

HiC Workshop Feedback Survey



QUESTIONS

RESPONSES 17

17 responses



- SUMMARY
- INDIVIDUAL

Accepting responses ☒

About you

Email address

17 responses

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May we contact you by email in the future to take part in user research activities?

17 responses

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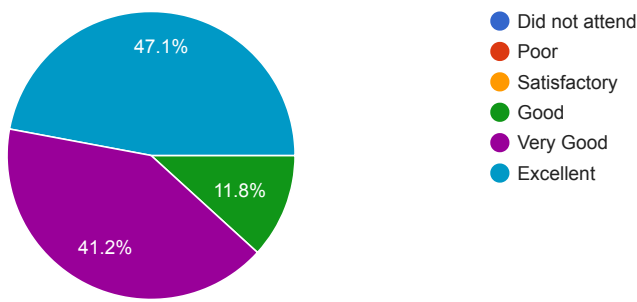
QUESTIONS

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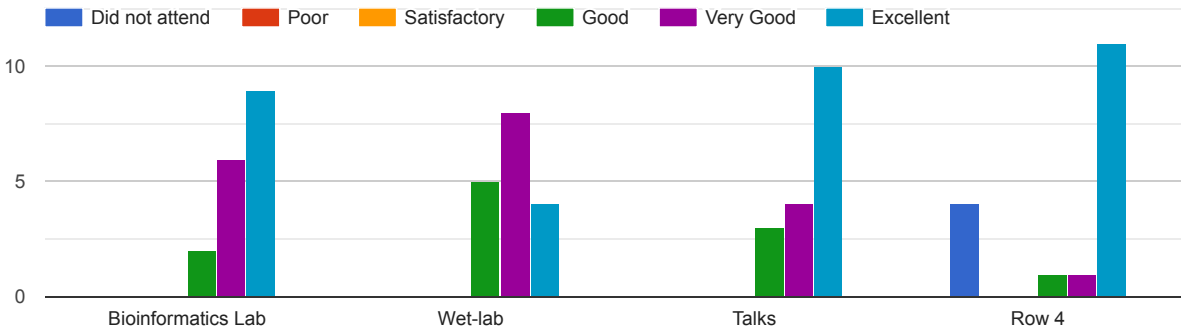
Course content

Please tell us your overall rating for the entire course.

17 responses



Please rate each section of the course.



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QUESTIONS

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obtain enough data at the end. During the bioinformatics lab there are some sections that could be explained with more extension because it could be good to understand the implications of use the appropriate parameters.

Wet-lab is a little bit difficult with a lot of people.

I liked the course but sometimes more time is necessary to improve both lab or in silico understanding.

I think different bioinformatic or wet-lab backgrounds in the students determine the effectiveness of the workshop. Personally I think bioinformatic tools explanation were very fast and requires additional time.

To program more practical parts after lunch so we can move and wake up from digestion

What was the best part of the course?

17 responses

Last day of bioinformatics, R session

the integration in the experimental part

Wet-lab

Bioinformatics lab.

The best part of the course was know all the logarithms needed to analyze Hi-C data

Both, bioinformatics and lab were excellent.

The first six sections of the bioinformatics lab

The use of just a minimal set of data to advance in the bioinformatics lab

the personalized attention was

Complementing the learning of both wet lab and bioinformatics was excellent.

Seeing from beginning to end the experimental generation and the computational analysis of Hi-C data.

People of the course make me feel really comfortable and the practice was very util in my research

The talks about this new tech and area of research.

Get involved with the tools for Hi-C analysis. Get an update of how to manage data and learn some programming.

To being able to follow the all the HiC data analysis steps and to identify possible bias sources both experimental and how to filter them. And how to interpret them. The talks from the instructors were very useful as they provided examples from their own research projects.

I will say that the best part of this course was the whole bioinformatics part, because I did not have expertise in this area. The instructors were very clear and very supportive. I really enjoyed working in the computer, condong and all that stuff, It was really fun and didactic

All helpers were 100% willing to help and support at all moments

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I think that is necessary focus and to get better the explanations in Bioinformatic

R

The worst part of the course was the little time there was to understand each command

All course was great.

Differential interactions

The wet lab protocol could be optimized

the time , is too much knowledge for only a week, but the instructors they did it great despite of that

Lack of some lab equipments caused losing time during the wet lab.

