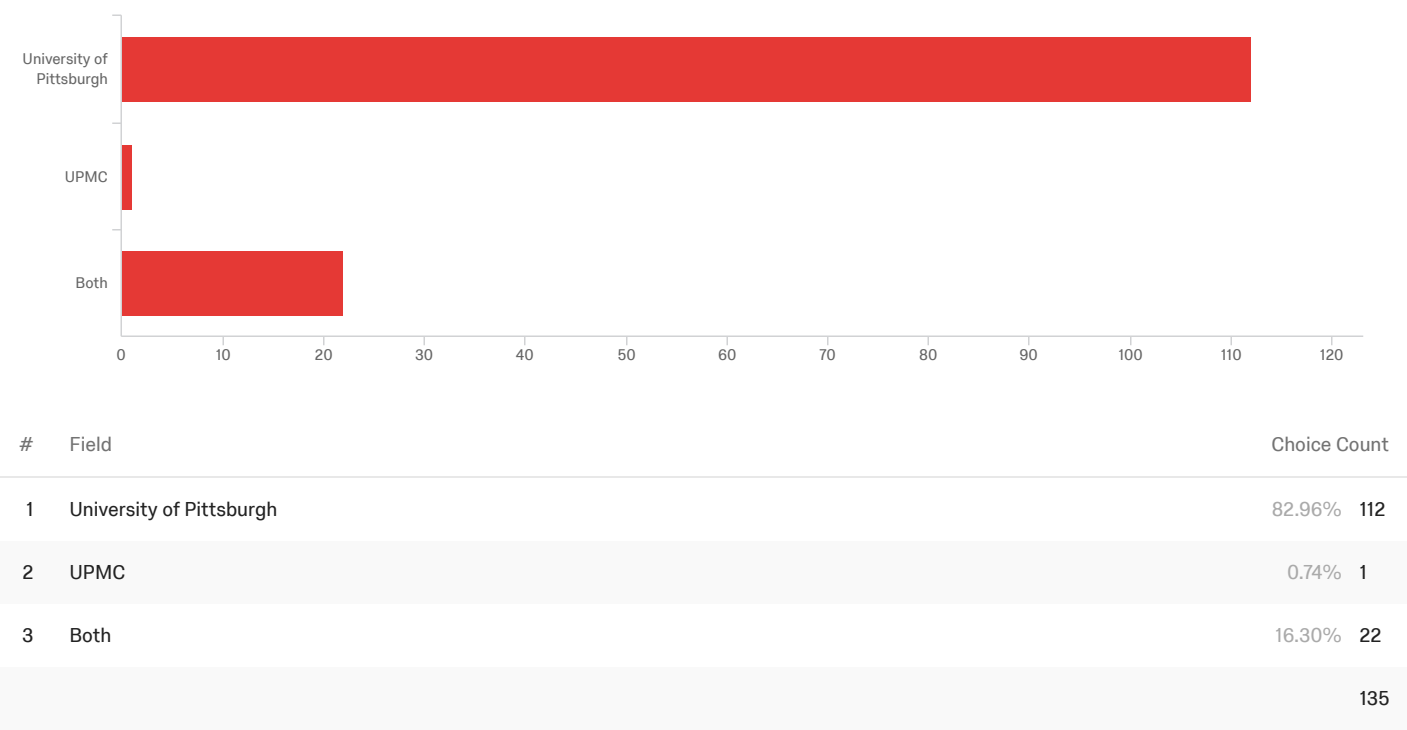


Default Report

HSLs MBIS Services Survey
January 9, 2019 12:45 PM EST

Q1.2 - What is your affiliation?



Showing rows 1 - 4 of 4

Q1.3 - What is your department?

What is your department?

