also in the specification of the cell fate at megakaryocyte erythrocyte progenitor (MEP). The project aim to identify the possible partners of SMIM1-membrane multi-protein complex, obtain a detailed understanding of the mechanism/s by which SMIM1 plays a role in fate commitment at MEP stage and in iron uptake, by making use of lentiviral overexpression and knockdown of SMIM1, induced pluripotent stem cells derived from VEL negative donors, SMIM1 knockout in induced pluripotent stem cells using CRISPR/Cas9n system and SMIM1 knockout mice.	2/26/2016 12:13 PM
9	Association methods for genomic and ontological phenotype data	2/26/2016 11:54 AM
10	Performing rnaseq on hscs, megakaryocytes and platelets from clinical samples	2/26/2016 11:12 AM
11	I work on signal and image processing techniques for fast and automatic reconstruction and compression of events in the sub detectors of the ALICE experiment in the LHC.	2/25/2016 4:23 PM
12	I work on the genetic risk related to type 2 diabetes	2/25/2016 1:50 PM
13	I work on identifying mutations, using gene sequencing, in coagulation disorders	2/25/2016 10:14 AM
14	Structural bioinformatics and x-Ray crystallography of superoxide dismutase enzymes	2/25/2016 9:36 AM
15	I am using thermography to identify changes in the diabetic foot. On another study I use thermography to identify success of revascularization.	2/25/2016 6:44 AM
16	In my project, I work on identifying new or known gene variants in family members affected with osteoporosis using next generation sequencing.	2/24/2016 5:21 PM
17	Fetal hemoglobin and beta thalassaemia.	2/24/2016 3:34 PM
18	My PhD will focus on Herceptin-resistant breast cancer with particular focus on specific molecular pathways. Although still at an early stage, RNA-seq might be required further on during the study.	2/24/2016 2:02 PM
19	Genetics of inherited diseases	2/24/2016 11:17 AM
20	I work on the link between splicing defects and neurodegenerative disorders	2/24/2016 7:03 AM
21	genetics	2/22/2016 2:21 PM

22	I work on deciphering the molecular mechanisms that regulate the expression of genes involved in cardiovascular diseases, with specific focus on epigenetic regulation and non-coding regions.	2/22/2016 9:40 AM
23	Analysis of RNAseq data from primary erythroid progenitor cells, & analysis of WGS data from clinical samples	2/19/2016 3:31 PM
24	I work on long rang enhancers and proving that they influence the expression of a gene by binding different transcription factors. Additional I want to use RNA-seq data to elucidate the effect of a point mutation in a patient on the different pathways in megakaryocytes.	2/17/2016 1:00 PM
25	Genetics and pathophysiology of kidney diseases	2/16/2016 3:57 PM
26	Molecular characterisation of Triple Negative Breast Cancer using multiplex RNA expression	2/16/2016 12:37 PM
27	Functional effects of molecular genetic associations with drug response or disease characteristics, with a main focus on COPD and asthma.	2/15/2016 2:49 PM
28	To find new mechanisms of globin gene expression	2/15/2016 9:08 AM
29	I work on the genetic predisposition and molecular biology of pituitary tumours using a variety of techniques, mostly based on cell culture in vitro models and functional studies of different molecular pathways.	2/11/2016 12:11 PM
30	The genetics of heritable dental anomalies	2/11/2016 9:20 AM
31	Interested in phylogenetic relationships.	2/11/2016 9:03 AM
32	We are investigating the influence of variants in inflammatory-related genes on mRNA expression levels and will soon start RNA_seq to determine any differentially expressed genes in relation to myocardial infarction and inflammation.	2/11/2016 6:43 AM
33	I work on inherited diseases, family studies and their analysis with next generation sequencing technique.	2/10/2016 1:03 PM
34	De novo genome sequencing of novel strains of cyanobacteria and microalgae, a study of their biochemistry, and application of their metabolites to biomedicine.	2/10/2016 9:26 AM
35	Microbial genomics	2/10/2016 9:11 AM
36	I am using NGS (whole exome or targetee sequencing) in a family study to detect mutations that may account for specific inherited diseases.	2/10/2016 6:10 AM
37	Changes in protein function resulting from lysine methylation	2/9/2016 9:04 PM
38	I am researching the analysis of pollen identification in honey through the use of NGS	2/9/2016 5:02 PM
39	1) Identification of disease causing mutations in patients with rare diseases using exome sequencing 2) Identification of mutations within selected pathways in samples from the Maltese acute myocardial infarction (MAMI) study using HTS of selected genes	2/9/2016 4:34 PM
40	Population and Forensic Genetics, mitochondrial genetics	2/9/2016 12:26 PM
41	I am starting a PhD in Bioinformatics (Structural and Molecular Biology)	2/8/2016 8:46 PM
42	I work on Platelet biology and genetics to study candidate genes in Autism spectrum disorders (ASD)	2/8/2016 4:20 PM
43	I work on granule biogenesis during megakaryopoiesis starting from insights of known and novel genetic granule deficiencies.	2/8/2016 4:15 PM

Q9 Have you used any high-throughput sequencing applications in your research so far?