There wasn't really a "worst" part, but perhaps it would be useful to have a space between sessions (I know it's really difficult to put together a workshop schedule, but perhaps it could be instead of a coffee break) where a discussion about applications of Hi-C analysis could take place; not necessarily from the workshop staff, maybe students could propose/ask potential ways to implement the Hi-C technique in the context of biological research projects.

The extraction hood

Everything was good actually but probably we need more time to improve lab skills.

The fast pace

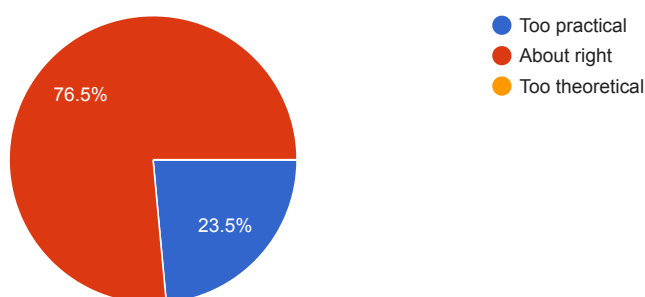
I was unable to install the packages on R studio so I could not work on the last practical part. But I think I might be able to perform this part later on my own.

Not sure I wouldn't say that the workshop had a "worst part", everything was very good, amazing quality.

The extraction hood was not working and that was bad because we worked with toxic substances

The balance of theoretical and practical content across the course was

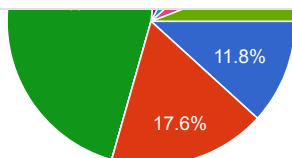
17 responses



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- Frequently
- only R
- I used R and bash but it was interesting the part of Docker and H...
- some of them. The basic tools that...

Other (please specify)

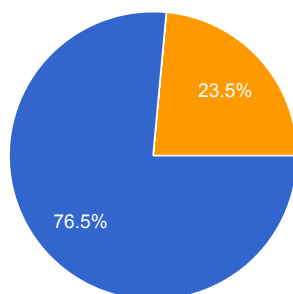
2 responses

its my first time with HiC software

Probably my impressions are skewed because of expertise training on wet lab but deficient in programming language and interfaces.

Will you use the tools and/or data resources covered in the course in your future work?

17 responses



- Yes
- No
- Maybe

Comments

3 responses

Definitely the learning will be useful for my future career as scientist.

Thanks to this course I will front the bioinformatic black box very well and I learn a lot

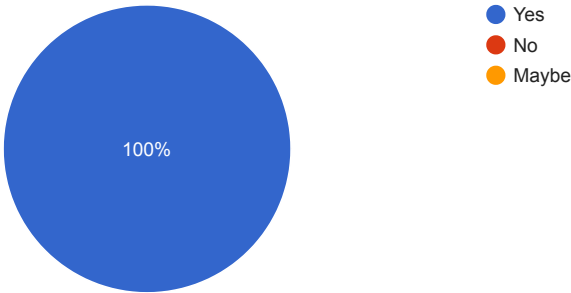
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1 / responses



Comments

5 responses

- You did a great job! Thanks for create this kind of workshops in Mexico.
- thanks
- Súper yes!
- Thanks all the organizers and instructors for this amazing course
- Absolutely, it was a great experience in every aspect. Since first day the whole experience was terrific: the course, the talks, the wet-lab part, the supportative staff, everything.

Course logistics

The overall course organisation (including: registration, accommodation, assistance) was:

17 responses

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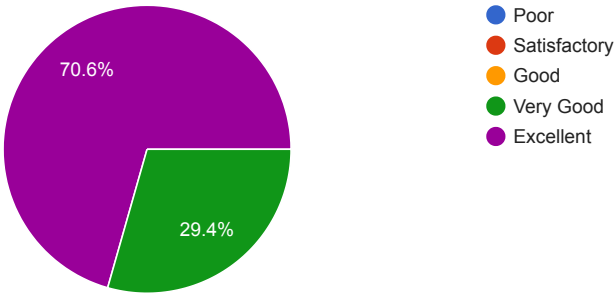
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The breakfast at hotel always was the same.

The catering provided during the course was:

17 responses



Comments

1 response

setbacks were during the days of the course are not related to organizers and additional employees.

The accommodation you stayed in during the course was:

17 responses

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2 responses

I did not used the accommodation
does not apply

Any other comments?

2 responses

I loved the course, thank you so much for share your experience and knowledge.
I am very grateful for the oportunity to participate in the workshop.

Thank You