Starzl transplantation institute

Transplant surgery

Medicine

Medicine

Pharmacology & Chemical Biology

Department of Medicine - Division of Infectious Diseases

pathology

Human Genetics

medicine

Infectious Diseases & Microbiology

Neurosurgery

Cell Biology

DBMI

Pediatrics

Computational and Systems Biology

Medicine

IDM

Infectious diseases

Genomics Core

EOH

Medicine/Pulmonary

nursing

Pathology

Medicine

GSPH, Infectious Diseases and Microbiology

Department of Medicine

pediatrics

Environmental and Occupational Health

PACCM

Pathology

VMI

Medicine

Psychiatry

Microbiology and Molecular Genetics

Neurology

computational&systems biology dept

Pediatrics

Surgery

Immunology

psychiatry

Pediatrics

Neurological Surgery

Pathology

Human Genetics

IDM. GSPH

Medicine

EOH

IDM

Pediatrics

IDM

IDM

Infectious Diseases and Microbiology

surgery

Surgery

neurology

Neurological Surgery

Cellular and Molecular Pathology

Medicine

Department of Surgery

EOH

cell biology

Pathology

Medicine

mmg

Ophthalmology

OBGYN

Human Genetics

Pediatrics

Genomics Research Core

MMG

Ophthalmology

Medicine

Medicine

Bioengineering

nursing

Health Promotion and Development

Physics and Astronomy

MMG

Peds

psychiatry

Computational and Systems Biology

Pediatrics: Medical Genetics

Bioengineering

PATHOLOGY

Biomedical Informatics

Pharmacy

Biomedical Informatics

Medicine

Epidemiology

radiology

Immunology

Pharmacy

Pediatrics

ECE

Immunology

Pathology and Bioengineering

pathology

Pathological

medicine

Immunology

Ophthalmology

medicine

Pediatrics

Pathology

magee women research institute

Developmental Biology

Biological Sciences

ophthalmology

Biological Sciences

Medicine

Pathology

medicine

Surgery

Molecular Biophysics and Structural Biology

Human Genetics

Medicine

nursing

Pharmacology

Biological Sciences

Biological Sciences

School of Nursing

Medicine

IDM

Immunology

Computational & Systems Biology

Neurobiology

MMG

Structural Biology

Medicine

Department of Pharmaceutical Sciences

Human Genetics

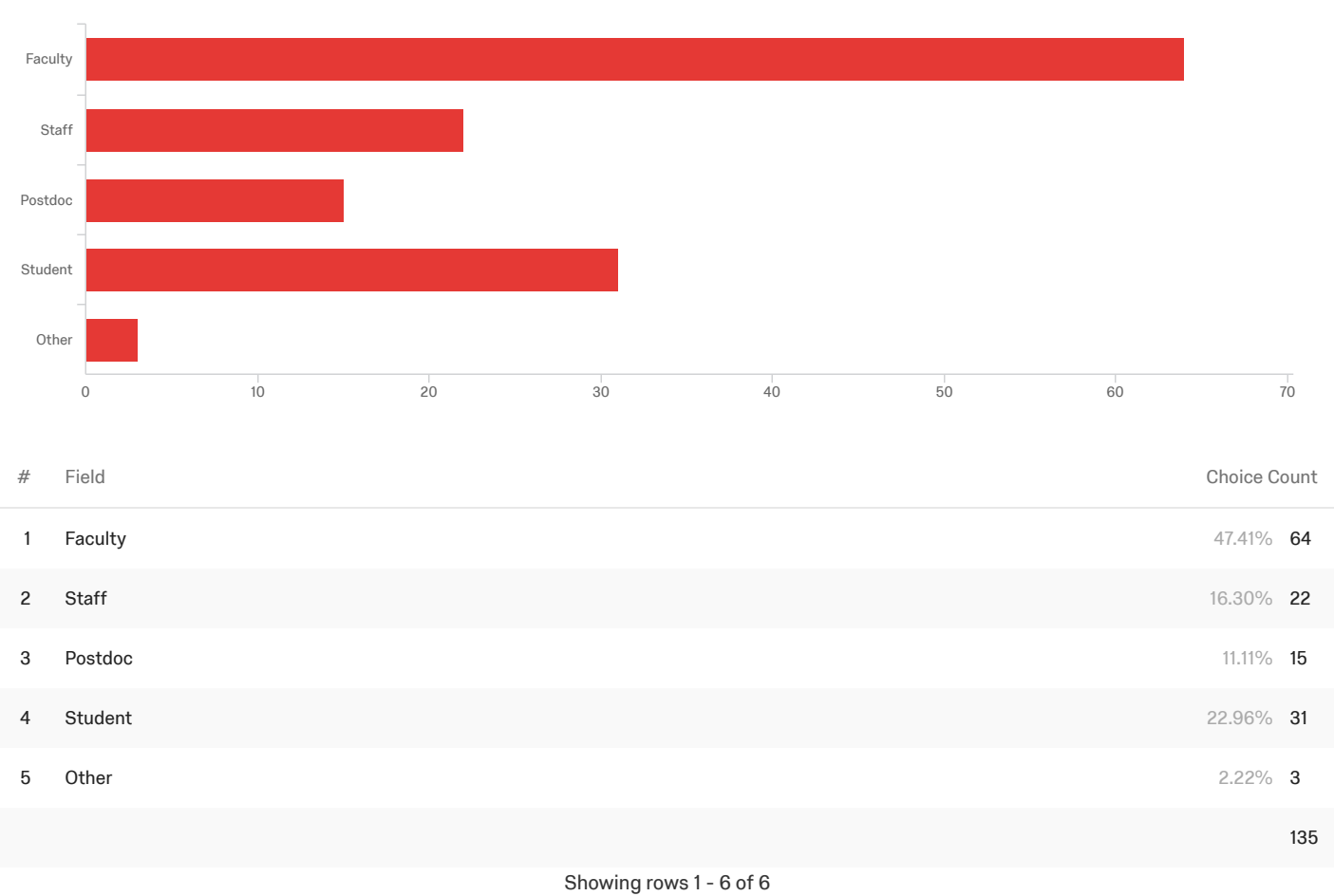
Immunology

human genetics

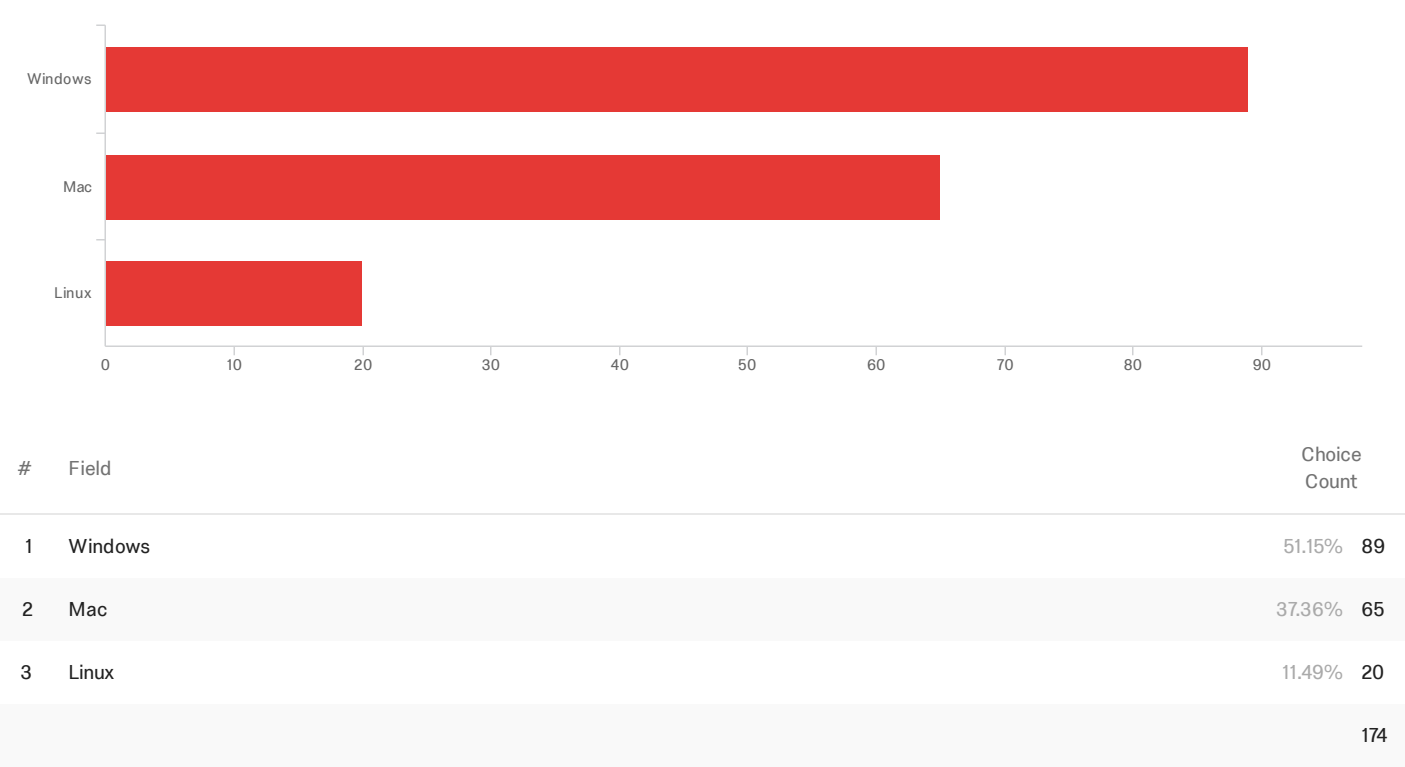
immunology

Biological Sciences

Q1.4 - What is your role?



Q1.5 - What operating system do you use? (select all that apply)

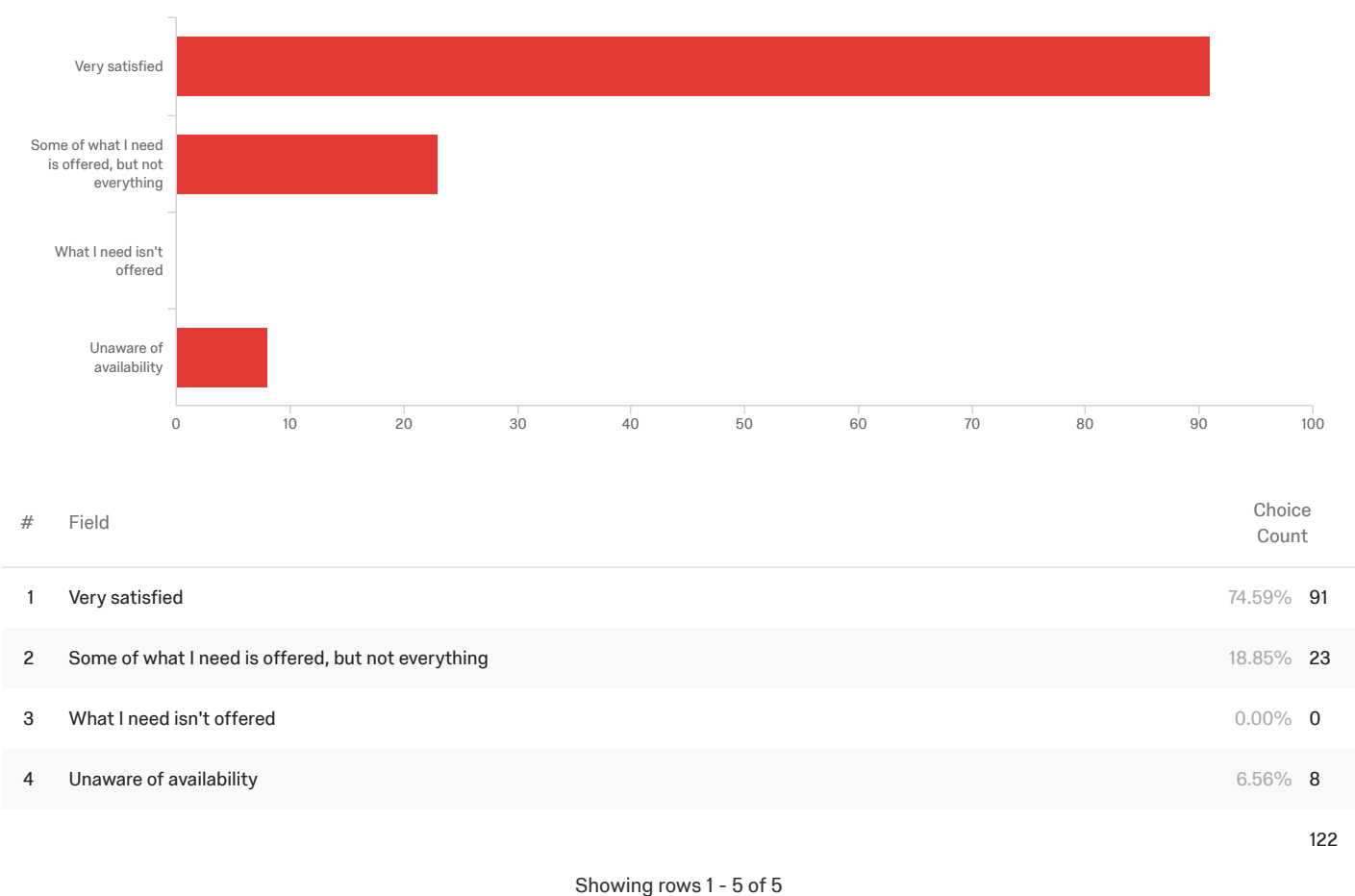


Showing rows 1 - 4 of 4

Q2.2 - How satisfied are you with the selection of commercial software that MBIS

licenses? Examples: CLC Genomics Workbench, Ingenuity Pathway Analysis (IPA),

ePath3d, etc. (hsls.libguides.com/molbio/licensedtools/resources)



Q2.3 - Are there any commercial software packages you would like us to offer?

Are there any commercial software packages you would like us to offer?

Molecular modeling software PyMol is used by lots of researchers in protein structural and function studies.

Transfac is outdated and cannot be accessed now. We would also like access to RNA-seq analysis software using Partek

no

Omeisha

N/A

Snapgene

Partek Flow, Flowjo

not at this time

Omeisha

imaris

Adobe Photoshop (this could be helpful for analyzing images, and making figures)

no

Fabric genomics

Snap Gene

Yes, Quertle (Quetzal) subscription for University users

IPA Causal Analysis and Biomarker Identification

primer premier 5

Flowjo

Nova products that is currently not included in Lasergene

Software to predict transcription factor binding sites to the genes

It is nearly impossible to use Lasergene these days. I always get a message that all licenses are in use. I have switched to CLC, which is really nice, but we have old data in Lasergene that I have trouble accessing.

IPA Causal Network Analysis (Advanced Analytics)

We do a lot of mouse genetics. Colony tracking software would be helpful.

Adobe Suite? Acrobat, illustrator, and photoshop.

None.

Clone Manager

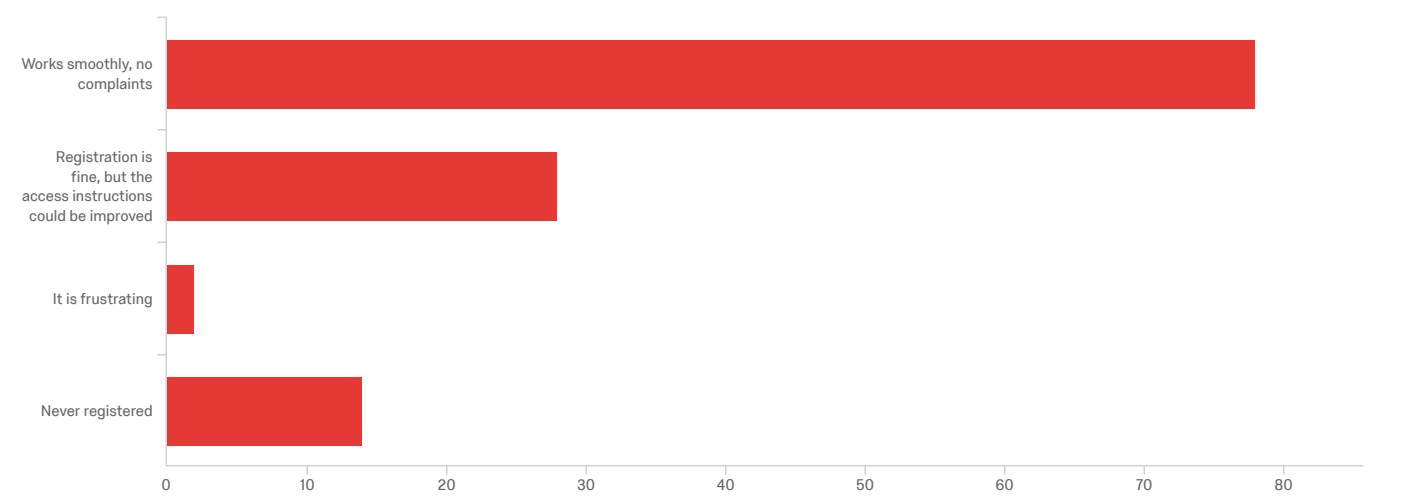
Oligo 7

<https://www.pharmapendium.com/#/login> , this software is great for us, we previous have the evaluation license if I am right as we can login with pitt email address, but now it dosen't provide anymore.

Not at this time

Showing records 1 - 29 of 29

Q2.4 - How satisfied are you with the MBIS commercial software registration process, including delivery of access instructions?