Answered: 43 Skipped: 12



Answer Choices	Responses	
Yes	**44.19%**	19
No	**55.81%**	24
Total		**43**

#	If Yes, please specify which one	Date
1	Next Generation Sequencing	3/1/2016 8:34 AM
2	Targeted sequencing NGS and exome sequencing (still to be analysed)	2/29/2016 8:58 PM
3	Library preparation for exome sequencing and targeted gene panel sequencing.	2/28/2016 11:20 PM
4	But used by collaegues in bioinformatic team	2/26/2016 1:43 PM
5	WGS	2/26/2016 11:54 AM
6	Rna seq	2/26/2016 11:12 AM
7	GWS	2/24/2016 3:34 PM
8	Exome sequencing	2/24/2016 11:17 AM
9	RRBS	2/22/2016 9:40 AM
10	Complete Genomics proprietary machines	2/19/2016 3:31 PM
11	My research is based on exome sequencing of the BPD-BRIDGE study. But I did not handle any data myself.	2/17/2016 1:00 PM
12	Microarrays for RNA profiling	2/11/2016 12:11 PM
13	Sequencing of candidate genes on a HiSeq4000	2/11/2016 6:43 AM
14	RNA-seq	2/9/2016 9:04 PM
15	exome sequencing	2/9/2016 4:34 PM
16	The ASD candidate genes I selected and am working on were obtained by using whole genome and whole exome sequencing of the ASD patients in University of Cambridge.	2/8/2016 4:20 PM
17	WES/WGS was performed on patients' samples at the University of Cambridge. I'm now verifiying and characterizing the resulting candidate genes for their disorders.	2/8/2016 4:15 PM

Q10 What are your future research plans? Please indicate if you intend to start using any new applications (e.g. RNA-seq,...) that you have not previously used.

