

GCC 2021 BoF, Wednesday, July 7th

Addressing common misconceptions about Galaxy

<https://app.slack.com/client/T0222FLLLFQ/C02572RGA1G>

Participants (with a misconceptions they have encountered)

- Hans-Rudolf Hotz
 - No one is using Galaxy in the US
- Simon
 - Galaxy is only for teaching
 - Galaxy can't be used for serious research
- Gareth
 - Galaxy is only for microbes / small datasets
- Björn:
 - Galaxy is not used by serious bioinformaticians. Not for real scientists.
 - Which audience are we trying to address misconceptions? Are “data scientists” who we are trying to convince to use Galaxy more?
 - Answer: Researchers, institutional bioinformaticians, institute heads / funders

added later:

- Anne Fouilloux
- Johan Gustafsson
- Sarah Williams
- Sharon Elaine D'Souza
- Ross Lazarus

How can we tackle these misconceptions

1) Simon: *More advanced education.* There are a lot of “Basic Galaxy” or “Galaxy 101” tutorials but there are very few that address intermediate or advanced Galaxy topics. It would be really good to see some tutorials that tackle “Galaxy at scale” or “Advanced Galaxy interface techniques” or “Advanced workflows” etc.

2) Simon: *Really good user stories.* We all know of good user stories from our servers. We could promote these stories around different communities. With serious publicity and highlighting of these researchers and their work. Can we target non-Galaxy seminar series etc. Ask the power users to be “Galaxy Missionaries” (maybe a poor choice of words) in their communities or at conferences like ISMB or ABPHM or PAG etc etc.

3) Simon: *Talk about Galaxy as a tool dissemination vehicle.* Do you want to get your tool to a massive audience and get lots of citations? Make it work on Galaxy! We can help.

4) Bigger focus on cmd line access to Galaxy? Together with community champion bioinformaticians (including science driver projects / initiatives). Education on Galaxy API and language bindings.

5) Björn: promote Galaxy as a data management system

6) Johan: *better / targeted / tailored promotion of interactive tools* to communities as the connection between wrapped tools and flexible bioinformatics using R/python?

- Combined with structured community onboarding / training...?

7) Simon: address different audience differently to tackle the misconceptions

- Researchers/Life scientists
- Data scientists/Bioinformaticians
- Bioinformatics core facilities
- Funders
- Others?

8) Simon: promote Galaxy as a source for help

9) Björn: talk to / approach the big projects (use cases: VGP, Human Cell Atlas)

10) <your idea>

zoom chat

08:14:01 From Björn Grüning to Everyone : Hi Sarah!

08:14:27 From Sarah Williams to Everyone : Hi! Took me a while to find the link :)

08:38:49 From Sharon Elaine D'Souza to Everyone : I would like to say I also had a misconception that in Galaxy there is no coding involved. But by attending the researchers session I learned that people who can code are free to choose their own tools from the tool sched. Maybe these videos should be promoted more so that end users have a better understanding.

08:39:45 From Björn Grüning to Everyone : Sharon, thanks for sharing! Do you have an idea how we can communicate that better? :)

08:40:18 From Sharon Elaine D'Souza to Everyone : Brief video introductions particularly on YouTube can help

08:40:41 From Sharon Elaine D'Souza to Everyone : according to me. Happy to provide some insight:)

08:40:57 From Simon Gladman to Everyone : You tube has been a boon to us in the training space. Using it for promotion is a great idea Sharon!

08:41:14 From Sharon Elaine D'Souza to Everyone : Thank you

08:41:31 From Simon Gladman to Everyone : Can you see the document?

08:41:37 From Simon Gladman to Everyone :
https://docs.google.com/document/d/1UlrZWMnqJxQtHgmyAi-0q_sPnKE7401MoM1XPxnDQGg/edit

08:42:13 From Sharon Elaine D'Souza to Everyone : Yes we can

08:42:47 From Gareth Price to Everyone : thanks everyone, great discussion. Can't imagine how much we would have shared if we'd done this around a pub table in Ghent?!?! That said, daycare calls - see you in a couple of hours online (with a 4yr on my lap)

08:43:59 From Sarah Williams to Everyone : Having come recently to galaxy - I've had misconception that I'd need to re-learn and restructure my familiar workflows and adapt them to 'galaxy' way (using only galaxy available tools). Written domain-specific examples with modern tools have helped there.

08:45:18 From Johan Gustafsson to Everyone : +1

08:46:12 From Sharon Elaine D'Souza to Everyone : One way to promote Galaxy can also be by targeting participants of the iGEM competition.

08:46:40 From Sharon Elaine D'Souza to Everyone : These tools can prove to be very useful to these contestants.

08:46:47 From Björn Grüning to Everyone : Sarah, what has helped you to overcome that? Just writing tools?

08:47:42 From Björn Grüning to Everyone : and to be honest, your fears are true, you are always restricted to the tools in Galaxy - but we can explain it why this is. Its because of security and because you are not alone on that server. Are we not explaining that enough?

08:48:16 From Simon Gladman to Everyone : I think we are. I think it all just needs to be a continuous process.

08:48:19 From Sarah Williams to Everyone : I haven't even got that far with galaxy yet - but seeing the focussed things like human cell atlas galaxy with a lot of familiar things listed has helped.

08:48:57 From Simon Gladman to Everyone : ^Good example

08:53:21 From Björn Grüning to Everyone : humancellatlas.usegalaxy.eu/

08:55:01 From Björn Grüning to Everyone : don't want to be the party pooper, but we have only 5min

08:56:45 From Ross Lazarus to Everyone : Good TimeZone everyone

08:56:53 From Sharon Elaine D'Souza to Everyone : thank you bye