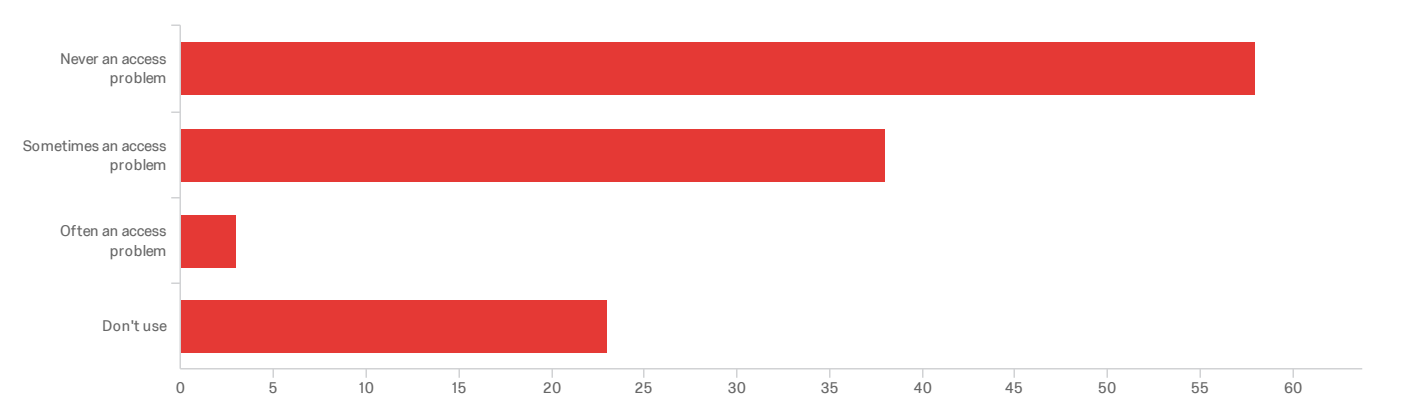


#	Field	Choice Count
1	Works smoothly, no complaints	63.93% 78
2	Registration is fine, but the access instructions could be improved	22.95% 28
3	It is frustrating	1.64% 2
4	Never registered	11.48% 14

122

Showing rows 1 - 5 of 5

Q2.5 - Are you able to access MBIS commercial software when you need it?



#	Field	Choice Count
1	Never an access problem	47.54% 58
2	Sometimes an access problem	31.15% 38
3	Often an access problem	2.46% 3
4	Don't use	18.85% 23

Q2.6 - If you have had an access problem, please list the problematic resource(s).

If you have had an access problem, please list the problematic resource(s).

Vector NTI sometimes cannot be connected.

Sometime, I can't connect to server, and the job take a little long time to finish.

mac based

Transfac

Pathway for a student that is unaffiliated with a particular laboratory / research group is particularly onerous.

N/A

IPA

I've had the most trouble w/ Transfac. I have to get a new password everytime it seems. For the most part getting the software from HSLS is great, but I have had a few problems I've had to work through. I have always gotten great responses and help from the team to get it working.

our lab has occasional difficulty accessing some resources, such as sequencher, because licenses are all in use. this is occasional and in general does not cause big problems.

Not able to use at CHP

Sequencher

Sequencher is sometimes limited in license usage

problem getting license (Partek)

DNASStar

I have not used the software recently, but in the past access was smooth and I had no problem.

I would to know if Blast2GO accessible of Pitt Users?

I used to be able to access remotely if logged into Pitt VPN connection but more difficult now. Sometimes there are not enough licenses for Sequencher so we ended up purchasing 2 licences for the lab.

Login - and use

Have had trouble logging in and using IPA and Transfac from home. Also have had trouble using on UPMC computers, they will run when VPN connected but then the UPMC microsoft word licence stops working.

Sometimes the number of licenses becomes an issue.

Ingenuity

Distinguishing generic login page from Pitt-specific login page of Correlation Engine

Sequencher

Sometimes I cannot log in due to maximum number of login

Been used by more than 4 other users

Problems noticed after new computer due to missing plug in.

When I updated my CLC genomics Workbench, I was not being able to use it, because the licensing setting didn't get carried over to the new version. Since I could not remember how I set it up last time, I ended up re-registered for the product again, so I could see the instruction for license setting.

Lasergene.

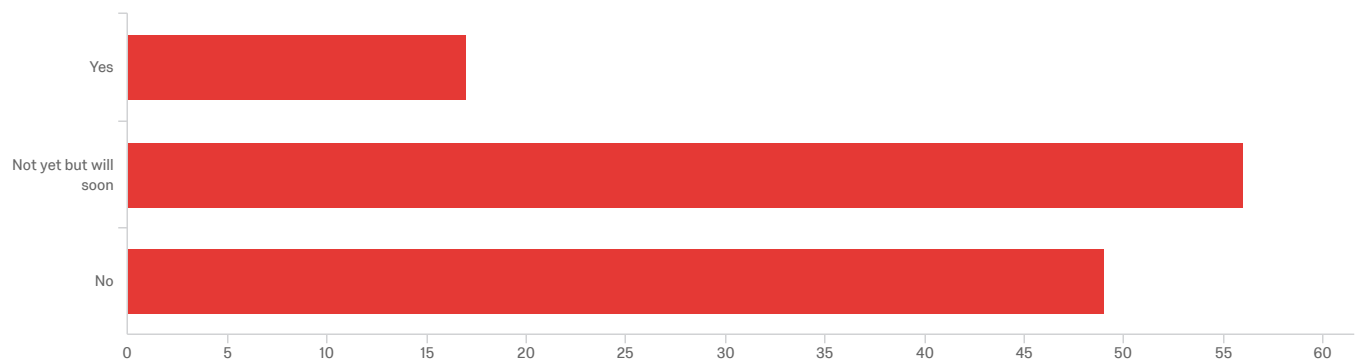
IPA, IVA

I cannot access to DNASTar in the daytime

Lasergene

Showing records 1 - 31 of 31

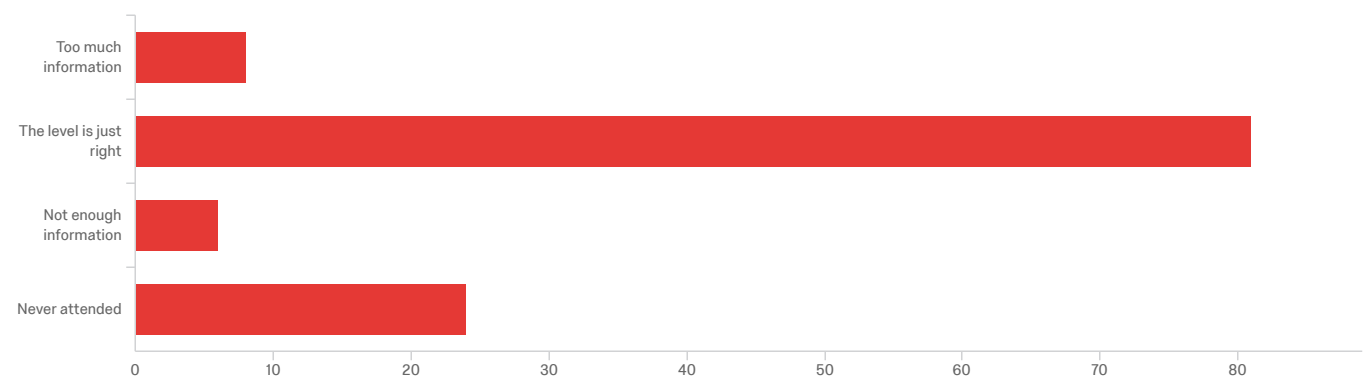
Q2.7 - Have you referenced any MBIS commercially licensed software tools in one of your publications?



#	Field	Choice Count
1	Yes	13.93% 17
2	Not yet but will soon	45.90% 56
3	No	40.16% 49
		122

Showing rows 1 - 4 of 4

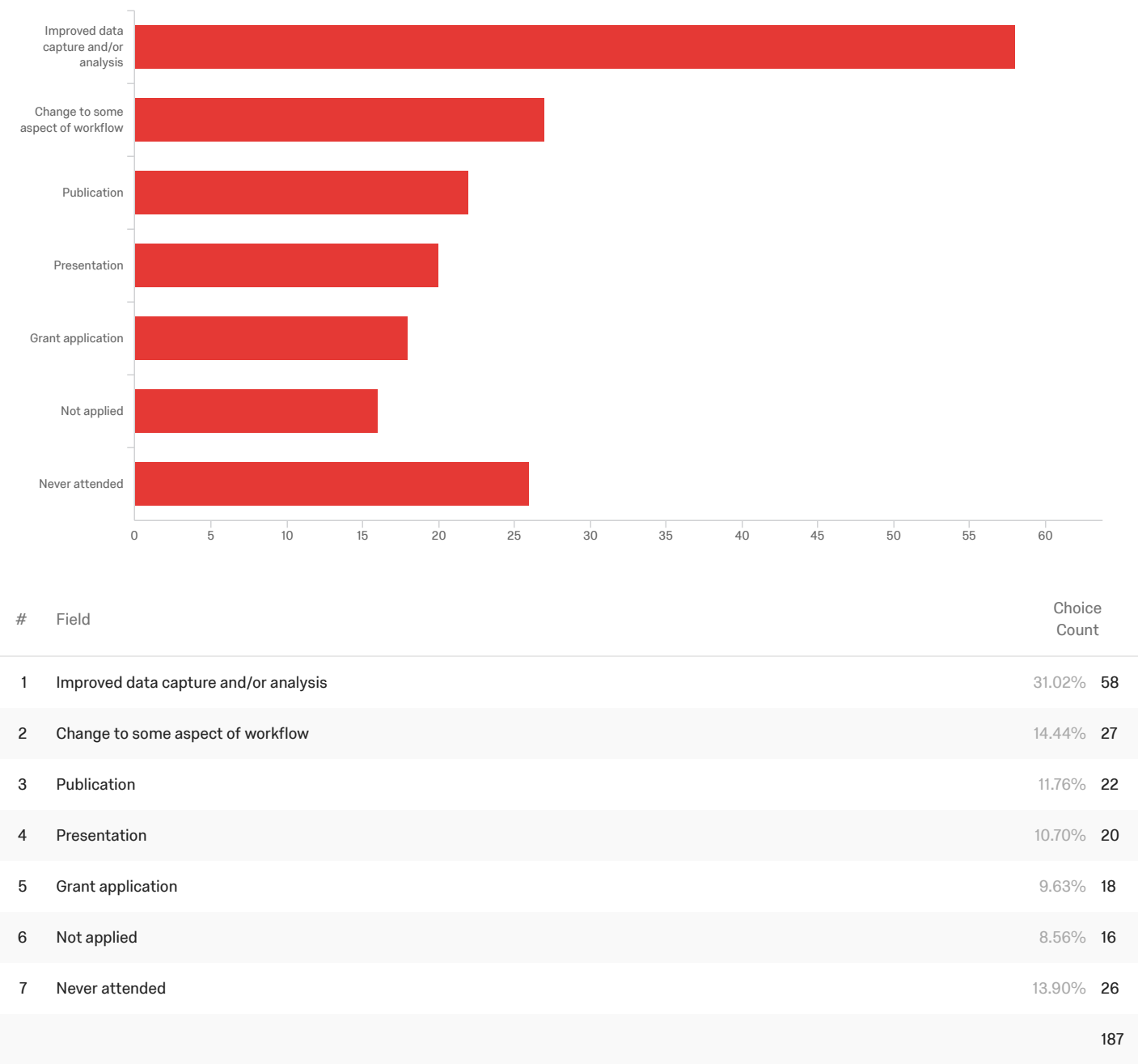
Q3.2 - How satisfied are you with the MBIS workshops level of training, on average?