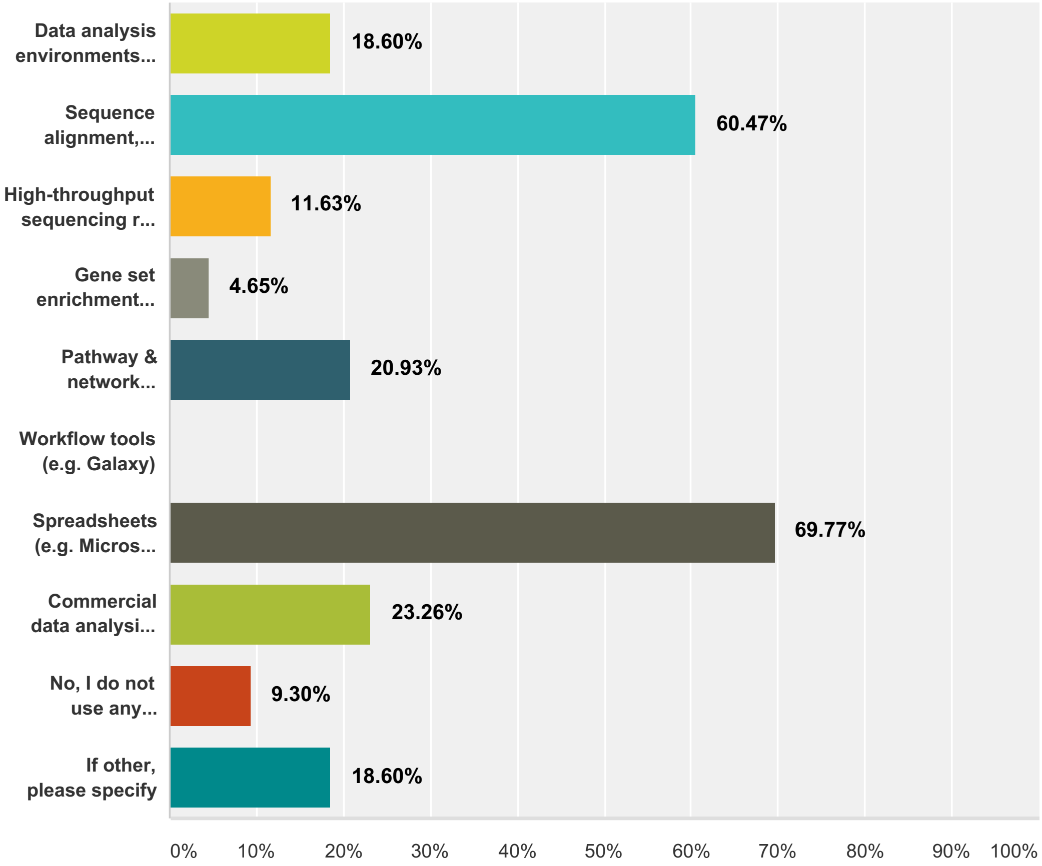
Answered: 43 Skipped: 12

#	Responses	Date
1	Yes, I would like to start working with sequencing of genes in order to identify closely related species.	3/3/2016 12:25 PM
2	Enlarging my sample size and analysing all the data in relation to clinical information and cellular models.	3/2/2016 7:07 AM
3	Until now, I am to focus more on the analysis of data generated by Next Generation Sequencing	3/1/2016 8:34 AM
4	Not sure what applications my future research plans will hold.	2/29/2016 8:58 PM
5	My future research plans involve the application of gene pathway analysis, such as through the use of KEGG and GO databases, and possibly other functional work on the candidate genes identified during my research project,	2/28/2016 11:20 PM
6	I am setting up an Embryology lab , and this will require new applications	2/26/2016 10:54 PM
7	RNA seq of induced megakaryocytes and patient derived platelets	2/26/2016 1:43 PM
8	I would like to compare the transcripts of my different knockouts in different conditions by RNA-seq.	2/26/2016 12:13 PM
9	Incorporate more prior information about individual variants	2/26/2016 11:54 AM
10	Methylome seq	2/26/2016 11:12 AM
11	I would be interested to collaborate with life scientists on issues related to processing of big datasets.	2/25/2016 4:23 PM
12	at the moment there is any plan but it might be in future	2/25/2016 1:50 PM
13	It would be ideal if I could make use of these techniques during my Masters. I plan to continue my studies for Phd	2/25/2016 10:14 AM
14	I intend to start using Amber tools for molecular dynamics and electrostatics studies.	2/25/2016 9:36 AM
15	My research fellow ends this coming November, I would like to embark on another project or continue to lecture.	2/25/2016 6:44 AM
16	I plan to use whole genome sequencing	2/24/2016 5:21 PM
17	RNA sequencing	2/24/2016 3:34 PM
18	As biomedical scientist employed by MDH, NGS (genomic) will be a very important inclusion in our test repertoire. RNA-seq might be required during my PhD studies.	2/24/2016 2:02 PM
19	More exome sequencing, whole genome sequencing and RNAseq for quantitation.	2/24/2016 11:17 AM
20	RNA-Seq of brain-specific mutants	2/24/2016 7:03 AM
21	no	2/22/2016 2:21 PM
22	I would like to continue with bisulfite sequencing but also RNA-sequencing	2/22/2016 9:40 AM
23	Same platforms as above	2/19/2016 3:31 PM
24	I will use RNA-Seq for the first time. So I would like to be trained in analyzing the data.	2/17/2016 1:00 PM
25	Whole genome sequencing, proteomic analysis	2/16/2016 3:57 PM
26	RNA sequencing and exome sequencing	2/16/2016 12:37 PM
27	Transcriptome-wide gene expression in mammalian primary cells and cell lines, ideally via RNA-seq. However would consider Affymetrix expression arrays if RNA-seq cost proves prohibitive !	2/15/2016 2:49 PM
28	Whole genome sequencing of selected patients and RNA sequencing in experimental methods and cell cultures	2/15/2016 9:08 AM
29	NGS or exome sequencing depending on availability	2/11/2016 12:11 PM
30	Analysis of subjects using NGS	2/11/2016 9:20 AM
31	RNA-seq	2/11/2016 9:03 AM

32	using exon sequencing and RNA_seq (these are new applications as till now we have analysed data from a candidate gene approach only)	2/11/2016 6:43 AM
33	I am currently using the Illumina GAIIx analyser and the Covaris bioanalyser. I don't think I will be using any other new analysers.	2/10/2016 1:03 PM
34	ongoing and future: data analysis and interpretation of de novo sequencing data	2/10/2016 9:26 AM
35	HIV resistance testing and cross border transmission of pathogens such as TB	2/10/2016 9:11 AM
36	In the very near future I will carry out data analysis from whole exome and candidate gene sequence data of NGS to identify possible disease causing variants	2/10/2016 6:10 AM
37	No plans for high throughput yet	2/9/2016 9:04 PM
38	Plant Varieties identification through NGS	2/9/2016 5:02 PM
39	1) Further pathway analysis in the MAMI collection 2) RNA-seq of selected individuals with differential white cell responses to stimulation	2/9/2016 4:34 PM
40	Full mitochondrial genome sequencing, Control-region mitochondrial sequencing, Target sequencing	2/9/2016 12:26 PM
41	My research plan are to develop computational methods for classifying proteins into evolutionary families. I am at the start of my PhD and I am still at the start of the process.	2/8/2016 8:46 PM
42	I will analyze the Whole exome sequencing data from the patients to check for other already published candidate genes. Also, I will use the RNA - seq data for my candidate genes in megakaryocytes to study the splice variants and/or splice defects.	2/8/2016 4:20 PM
43	RNA-seq will be performed on patient and control samples. These patients have mutations in a non-coding RNA important for the splicing of many genes. The presence of differential splice events will be evaluated in mature megakaryocytes.	2/8/2016 4:15 PM

Q11 Which software do you use to analyze your data? Please select all that apply.

Answered: 43 Skipped: 12



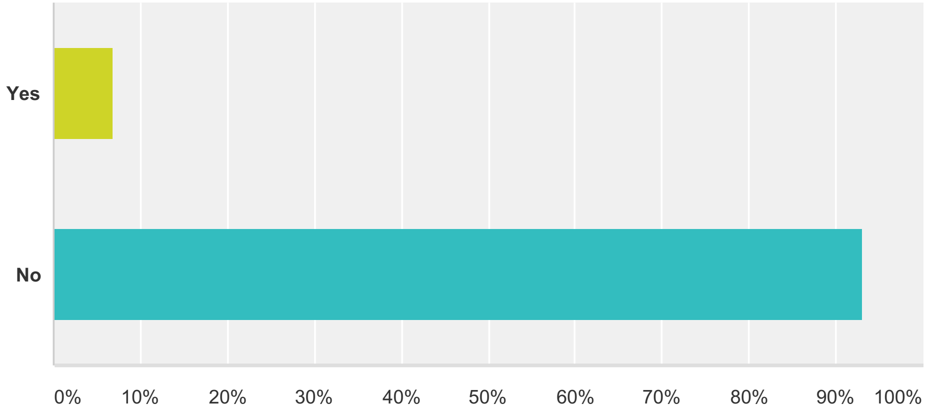
Answer Choices	Responses	
Data analysis environments (e.g. R/Bioconductor, Matlab, Python/Pandas....)	**18.60%**	8
Sequence alignment, similarity & homology tools (e.g. Blast, Clustal,...)	**60.47%**	26
High-throughput sequencing read alignment and assembly programs (e.g BWA, Bowtie,...)	**11.63%**	5
Gene set enrichment testing tools (e.g DAVID, GO)	**4.65%**	2
Pathway & network analysis tools (e.g. Cytoscape, Biocarta, Ingenuity,...)	**20.93%**	9
Workflow tools (e.g. Galaxy)	**0.00%**	0
Spreadsheets (e.g. Microsoft Excel)	**69.77%**	30
Commercial data analysis software packages	**23.26%**	10
No, I do not use any software	**9.30%**	4
If other, please specify	**18.60%**	8
Total Respondents: 43		

