Final Survey

BioStore SEQAN

1 Please give us the first
4 characters of your ID: *ghuu* · · · · · · · · · · ·

2 What did you particularly **like** in the installation process?

> *step-by-step doku for different platforms*

3 What did you particularly **dislike** in the installation process?

4 What did you particularly **like** about SeqAn?

> *tags*

5 What did you particularly **dislike** about SeqAn?

> *unfinished documentation*

6 How would you rate the workshop altogether?

☐	☐	☐	☐	☒
Very bad	Bad	Average	Good	Very good

7 How would you rate the organization of the workshop?

☐	☐	☐	☐	☒
Very bad	Bad	Average	Good	Very good

8 How helpful was the assistance by the SeqAn staff?

☐	☐	☐	☒	☐
Hardly helpful	Below averagely helpful	Averagely helpful	Above averagely helpful	Extraordinarily helpful

9 What do you think about the duration of the workshop?

☐	☐	☒	☐	☐
Far too short	Too short	Good	Too long	Far too long

Final Survey

BioStore   SeqAn

10 How would you rate the pure online tutorials (not their integration in the workshop)?

○	○	○	○	⊠
Very bad	Bad	Average	Good	Very good

11 Why did you attend to this workshop?

⊠   ○   ○

I'm currently working   I'm currently working   I was just curious
on a project where   on a project where I
I'm expected to use   think SeqAn does
SeqAn   the job

Other reason

12 Did the workshop meet your expectations?

Yes, it was great to get in touch with the seqAn staff

13 What functionality of SeqAn are you using?
What functionality do you miss?

ProfileChar, JournalStrings
missiting possebility to store floats in ProfileChar.count

What is / would be your preferred way to develop with SeqAn?

○   ⊠

As a framework   As a library
(create apps)   (include SeqAn
                  headers in own
                  program)   Other

14 Will you use SeqAn in the future?

⊠   ○

Yes, why? →   No, why? →   *Doing a praktikum. If functionality*
                              is missing, I can learn to program it.

15 What do / did you study?

Bioinformatik

16 What is your currently highest degree?

Abitur

Final Survey

BioStore SEQAN

1 Please give us the first
4 characters of your ID: _ _ _ _   • • • • • • • • • • •

2 What did you particularly **like** in the installation process?

> It was pretty easy as the description of how to get it done was quite detailed.

3 What did you particularly **dislike** in the installation process?

> I believe using Windows as the OS is a disadvantage, because the checkout or some other step too a lot of time, which is not the case using Linux.

4 What did you particularly **like** about SeqAn?

> I think it's a good idea and very helpful/useful for Bioinformaticians.

5 What did you particularly **dislike** about SeqAn?

> There is a bunch of things that can be improved.

6 How would you rate the workshop altogether?

☐ Very bad   ☐ Bad   ☒ Average   ☐ Good   ☐ Very good

7 How would you rate the organization of the workshop?

☐ Very bad   ☐ Bad   ☒ Average   ☐ Good   ☐ Very good

8 How helpful was the assistance by the SeqAn staff?

☐ Hardly helpful   ☐ Below averagely helpful   ☐ Averagely helpful   ☒ Above averagely helpful   ☐ Extraordinarily helpful

9 What do you think about the duration of the workshop?

☐ Far too short   ☐ Too short   ☒ Good   ☐ Too long   ☐ Far too long

Final Survey

BioStore   SeqAn

10 How would you rate the pure online tutorials (not their integration in the workshop)?

☐ Very bad   ☐ Bad   ☒ Average   ☐ Good   ☐ Very good

11 Why did you attend to this workshop?

☒ I'm currently working on a project where I'm expected to use SeqAn

☐ I'm currently working on a project where I think SeqAn does the job

☐ I was just curious

[   ]
Other reason

12 Did the workshop meet your expectations?

Not quite. I was actually expecting a little bit more.

13 What functionality of SeqAn are you using?
What functionality do you miss?

[   ]

What is / would be your preferred way to develop with SeqAn?

☐ As a framework (create apps)

☒ As a library (include SeqAn headers in own program)

[   ]
Other

14 Will you use SeqAn in the future?

☒ Yes, why? →   ☐ No, why? →

I think it could save a lot of time while programming as a lot of Algorithms are already implemented.

15 What do / did you study?

As I've ~~tried it~~ made use of it before, I learned especially about recent developments / improvements like SequenceStream

16 What is your currently highest degree?

[   ]

Final Survey

BioStore SEQAN

1 Please give us the first
4 characters of your ID: Z S r C · · · · · · · · · · · · ·

2 What did you particularly **like** in the installation process?

Altogether very detailed explanation what to do

3 What did you particularly **dislike** in the installation process?

minor mistakes { Unstimmonigkeiten zwischen Text und
screen shots (very minor)

4 What did you particularly **like** about SeqAn?

Very many helpful functions and Classes.