#	Field	Choice Count
1	Too much information	6.72% 8
2	The level is just right	68.07% 81
3	Not enough information	5.04% 6
4	Never attended	20.17% 24

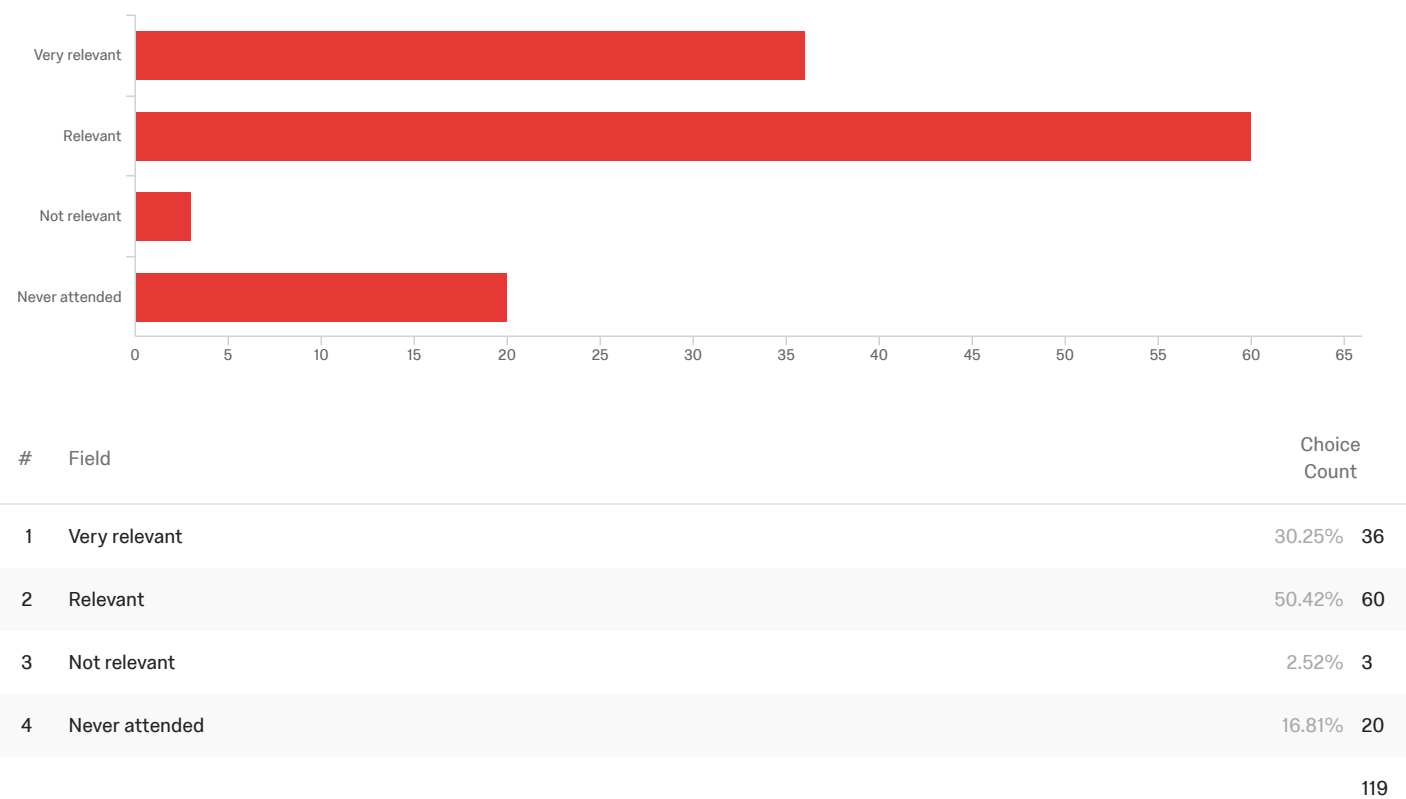
Q3.3 - If you've attended an MBIS workshop, how have you applied what you've learned?

(select all that apply)



Showing rows 1 - 8 of 8

Q3.4 - How relevant are MBIS workshop topics to your needs, on average?



Showing rows 1 - 5 of 5

Q3.5 - Are there any workshop topics you would like us to cover?

Are there any workshop topics you would like us to cover?

Big data mining

An introduction to biomedical programming using R

Bioinformatic analysis of high throughput data such as proteomics to non-bioinformatics person - Although biologist know what softwares to use for analysis there is no definite system to know what things should be in the manuscript.

no

It would be neat if classes could be run together w/ the Frank/Sam people. They have their own classes which are also expanding in topic but can sometimes be too much for the non-expert. A series of classes that worked together w/ the cluster to focus on using tools like HOMER, bedtools, etc for genomics users would be great. Could also highlight what GUI software like CLC or Partek can do, and what you really need the cluster, Linux and R for. I admit these would take work to develop but would be a huge help for many investigators.

some time spent on R/bioconductor might be useful, though it's not comercial

using R

Better overview of open source tools.

Maybe a basic photoshop class and what is an isn't appropriate for figure manipulation

not sure

Nanosting and miRNA data analysis

Offer training modules on website (could be recording of previous workshops) so we can access as needed in case the training needed is not offered frequently

Python, matlab, Bionetgen for beginners

Programming in R

scientific drawing

R programming

More in Depth ATAC-seq

Microbial taxonomy with next generations sequencing. Using Excel scripts and SEQL language for data analysis.

RNAseq using CLC genomics workbench that tailors for prokaryotes

not sure yet

For IPA, would like to know more about the choices within the analysis.

Statistics. When to use and not to use basic stat tests like t-tests, ANOVA, Chi square, etc...

Topics on Epigenetic

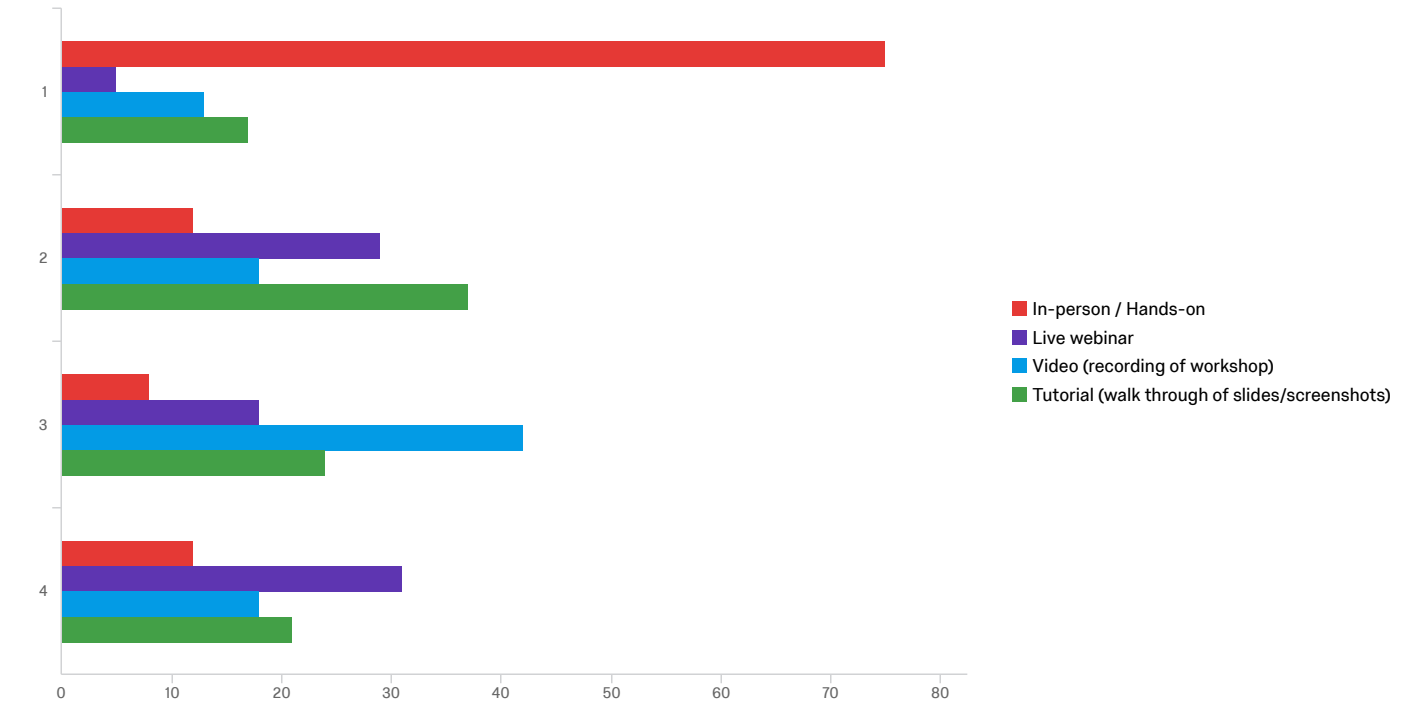
I just found out about this service, but this is awesome. I plan to have my trainees participate in this training.

Analysis of NGS data using command line

Not at this time

Showing records 1 - 27 of 27

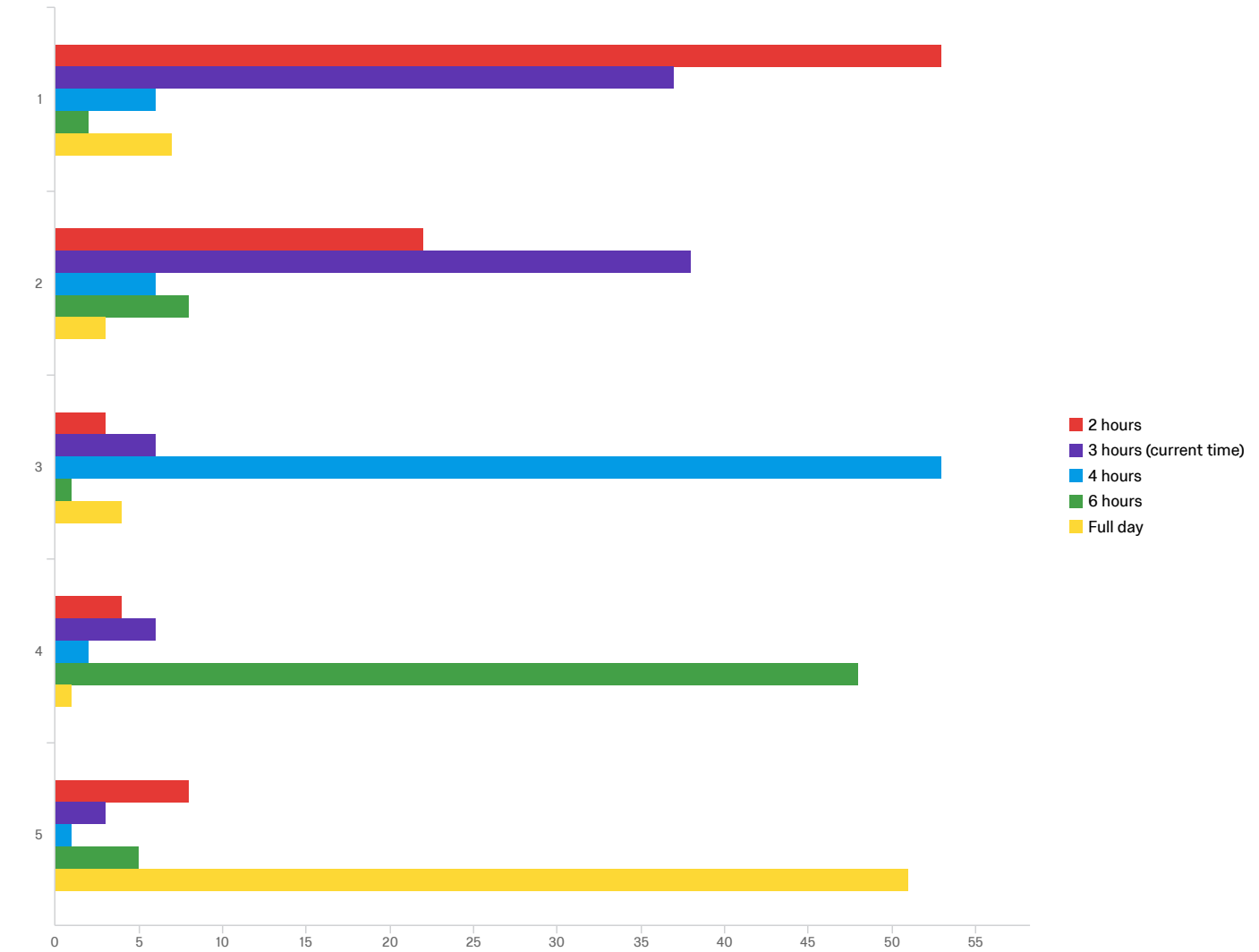
Q3.6 - What is your preferred mode for workshops? rank the order--1 is highest you do not have to rank them all