#	If other, please specify	Date

1	Rapidminer	3/2/2016 7:07 AM
2	Genespring, Vector NTI plus several online tools	2/15/2016 2:49 PM
3	SPSS	2/15/2016 9:08 AM
4	Geneious,	2/11/2016 9:03 AM
5	NextGene Software	2/11/2016 6:43 AM
6	phylogenetics software, online tools for prediction of molecular structures and reactions	2/10/2016 9:26 AM
7	I will need to use EMMA for mt Genome sequencing, NetworkNETWORK is software to calculate and draw quasi-median networks. They are useful to examine the quality of an mtDNA dataset. http://empop.online/tools, http://empop.online/downloads	2/9/2016 12:26 PM
8	Sanger sequencing analyzer softwares	2/8/2016 4:20 PM

Q12 Do you have any experience with writing programs to analyse your data?

Answered: 43 Skipped: 12

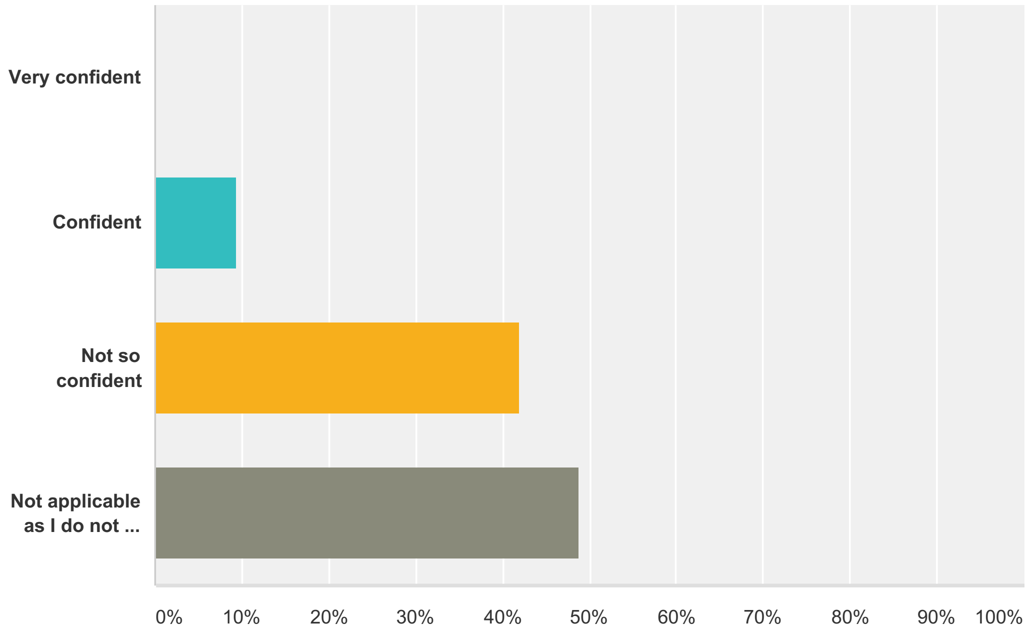


Answer Choices	Responses	
Yes	**6.98%**	3
No	**93.02%**	40
Total		**43**

#	If yes, please specify which programming language(s) you use.	Date
1	R, C++	2/26/2016 11:54 AM
2	R, Python, MATLAB, C/C++, Java	2/25/2016 4:23 PM
3	R, Python, Java	2/8/2016 8:46 PM

Q13 How confident are you with web-based software tools, e.g. Galaxy?

