

This questionnaire collects your views about how easy/difficult it is to use the SeqAn library. It includes a series of questions that encourage you to think about the ways you need to use SeqAn, and whether it helps you to do the things you need.

Section 1 Background Information

What are you studying / did you study?

computer science, bioinformatics, biotechnology, ...

What describes your work style best?

Systematic Pragmatic Opportunistic

How long have you been using SeqAn?

6 days weeks months years

Do you consider yourself proficient in its use?

To what extent?

Never used, beginner, advanced, expert, ...

Have you used other similar systems?

If so, please name them.

What do you mainly use SeqAn for?

What are typical products you create with SeqAn?

How durable are the products you create?

throw-away / rarely used regularly used and improved other

Section 2 When using SeqAn, what proportion of your time do you roughly spend

... exploring SeqAn's functioning and function scope

0 %

... understanding and debugging code

0 %

... implementing code

0 %

... reorganising and restructuring your code

0 %

Section 3 Questions About the API

While answering the following questions, please think of SeqAn itself and the tools you use while working with it (e.g. your IDE, the online documentation, etc.)

When you need to make changes to your code what are the particular changes that are especially difficult to make? Which ones?

Do some things in SeqAn seem especially complex or difficult to work out in your head (e.g. when combining several things)? What are they?

How clearly do the API components map to bioinformatics? Which parts seem to be a particularly strange way of doing something?

Can you check your progress whenever you like? If not, why not?

Can you go about your task in any order you like, or does SeqAn force you to think ahead and make certain decisions first?

What decisions do you need to make in advance? What sort of problems can this cause in your work?

Do the levels of abstraction¹ used in SeqAn make sense to you? If not, please name the ones that pose the biggest problems and why?

¹ such as String, Dna, globalAlignment, RecordReader, localAlignment, Gaps, Score, Finder, Iterator, length, Align, Reference, Segment, Infix, ...

How much of a programming task can be completed within a single line of code?

Does the amount of code required for a typical task seem just about right, too much, or too little? Why?

Do some kinds of mistake seem particularly common or easy to make? Which ones?

Do you often find yourself making small slips that irritate you or make you feel stupid? What are some examples?

When using SeqAn, is it easy to know what classes and methods to use when writing code?

Are there parts that you really don't know what they mean, but you use them just because it's always been that way? What are they?

Is it possible to easily play around with ideas (e.g. when you aren't sure which way to proceed)?

What features help you to do this?

What stops you from playing around?

Are there parts of SeqAn where some things ought to be similar, but are actually different? What are they?

How easy/difficult is it for you to get started with SeqAn?

What are the learning resources you used most?

What are the learning resources you missed?

Section 4 Personal Opinion

After completing this questionnaire, can you think of obvious ways that the design of SeqAn could be improved? What are they? Could it be improved specifically for your own requirements?

How was it for you to complete this questionnaire?

Send questionnaire