5 What did you particularly **dislike** about SeqAn?

Inconsistency

6 How would you rate the workshop altogether?

☐ Very bad ☐ Bad ☐ Average ☒ Good ☐ Very good

7 How would you rate the organization of the workshop?

☐ Very bad ☐ Bad ☐ Average ☐ Good ☒ Very good

8 How helpful was the assistance by the SeqAn staff?

☐ Hardly helpful ☐ Below averagely helpful ☒ Averagely helpful ☐ Above averagely helpful ☐ Extraordinarily helpful

9 What do you think about the duration of the workshop?

☐ Far too short ☒ Too short ☐ Good ☐ Too long ☐ Far too long

Final Survey

BioStore   SEQAN

10 How would you rate the pure online tutorials (not their integration in the workshop)?

☐ Very bad   ☐ Bad   ☒ Average   ☐ Good   ☐ Very good

11 Why did you attend to this workshop?

☒ I'm currently working on a project where I'm expected to use SeqAn

☐ I'm currently working on a project where I think SeqAn does the job

☐ I was just curious

Other reason

12 Did the workshop meet your expectations?

Yes, Completely

13 What functionality of SeqAn are you using?
What functionality do you miss?

as a library, Dna -type is very useful in combination with Profile Char / Missing: Profile Char<Dna>. count als float ode double for ward version.

What is / would be your preferred way to develop with SeqAn?

☐ As a framework (create apps)

☒ As a library (include SeqAn headers in own program)

Other

14 Will you use SeqAn in the future?

☒ Yes, why? →   ☐ No, why? →

Very useful for handling genomic data

15 What do / did you study?

Bioinformatics Bsc

16 What is your currently highest degree?

Abitur

SeqAn — BioStore Workshop, 4th - 6th Sept. 2012
Final Survey

BioStore SEQAN

1 Please give us the first
4 characters of your ID: __ __ __ __ • • • • • • • • • • • •

2 What did you particularly **like** in the installation process?

straight forward

3 What did you particularly **dislike** in the installation process?

svn co is slow

4 What did you particularly **like** about SeqAn?

quite easy to get started, good documented with tutorial

5 What did you particularly **dislike** about SeqAn?

too many global functions, a more OO way would be easier (STL like)

6 How would you rate the workshop altogether?

☐	☐	☐	☒	☐
Very bad	Bad	Average	Good	Very good

7 How would you rate the organization of the workshop?

☐	☐	☐	☐	☒
Very bad	Bad	Average	Good	Very good

8 How helpful was the assistance by the SeqAn staff?

☐	☐	☐	☒	☐
Hardly helpful	Below averagely helpful	Averagely helpful	Above averagely helpful	Extraordinarily helpful

9 What do you think about the duration of the workshop?

☐	☐	☒	☐	☐
Far too short	Too short	Good	Too long	Far too long

Final Survey

BioStore **SEQAN**

10 How would you rate the pure online tutorials (not their integration in the workshop)?

○ Very bad   ○ Bad   ○ Average   ⊠ Good   ○ Very good

11 Why did you attend to this workshop?

○ I'm currently working on a project where I'm expected to use SeqAn

○ I'm currently working on a project where I think SeqAn does the job

⊠ I was just curious

[ ]

Other reason

12 Did the workshop meet your expectations?

✓

13 What functionality of SeqAn are you using?
What functionality do you miss?

n/a

What is / would be your preferred way to develop with SeqAn?

○ As a framework (create apps)

○ As a library (include SeqAn headers in own program)

[ ]

Other

14 Will you use SeqAn in the future?

○ Yes, why? →   ○ No, why? →

depends on the future

15 What do / did you study?

Informatik

16 What is your currently highest degree?

Dipl. - Inform.

Final Survey

BioStore SEQAN

1 Please give us the first
4 characters of your ID: _Zur8_ · · · · · · · · · · · ·

← or similar

2 What did you particularly **like** in the installation process?

It worked! even on Windows with VS !

3 What did you particularly **dislike** in the installation process?

4 What did you particularly **like** about SeqAn?

It is rapidly getting better and easier to program

5 What did you particularly **dislike** about SeqAn?

Non STL - style

6 How would you rate the workshop altogether?

☐ Very bad   ☐ Bad   ☐ Average   ☒ Good   ☐ Very good

7 How would you rate the organization of the workshop?

☐ Very bad   ☐ Bad   ☐ Average   ☒ Good   ☐ Very good

8 How helpful was the assistance by the SeqAn staff?

☐ Hardly helpful   ☐ Below averagely helpful   ☒ Averagely helpful   ☐ Above averagely helpful   ☐ Extraordinarily helpful

9 What do you think about the duration of the workshop?

☐ Far too short   ☐ Too short   ☒ Good   ☐ Too long   ☐ Far too long

Final Survey

BioStore   SEQAN

10 How would you rate the pure online tutorials (not their integration in the workshop)?

☐ Very bad   ☐ Bad   ☐ Average   ☒ Good   ☐ Very good

11 Why did you attend to this workshop?

☐ I'm currently working on a project where I'm expected to use SeqAn

☐ I'm currently working on a project where I think SeqAn does the job

☐ I was just curious

> I could imagine that
> SeqAn can be speed up
> my project

Other reason

12 Did the workshop meet your expectations?

> I would have liked a little bit more detail on how
> your tools (Razers, Mason) work under the hood.