Answered: 43 Skipped: 12

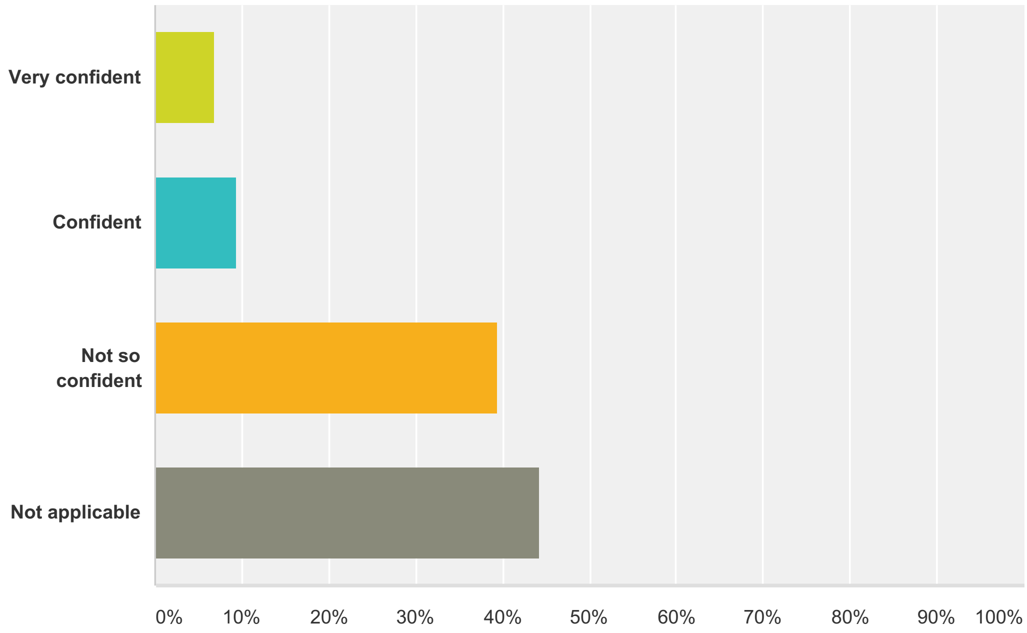


Answer Choices	Responses	
Very confident	**0.00%**	0
Confident	**9.30%**	4
Not so confident	**41.86%**	18
Not applicable as I do not use such tools	**48.84%**	21
Total		**43**

#	If you use any, please specify which ones	Date
1	I have used the Ensembl Variant Effect Predictor (VEP)	2/28/2016 11:20 PM
2	UCSC Genome Browser	2/26/2016 11:54 AM
3	I would like to use such tools in the near future	2/24/2016 2:02 PM
4	Several from the NCBI suite; mapping of transcription factor consensus sequences, generation of restriction maps, indel sequence deconvolution analysis, genome browsers such as IGV, ensembl tools, etc	2/15/2016 2:49 PM
5	Ingenuity pathway analysis and GeneSpring	2/11/2016 12:11 PM

Q14 How confident are you with command-line tools (e.g. Unix,.....)?

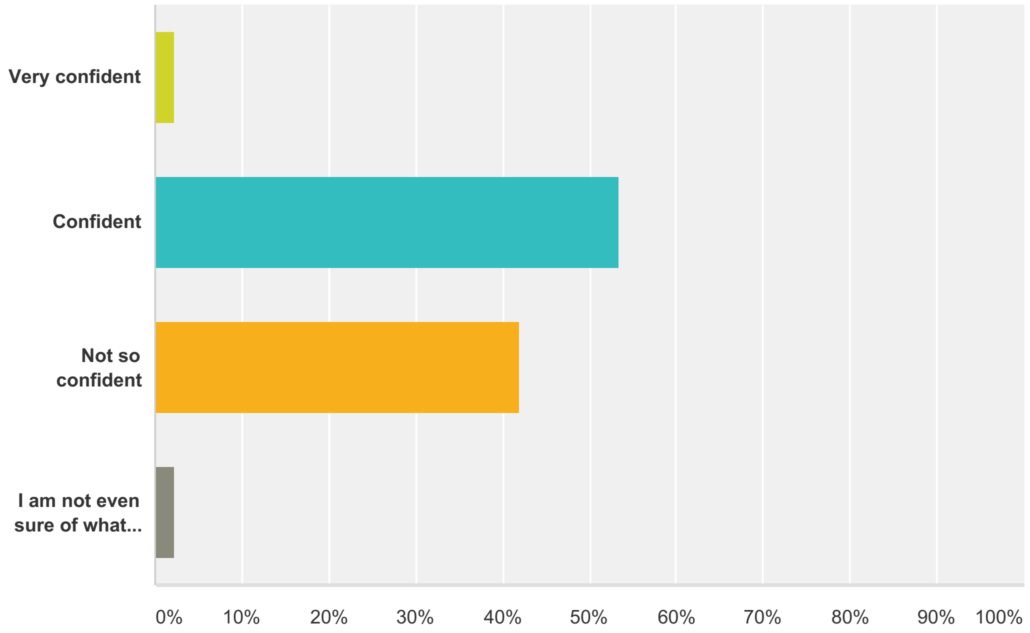
Answered: 43 Skipped: 12



Answer Choices	Responses	
Very confident	**6.98%**	3
Confident	**9.30%**	4
Not so confident	**39.53%**	17
Not applicable	**44.19%**	19
Total		**43**

Q15 How confident are you with statistics?