#	Field	1		2		3		4		Total
1	In-person / Hands-on	70.09%	75	11.21%	12	7.48%	8	11.21%	12	107
2	Live webinar	6.02%	5	34.94%	29	21.69%	18	37.35%	31	83
3	Video (recording of workshop)	14.29%	13	19.78%	18	46.15%	42	19.78%	18	91
4	Tutorial (walk through of slides/screenshots)	17.17%	17	37.37%	37	24.24%	24	21.21%	21	99

Showing rows 1 - 4 of 4

Q3.7 - What length of time do you prefer for hands-on workshops? rank the order--1 is highest you do not have to rank them all



#	Field	1	2	3	4	5	Total
1	2 hours	58.89% 53	24.44% 22	3.33% 3	4.44% 4	8.89% 8	90
2	3 hours (current time)	41.11% 37	42.22% 38	6.67% 6	6.67% 6	3.33% 3	90
3	4 hours	8.82% 6	8.82% 6	77.94% 53	2.94% 2	1.47% 1	68
4	6 hours	3.13% 2	12.50% 8	1.56% 1	75.00% 48	7.81% 5	64
5	Full day	10.61% 7	4.55% 3	6.06% 4	1.52% 1	77.27% 51	66

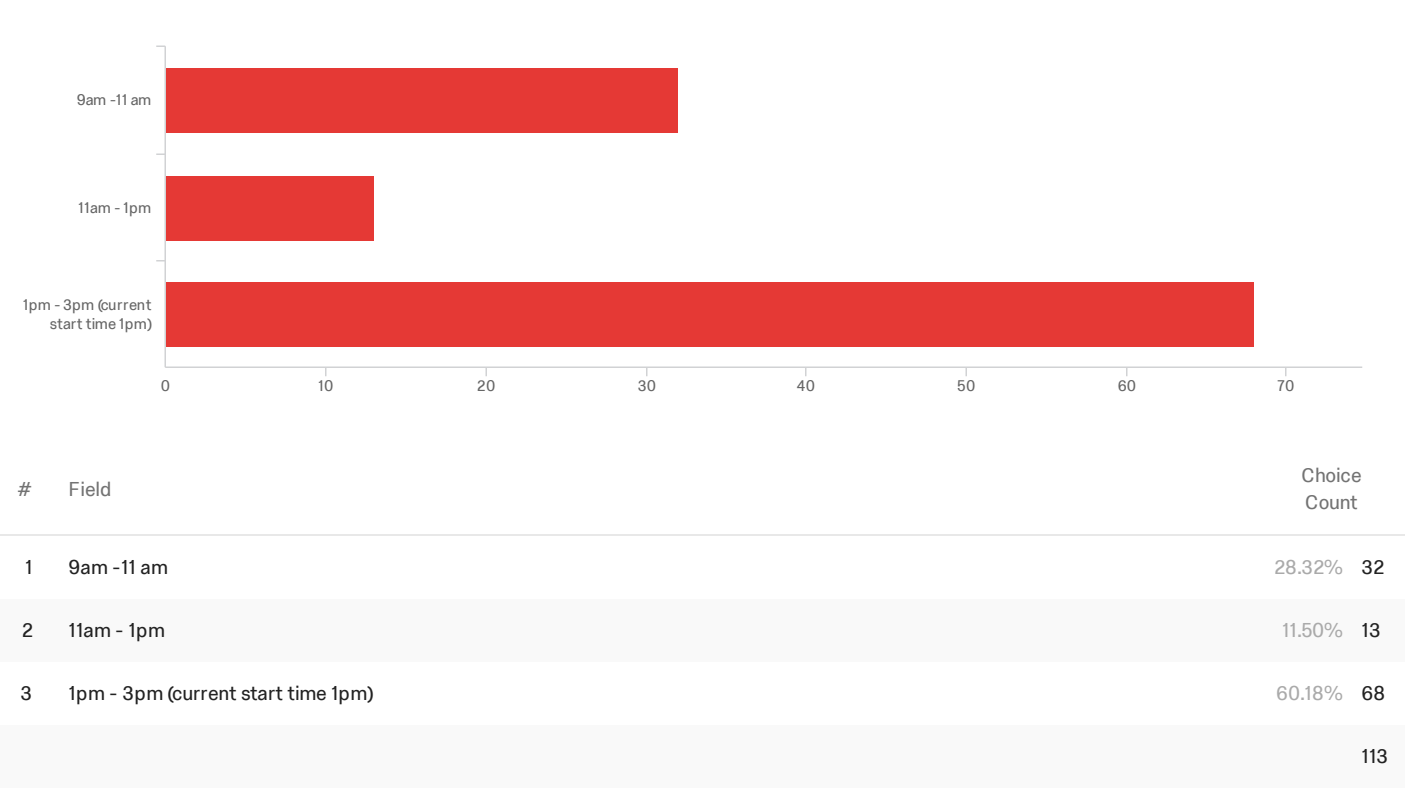
Showing rows 1 - 5 of 5

Q3.8 - What is your preferred day of the week for hands-on workshops? rank the order--1

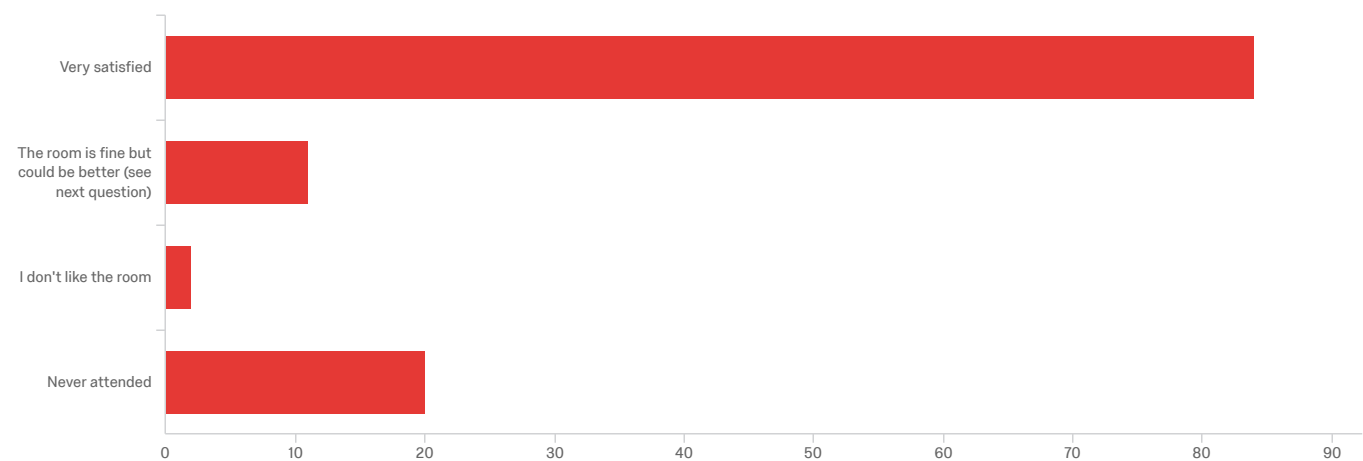
is highest you do not have to rank them all



Q3.9 - What is your preferred START time for hands-on workshops?



Q3.10 - How satisfied are you with the MBIS workshop classroom?



#	Field	Choice Count
1	Very satisfied	71.79% 84
2	The room is fine but could be better (see next question)	9.40% 11
3	I don't like the room	1.71% 2
4	Never attended	17.09% 20

117

Showing rows 1 - 5 of 5

Q3.11 - What would improve the classroom environment?

What would improve the classroom environment?

no

sometimes too warm

It can sometimes be hard to hear the speaker when you are sitting in the back row.

Maybe have a screen mirroring option on the computers on this desks if you are using your own computer.

