

# Bioinformatics infrastructure survey

Nick Loman (Birmingham, UK) and Tom Connor (Cardiff, UK) would like to provide evidence about the current state of bioinformatics data infrastructure for a grant application. We would really appreciate two minutes of your time to give us some feedback about your experiences doing bioinformatics.

(The anonymous responses will be available for all to see after the form is submitted, so please don't write anything you wouldn't want others to see. It would be nice to offer the responses for people to analyse and reuse. If you don't like that idea and you already added information to the form, Google will let you edit your response any time.).

## Are you located in the UK?

- ☐ Yes
- ☐ No
- ☐ Is Scotland still in the UK?

## How would you rate your level of bioinformatics expertise (0 = total n00b, 10 = Heng Li) ?

1 2 3 4 5 6 7 8 9 10

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## What things most frustrate you or limit your ability to carry out bioinformatics analysis?

Enter as many or as few as you wish

## Do you regularly use online genomic sequence resources e.g. NCBI or EBI to combine with your own data to perform integrated analysis?

- ☐ Yes
- ☐ No

## If no, why not?

## What is important when choosing which software to use?

- ☐ Already installed on server
- ☐ Best for job

- ☐ Quickest
- ☐ Word of mouth recommendation
- ☐ Graphical interface
- ☐ Good documentation
- ☐ Used in similar analysis
- ☐ Other:

**Where do you most often perform bioinformatics analysis?**

- ☐ Personal computer (laptop/desktop)
- ☐ Lab server
- ☐ Departmental server
- ☐ University server/cluster
- ☐ Cloud
- ☐ Other:

**What problems running software if any do you most often encounter with this solution?**

**If you train students, please say what in your view is the biggest challenge for training students in bioinformatics?**

Submit

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