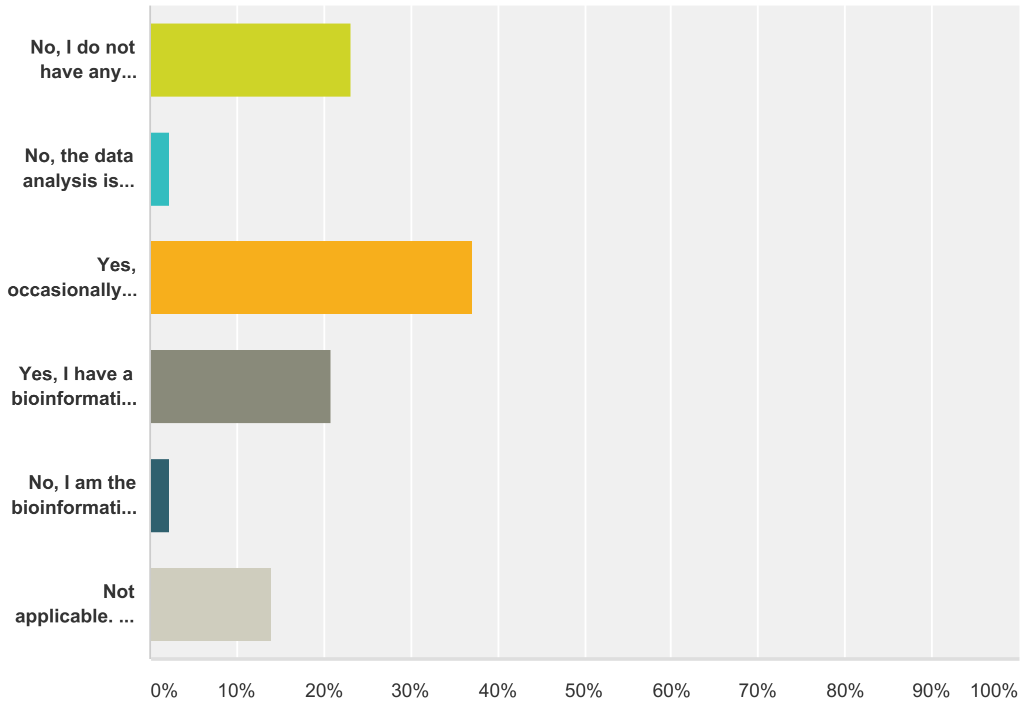
Answered: 43 Skipped: 12



Answer Choices	Responses	
Very confident	**2.33%**	1
Confident	**53.49%**	23
Not so confident	**41.86%**	18
I am not even sure of what statistics I need to know	**2.33%**	1
Total		**43**

Q16 Do you collaborate with a bioinformatician/statistician on the analysis of your data?

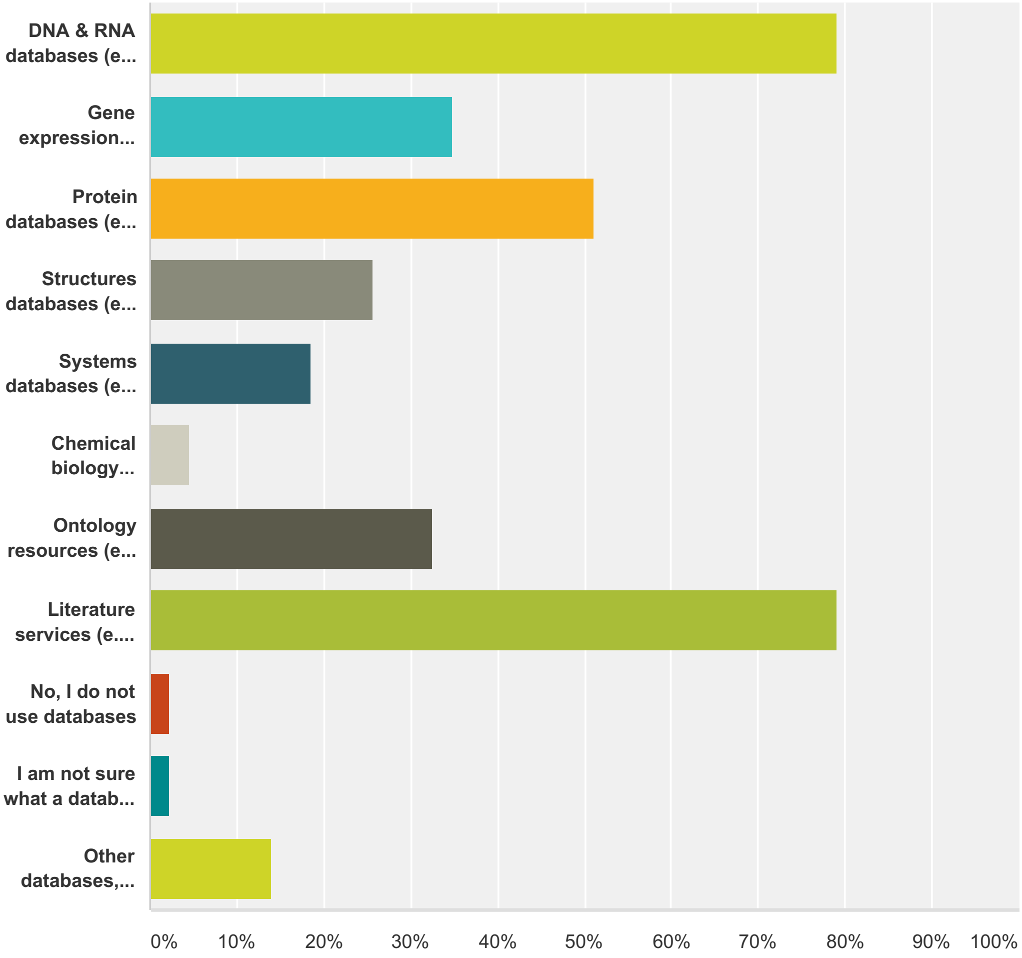
Answered: 43 Skipped: 12



Answer Choices	Responses	
No, I do not have any support. I am responsible for analyzing the data that I generate.	**23.26%**	10
No, the data analysis is carried out by someone else. I just receive a file with the results.	**2.33%**	1
Yes, occasionally I interact with a bioinformatician/statistician at my Institute, particularly when I get stuck and I don't know how to proceed.	**37.21%**	16
Yes, I have a bioinformatician in the group that helps me to design experiments and also provides support for the data analysis	**20.93%**	9
No, I am the bioinformatician in the group	**2.33%**	1
Not applicable. I do not do any data analysis at the moment.	**13.95%**	6
Total		**43**