no

Maintain temperature

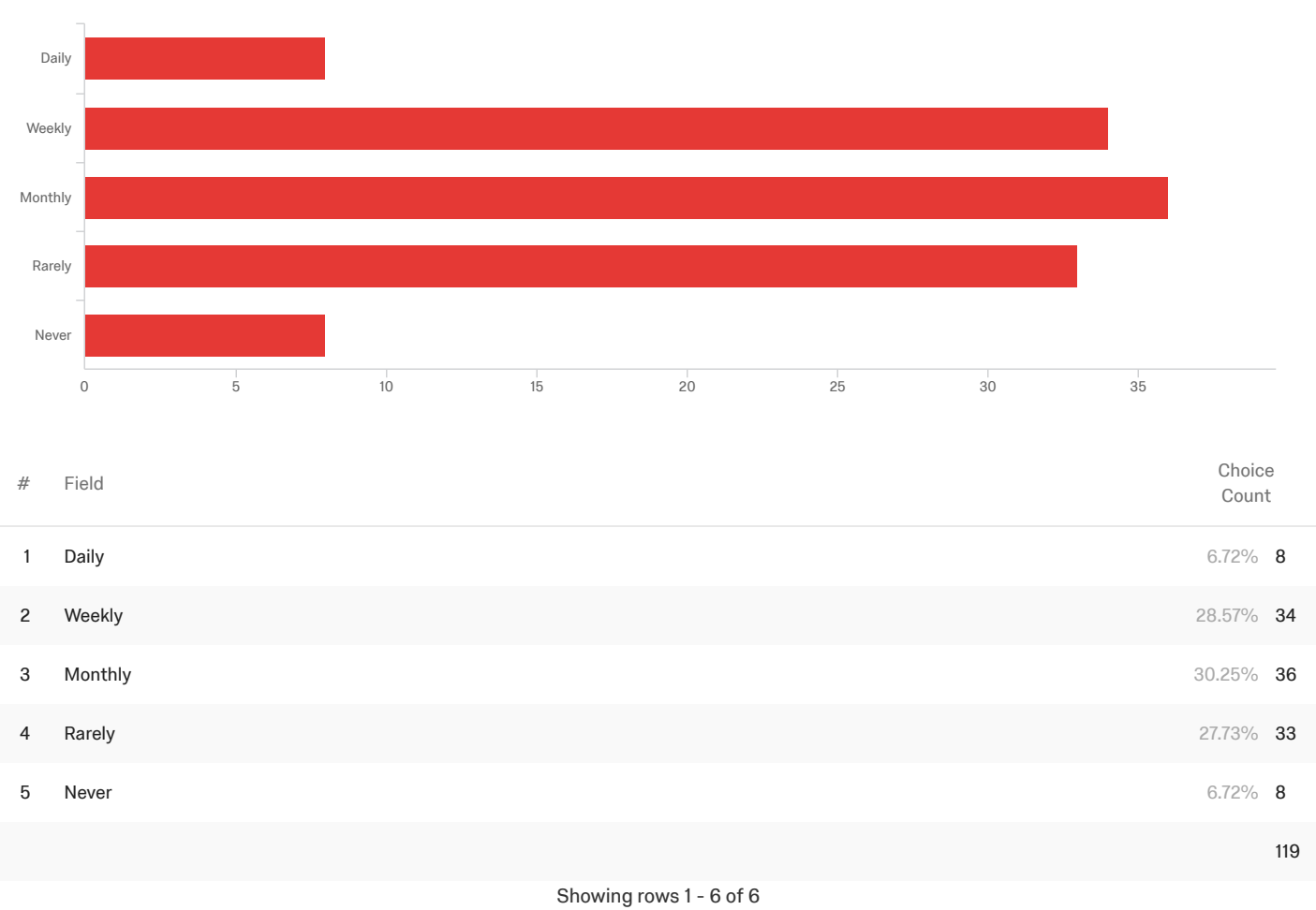
It's fine.

Larger

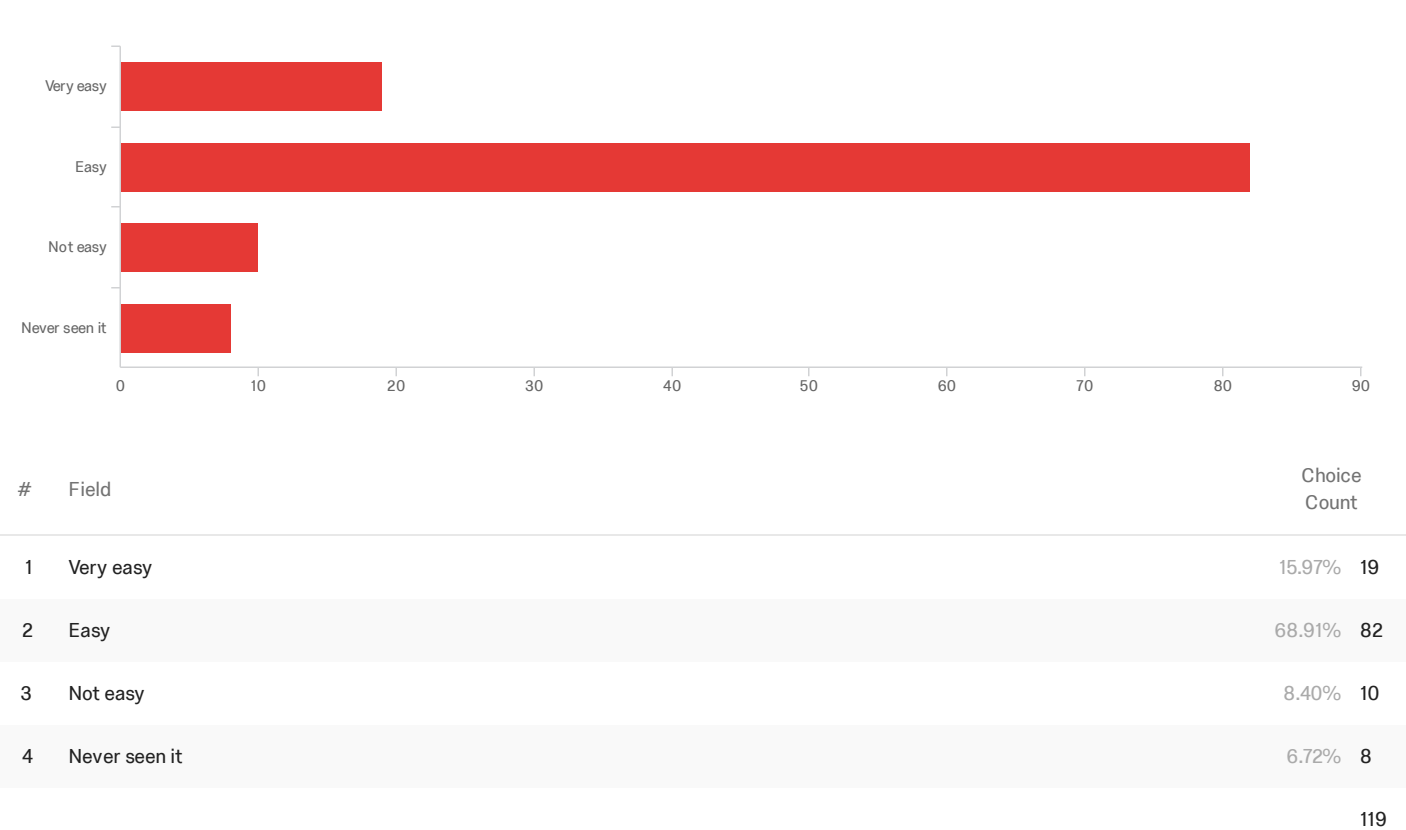
Could be a bit larger for workshops with larger crowds. Also could have a mixture of stations with and without computers to accommodate both those who wish to use the lab computers and those who want to use their personal laptops.

Showing records 1 - 9 of 9

Q4.2 - How often do you use some part of the MBIS website? (www.hsls.pitt.edu/molbio)



Q4.3 - How easy is it to find what you need on the MBIS website?



Showing rows 1 - 5 of 5

Q4.4 - Is there anything missing from the MBIS website that you wish was there?

Is there anything missing from the MBIS website that you wish was there?

I personally do not use the site often but lab members do.

N/A

The MBIS website is poorly organized since the upgrade. It takes longer to find things.

no

not at this time

Tutorial for some of some softwares such as ingenuity pathway analysis, metacore, etc. Could be recording of the courses that were not able to attend

Maybe a more descriptive and flashy (to call everyone's attention) button or link to HSLS software.

descriptions of the workshops

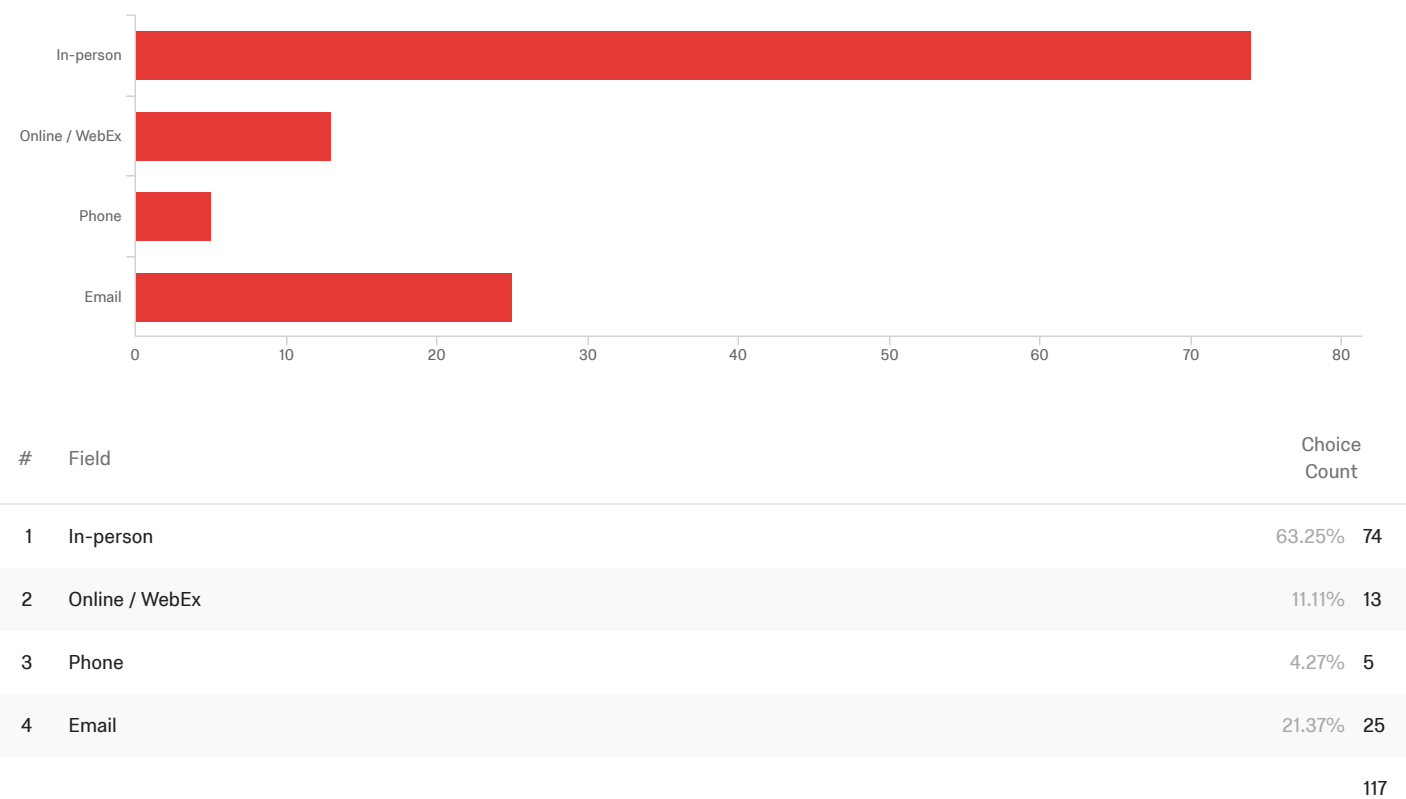
not sure: still adapting to new site

Level of comfort of use is not there yet.

N/A

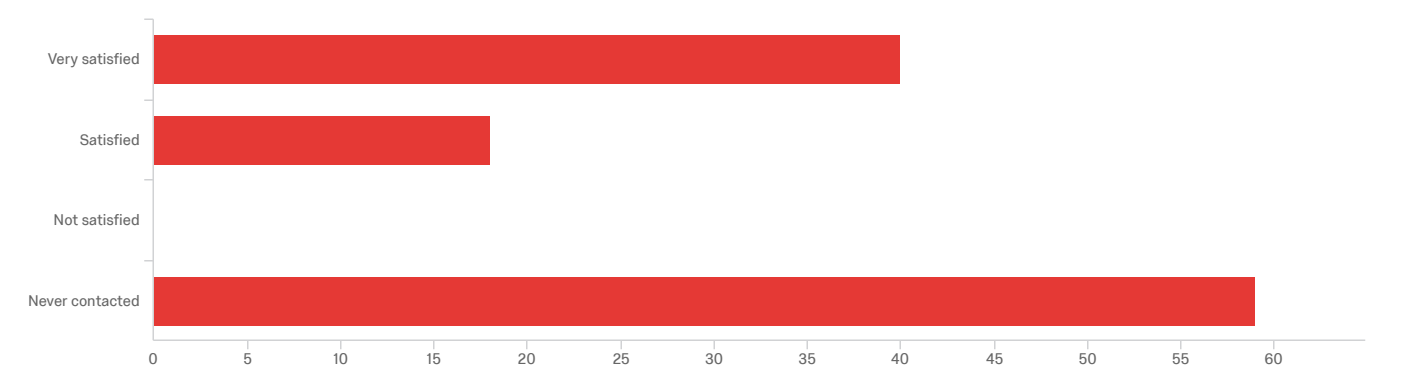
Showing records 1 - 11 of 11

Q5.2 - What is your preferred method for consultations, whether you've had one or not?



Showing rows 1 - 5 of 5

Q5.3 - If you've had an in-person consultation with MBIS, how satisfied are you with the experience?

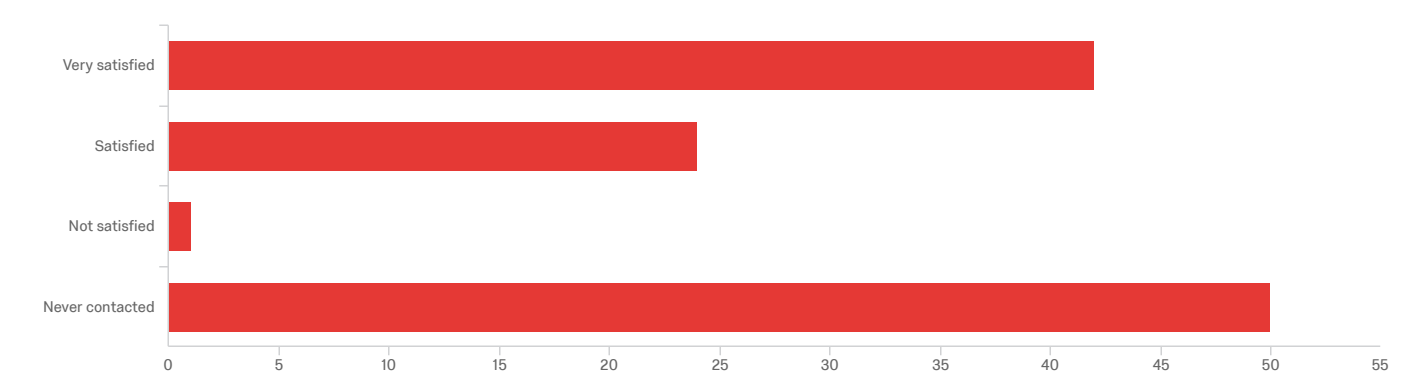


#	Field	Choice Count
1	Very satisfied	34.19% 40
2	Satisfied	15.38% 18
3	Not satisfied	0.00% 0
4	Never contacted	50.43% 59

117

Showing rows 1 - 5 of 5

Q5.4 - If you've contacted MBIS by phone or email, how satisfied are you with the speed of response?



#	Field	Choice Count
1	Very satisfied	35.90% 42
2	Satisfied	20.51% 24
3	Not satisfied	0.85% 1
4	Never contacted	42.74% 50

117

Showing rows 1 - 5 of 5

Q6.2 - What do you find most valuable about MBIS services & resources?

What do you find most valuable about MBIS services & resources?

Mainly IPA analysis, cytoscape and RNAseq analysis, and all other genomic sources are also required which are available MBIS.

Training on data services/software

Being updated about new softwares/ techniques

bioinformatic softwares

Resources are useful and help available when needed

Personal consultation

That the software is available to researchers throughout the University at no charge.

Easy to access and utility of information provided

Instruction and advice

Workshops and hands on class explaining software

Availability and tools and instruction on how to use them to enable me to perform my research.

N/A

It provides a good amount of needed software and good access to a large amount of information.

Help using CLC Genomics. Thanks Ansuman

The hands on training is excellent way to learn. The faculty have done a great job by going through the basics. For a person new to the subject its excellent to have something like this available in the university.

good quality

Software availability is great - having to purchase all this on our own would be a huge cost and probably prohibit users from gaining access. Classes are also great - I recommend them frequently to people Help from the staff (Ansuman and Carrie) is invaluable - having them to reach out to is a huge help to people and I frequently recommend people get in touch directly

bioinformatics tools are very expensive, it's extremely valuable to have access to them at no cost to our lab. expertise of people at MBIS is also very valuable to us.

The class on using clc and the consult service

It is comprehensive and up-to-date.

Lots of great resources and tutorials

What do you find most valuable about MBIS services & resources?

Hands on instruction and walk-throughs

software

They are easy to find and use once you know where to look.

Good training and sophisticated software

Availability of essential software tools along with a great training service and wonderful assistance.

Have very useful resources, personnel very well informed and very attentive.

The expertise and support from Ansuman and Carrie about software provided by HSLS. I also think it is very valuable all of the workshops that the library has to display their software selection.

I found the RNA-Seq workshop to be extremely helpful in introducing me to the CLC genomics workbench software. Both Ansuman and Sri were also great resources and met with me individually to help me with my project. I like that they didn't just do the work for me but explained what I needed to do and were able to help check my work. They also encouraged me to learn command line tools which I have started. A great team!

many data analysis software, paper figure drawing software

Access to software packages and also protocol resources

workshops and software

Correlation Engine

In-person instruction

many valuable analysis software for my study

Great resources with very knowledgeable and supportive staff

All of the MBIS services and resources are highly relevant and valuable given the current biomedical research trends. Most importantly, the MBIS staff are very knowledgeable, highly efficient and extremely helpful, making it possible for many of us to acquire the working knowledge to utilize MBIS softwares in remarkably short time.

Provide valuable information in how the software packages maximize data extraction

Up to date with software offerings.

Free commercial software

Digital access is generally very good though sometimes I still get to a dead end for digital access. Great staff

The fact that you guys spend so much time staying up to date with resources and making sure we have them available... so we don't have to.

The resources are available.

What do you find most valuable about MBIS services & resources?

learning how to use the resources available

Willingness and excitement to help

Helps the research pace.

The provide very useful software (and tech support) that our lab needs. This translates directly into saving money in the lab for other experiments.

software for pathway analysis.

In person hands on tutorials

Information on the Website, such as learning materials; Workshops; licensed tools.

a lot of resources available

I think this is an incredible resource for the University community and one that I will definitely be using more in the very near future. I described the MBIS software and resources in a recent "Facilities and Equipment" section for a grant proposal.

ansuman and carrie

Showing records 1 - 53 of 53

Q6.3 - What frustrations have you had with MBIS services & resources?

What frustrations have you had with MBIS services & resources?

Not being able to work in a real-world/ hands on scenario (which is changing I believe)

None

Unable to figure out the best option So personal consultation helps a lot

For some reason I always have trouble finding the seminar schedule when I want to refer people to it.

none

Finding a person available to talk to.

None to date.

N/A

The information needed to use any software requires considerable offsite searching. With the limited time that the library has it's probably too difficult for it to provide a more efficient workshop.

Im not frustrated

none

no

Limited licenses - trying to get onto Partek and # of users exceeds limit.

none at this time

Bias towards commercial pipelines, and a focus on outcomes without explaining the theory.

They are not overly advertised, so a little more advertisement would be nice.

Get connect with cloud from upmc computer

None

TRANSFACT does not always work on my browser and I have to delete cookies and take additional steps that make it difficult to access.

Some of the material is covered quickly in RNA-Seq and transcription courses but its tough to fit everything in 3hrs. Its complicated and requires individuals to actually be engaged and not learn passively looking at powerpoint. Not a complaint really there is just alot of material. I like the examples used in the workshops.

so far it's good

What frustrations have you had with MBIS services & resources?

no time to participate! Webinars to watch whenever would be helpful.

no

No frustration. They are doing great!

None.

0

Less than complete documentation to install software

being charged for papers that turn out to be useless by interlibrary loan (I think this is now free); quality of scanned material,

I haven't used them much to be able to say.

none

The in class workshops are unclear (too fast), and not good for Mac users (classroom equipment is PC only).

I wouldn't say it is a frustration, but there are a lot of offerings that I am not always clear on relevance to my area of focus. I don't always get a clear understanding from the descriptions.

The only frustration is that I didn't know about it earlier. I am a new faculty member. I purchased several of software packages you offer when I got here because I didn't know you offered them.

I did once or twice try to use Lasergene and a license wasn't available at the time, but generally I have not had a problem accessing the resources I wanted.

really none

Showing records 1 - 35 of 35

What frustrations have you had with MBIS services & resources?

Not being able to work in a real-world/ hands on scenario (which is changing I believe)

None

Unable to figure out the best option So personal consultation helps a lot

For some reason I always have trouble finding the seminar schedule when I want to refer people to it.

none

Finding a person available to talk to.

None to date.