Q17 Do you use scientific databases? Please select all that apply

Answered: 43   Skipped: 12



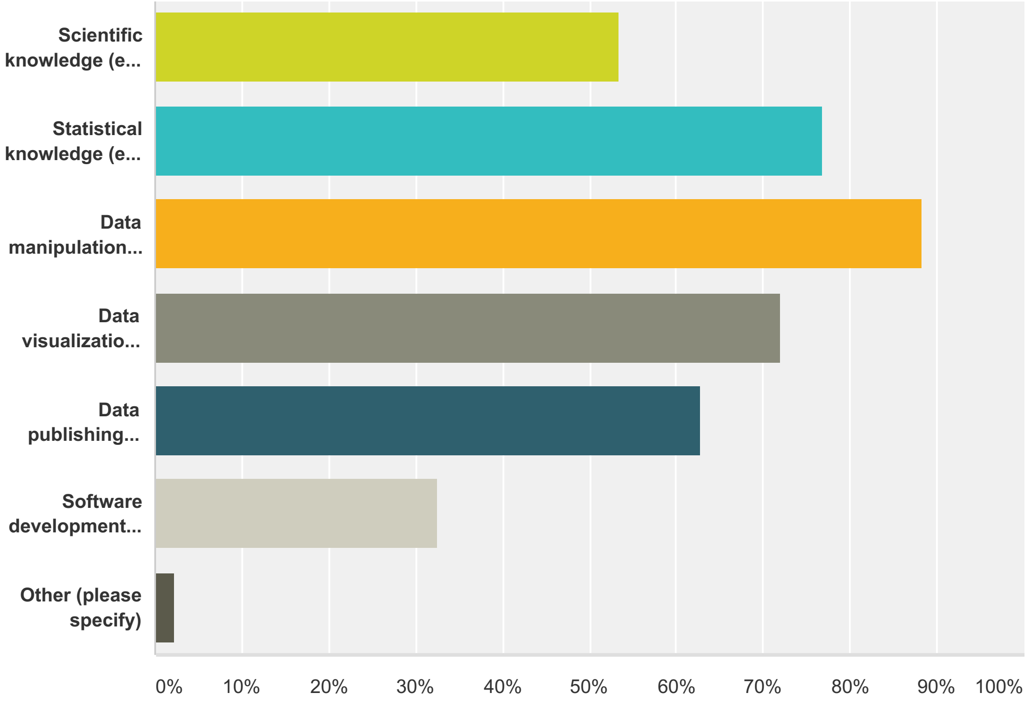
Answer Choices	Responses	
DNA & RNA databases (e.g. Ensembl, 1000 genomes, UCSC,....)	**79.07%**	34
Gene expression databases (e.g. ArrayExpress, Gene Expression Omnibus,...)	**34.88%**	15
Protein databases (e.g. Uniprot, Pfam, Intact,...)	**51.16%**	22
Structures databases (e.g. PDBe)	**25.58%**	11
Systems databases (e.g. BioModels, Reactome, KEGG,...)	**18.60%**	8
Chemical biology databases (e.g. ChEMBL,..)	**4.65%**	2
Ontology resources (e.g. Gene Ontology,..)	**32.56%**	14
Literature services (e.g. Pubmed,...)	**79.07%**	34
No, I do not use databases	**2.33%**	1
I am not sure what a database is	**2.33%**	1

Other databases, please specify	**13.95%**	6
Total Respondents: 43		

#	Other databases, please specify	Date
1	TCGA - cBIO Portal	3/2/2016 7:07 AM
2	Registers available at the Dept of Health Information, Malta	2/26/2016 10:54 PM
3	Not for this research, however my last MSc was in microbiology where I looked for different strains of ESBL	2/25/2016 6:44 AM
4	OMIM	2/16/2016 3:57 PM
5	Standford database for HIV	2/10/2016 9:11 AM
6	PhyloTree mt, PhyloTree Y, EMPOP, YHRD, MitoMap	2/9/2016 12:26 PM

Q18 What expertise would you like to acquire to be able to better handle the data that you generate? Please select all that apply

Answered: 43 Skipped: 12



Answer Choices	Responses	
Scientific knowledge (e.g. how should I design my experiment to obtain meaningful results?)	**53.49%**	23
Statistical knowledge (e.g. what statistics do I need to know to be able to analyze my data?)	**76.74%**	33
Data manipulation skills (e.g. what software is more appropriate to analyze my data? How does a specific software work?)	**88.37%**	38
Data visualization skills (e.g. how does my data look like? How do I interpret and present my data?)	**72.09%**	31
Data publishing skills (e.g. how do I publish my results?)	**62.79%**	27
Software development skills (e.g. how do I write software to analyse my data?)	**32.56%**	14
Other (please specify)	**2.33%**	1
Total Respondents: 43		

#	Other (please specify)	Date
1	Not applicable	2/25/2016 4:23 PM

Q19 What topics would you like to see covered in bioinformatics training courses organized by TrainMalta?