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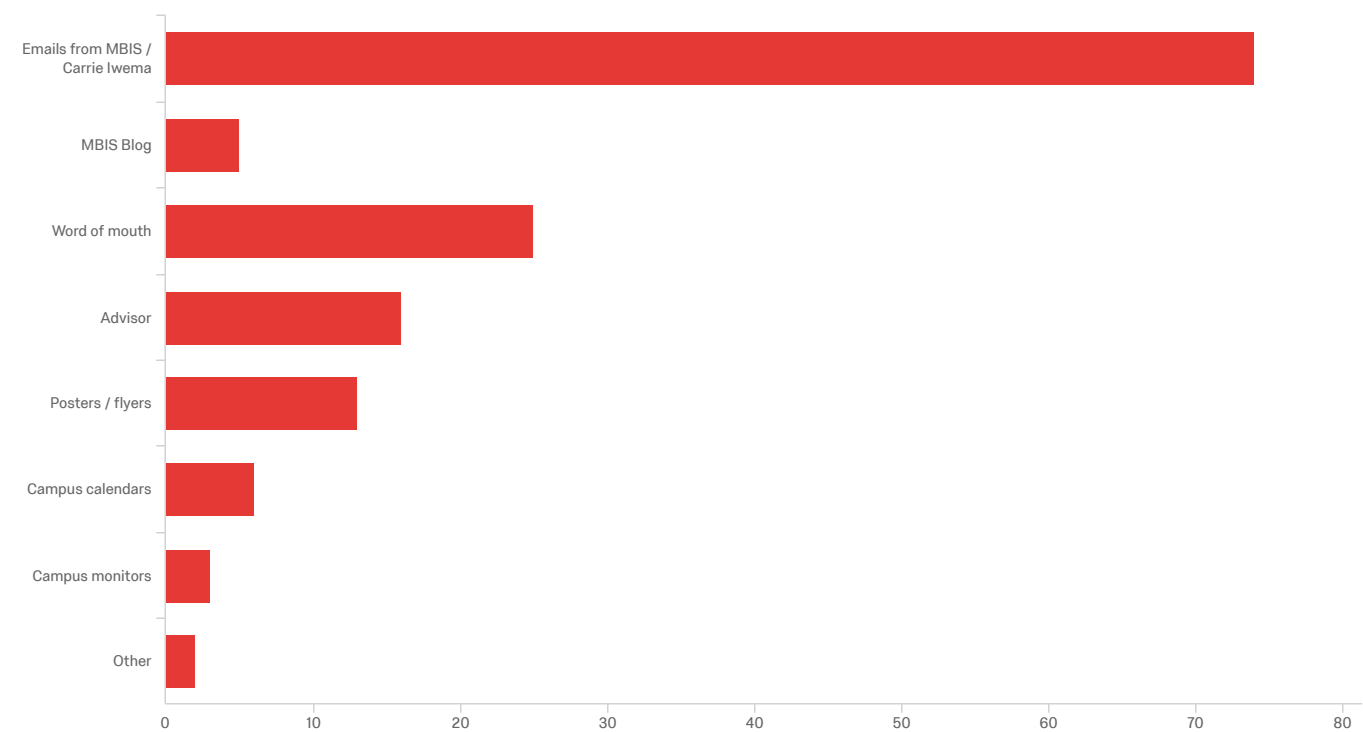
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really none

Showing records 1 - 35 of 35

Q6.4 - How do you find out about MBIS services & resources? (select all that apply)



#	Field	Choice Count
1	Emails from MBIS / Carrie Iwema	51.39% 74
2	MBIS Blog	3.47% 5
3	Word of mouth	17.36% 25
4	Advisor	11.11% 16
5	Posters / flyers	9.03% 13
6	Campus calendars	4.17% 6
7	Campus monitors	2.08% 3
8	Other	1.39% 2

144

Showing rows 1 - 9 of 9

Other

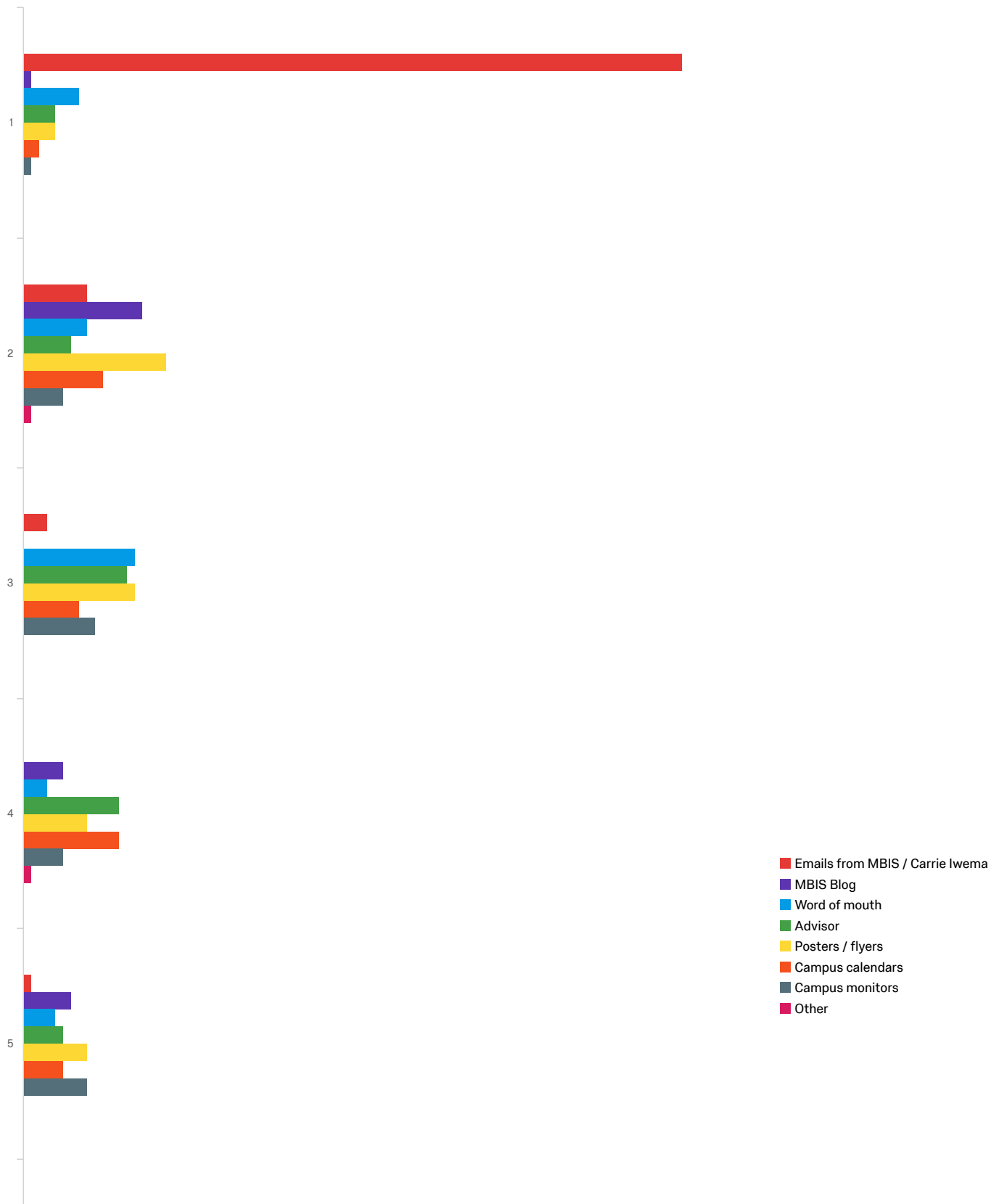
Other

Flash Class

cruising the library website

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Q6.5 - What do you think is the most effective way to advertise MBIS services & resources? rank the order--1 is highest you do not have to rank them all





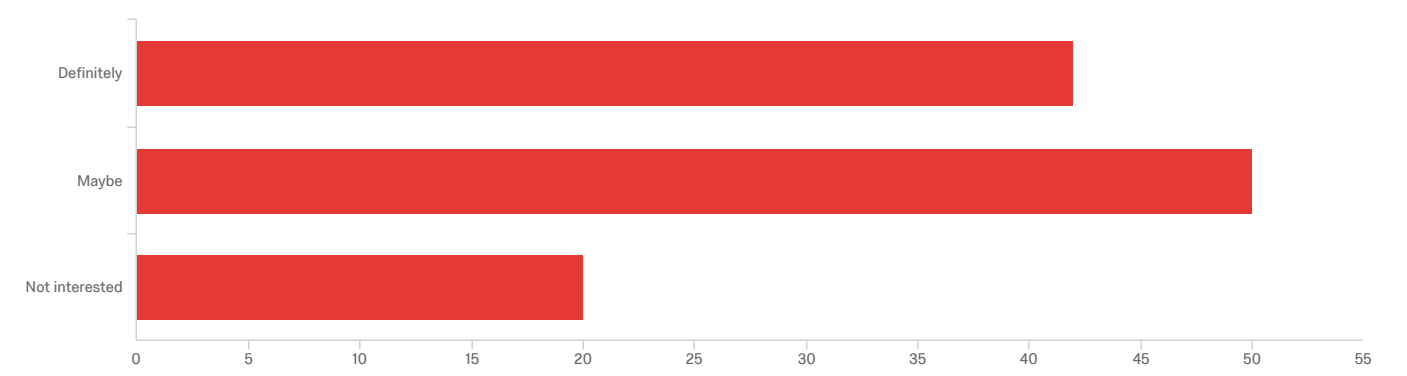
#	Field	1	2	3	4	5	6	7	8
1	Emails from MBIS / Carrie Iwema	82.18% 83	7.92% 8	2.97% 3	0.00% 0	0.99% 1	1.98% 2	0.99% 1	2.97%
2	MBIS Blog	2.17% 1	32.61% 15	0.00% 0	10.87% 5	13.04% 6	10.87% 5	17.39% 8	13.04%
3	Word of mouth	15.56% 7	17.78% 8	31.11% 14	6.67% 3	8.89% 4	17.78% 8	2.22% 1	0.00%
4	Advisor	8.16% 4	12.24% 6	26.53% 13	24.49% 12	10.20% 5	8.16% 4	6.12% 3	4.08%
5	Posters / flyers	7.14% 4	32.14% 18	25.00% 14	14.29% 8	14.29% 8	1.79% 1	5.36% 3	0.00%
6	Campus calendars	3.92% 2	19.61% 10	13.73% 7	23.53% 12	9.80% 5	19.61% 10	7.84% 4	1.96%
7	Campus monitors	2.33% 1	11.63% 5	20.93% 9	11.63% 5	18.60% 8	11.63% 5	23.26% 10	0.00%
8	Other	0.00% 0	14.29% 1	0.00% 0	14.29% 1	0.00% 0	0.00% 0	0.00% 0	71.43%

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Other

Other
You need a mechanism to notify new faculty
Showing records 1 - 1 of 1

Q6.6 - Would you be interested in workshops scheduled specifically for your lab/department?



#	Field	Choice Count
1	Definitely	37.50% 42
2	Maybe	44.64% 50
3	Not interested	17.86% 20
		112

Showing rows 1 - 4 of 4

Q6.8 - Any additional comments?

Any additional comments?

As in the past, we will contact MBIS contacts if there is a need. Thank you.

Thanks for your help

None

no

we are very pleased to have access to this resource, it's a pleasure working with the faculty and staff and the offerings are an extremely valuable resource

I had never accessed or analyzed RNAseq data myself. After the clc workshop and 2 consults I had all the data analyzed almost a complete manuscript prepared. I was shocked (positively) at how good the education and assistance was.

Thanks!

Maybe the library should have a short workshop displaying all of the software and services available from the molecular biology section. It is useful to know what all of the other software can do even if I don't need them right now.

Many thanks for your superb jobs, Ansuman and others!!

Ansuman does a great job teaching modern bioinformatics techniques to physicians.

Could slideshows used by the presenters be made available to attendees. I'm visually impaired and it is often hard for me to follow slideshows as I can't always see all the details or the presenter changes slides too fast for me to read everything.

The best day/time for the workshop varies based on the semester (class days and times vary)

This is a great resource. If there is anyway you could target new faculty to notify them about this, that would be awesome. I purchased three software packages when I got here that I could have got for free. Thanks, Jon

I'm generally quite impressed with the HSLS and MBIS services available at Pitt, which compare very favorably to other institutions I've attended.

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End of Report