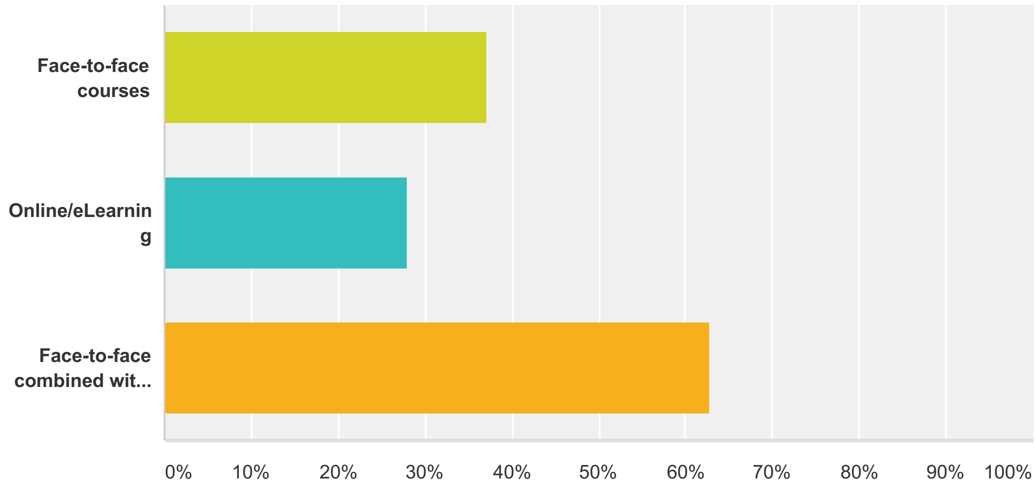
Answered: 28 Skipped: 27

#	Responses	Date
1	Not only human genetics.	3/3/2016 12:25 PM
2	How to present and interpret data	3/1/2016 8:34 AM
3	The bioinformatic process from when you receive bam files to scientific/statistical results understood by scientists, using command-line readily available software (such as Galaxy)	2/29/2016 8:58 PM
4	- Unix and Perl scripting for biologists - Statistical analysis using R - Determining the most appropriate statistical methods and software - Accessing public sequencing repositories - Use of bioinformatics software platforms for visualizing molecular interaction networks	2/28/2016 11:20 PM
5	All those mention in point 18.	2/26/2016 10:54 PM
6	Rather than topics as such I would like to see a stratified approach where the first sessions are relatively introductory.	2/26/2016 1:43 PM
7	Software use	2/25/2016 10:14 AM
8	Structural biology and protein homology modelling	2/25/2016 9:36 AM
9	- More exposure to online software sources and how can these be used/applied - Training on how to process raw data	2/24/2016 5:21 PM
10	GWS data RNA sequencing	2/24/2016 3:34 PM
11	Manipulation of NGS data	2/24/2016 2:02 PM
12	Data analysis of RNA-seq for quantitation purposes.	2/24/2016 11:17 AM
13	I am specifically interested in epigenomics in general	2/22/2016 9:40 AM
14	Mentioning of different available platforms used for genome seq @ exome & wgs level.	2/19/2016 3:31 PM
15	RNA-Seq and visualization of all the data already available in the databases (such as making a figure with long range enhancers interaction with promotors)	2/17/2016 1:00 PM
16	Introductory and basic bioinformatics and its application in practice	2/16/2016 12:37 PM
17	Experimental design and approaches to analysis of genomics and transcriptomics data, issues of statistical power, signal and noise in data, addressing of the differences in analysis output when the same data is analysed by different software packages, data formats suitable for package interoperability,	2/15/2016 2:49 PM
18	how to select appropriate software of specific applications and better understanding of different options available for high throughput data analysis	2/11/2016 12:11 PM
19	Analysis of data from RNA_seq experiments and assessing the effect of variants in a biological pathway approach	2/11/2016 6:43 AM
20	analysis of de novo data	2/10/2016 9:26 AM
21	Hands-on tutorials for data analysis software Statistics	2/10/2016 6:10 AM
22	Anything applicable to protein analysis especially mass spec	2/9/2016 9:04 PM
23	The basics of NGS	2/9/2016 5:02 PM
24	How to put together a data analysis pipeline to make me independent of commercial software	2/9/2016 4:34 PM
25	Training on Haplogroup assignment using EMMA and Network and Phylotree (mt and Y)	2/9/2016 12:26 PM
26	Biology for Computer Scientists	2/8/2016 8:46 PM
27	I would like to learn - -How and which statistical tests to use to analyse different data sets. -Analysis of whole genome and whole exome sequencing from raw data -Programming to create software to consolidate data regarding specific pathways or genes from all available published papers. -Exel programming to make data analysis easier -More useful online software for Molecular biology and complex genetics work	2/8/2016 4:20 PM

28	Statistical Analysis RNA-seq data analysis How to use online available databases Program in Excel Writing own programs for data analysis	2/8/2016 4:15 PM

Q20 How would you prefer training to be delivered to you?

Answered: 43 Skipped: 12



Answer Choices	Responses	
Face-to-face courses	**37.21%**	16
Online/eLearning	**27.91%**	12
Face-to-face combined with online	**62.79%**	27
Total Respondents: 43		

#	If other, please specify	Date
	There are no responses.	

Q21 Any other comment you would like to add?

Answered: 8 Skipped: 47

#	Responses	Date
1	No	2/26/2016 10:54 PM
2	Thanks	2/26/2016 1:43 PM
3	Software use and learning amongst students have been very limited. Softwares were made use during thesis only, if any. Statistical knowledge is also difficult for students as we dont have too much practise. Many softwares exists, and which to use or get the best data is a major headache.	2/25/2016 10:14 AM
4	I would prefer any online/face-to-face courses to be registered so that I would be able to access them at will, since I work part-time and study full-time.	2/24/2016 2:02 PM
5	Keep up the good work!	2/24/2016 7:03 AM
6	GOODLUCK !!	2/19/2016 3:31 PM
7	Prosit for the initiative and for your successful funding. Very much needed. Keep it up.	2/15/2016 2:49 PM
8	Very few bioinformaticians work in my field. There are none at the University of Malta who can help.	2/10/2016 9:26 AM