13 What functionality of SeqAn are you using?
What functionality do you miss?

> Nothing yet

What is / would be your preferred way to develop with SeqAn?

☒ As a framework (create apps)

☒ As a library (include SeqAn headers in own program)

Other

14 Will you use SeqAn in the future?

☒ Yes, why? →   ☒ No, why? →

> Probably, depends on how much
> time I have.

15 What do / did you study?

> Physics

16 What is your currently highest degree?

> Diploma

Final Survey

1 Please give us the first
4 characters of your ID: _p h r 0_ . . . .

2 What did you particularly **like** in the installation process?

many possibilities (Systems, Platform, Compiler)

3 What did you particularly **dislike** in the installation process?

Somehow magic; works but I don't now how (at first)

4 What did you particularly **like** about SeqAn?

Usefull / fast /

5 What did you particularly **dislike** about SeqAn?

hard to get an overview of functionality

6 How would you rate the workshop altogether?

☐	☐	☐	☒	☐
Very bad	Bad	Average	Good	Very good

7 How would you rate the organization of the workshop?

☐	☐	☐	☒	☐
Very bad	Bad	Average	Good	Very good

8 How helpful was the assistance by the SeqAn staff?

☐	☐	☐	☒	☐
Hardly helpful	Below averagely helpful	Averagely helpful	Above averagely helpful	Extraordinarily helpful

9 What do you think about the duration of the workshop?

☐	☐	☒	☐	☐
Far too short	Too short	Good	Too long	Far too long

Final Survey

BioStore   SEQAN

10 How would you rate the pure online tutorials (not their integration in the workshop)?

○ Very bad   ○ Bad   ○ Average   ○ Good   ⊗ Very good

11 Why did you attend to this workshop?

○ I'm currently working on a project where I'm expected to use SeqAn

⊗ I'm currently working on a project where I think SeqAn does the job

○ I was just curious

[   ]
Other reason

12 Did the workshop meet your expectations?

Y

13 What functionality of SeqAn are you using?
What functionality do you miss?

Reading and editing standard file formats

What is / would be your preferred way to develop with SeqAn?

⊗ As a framework (create apps)

○ As a library (include SeqAn headers in own program)

[   ]
Other

14 Will you use SeqAn in the future?

⊗ Yes, why? →   ○ No, why? →

See 4

15 What do / did you study?

Bioinformatics

16 What is your currently highest degree?

MSc

Final Survey

BioStore SEQAN

1 Please give us the first
4 characters of your ID: ＿ ＿ ＿ ＿ • • • • • • • • • •

2 What did you particularly **like** in the installation process?

It was just a installation process. Nothing special

3 What did you particularly **dislike** in the installation process?

— / ←—

4 What did you particularly **like** about SeqAn?

Modularity, ~~Ability~~ Functionality

5 What did you particularly **dislike** about SeqAn?

The language of the naming (vars...) sounds like
~~utter~~ marketing. One has to first learn all the meanings
(Fibres, fragmentStore ...)

6 How would you rate the workshop altogether?

Very bad	Bad	Average	Good	Very good
☐	☐	☐	☒	☐

7 How would you rate the organization of the workshop?

Very bad	Bad	Average	Good	Very good
☐	☐	☐	☒	☐

8 How helpful was the assistance by the SeqAn staff?

Hardly helpful	Below averagely helpful	Averagely helpful	Above averagely helpful	Extraordinarily helpful
☐	☐	☐	☒	☐

9 What do you think about the duration of the workshop?

Far too short	Too short	Good	Too long	Far too long
☐	☐	☒	☐	☐

Final Survey

BioStore   SEQAN

10 How would you rate the pure online tutorials (not their integration in the workshop)?

- ☐ Very bad
- ☐ Bad
- ☒ Average
- ☐ Good
- ☐ Very good

11 Why did you attend to this workshop?

- ☒ I'm currently working on a project where I'm expected to use SeqAn
- ☒ I'm currently working on a project where I think SeqAn does the job. *maybe*
- ☐ I was just curious

Other reason

12 Did the workshop meet your expectations?

Jepp.

13 What functionality of SeqAn are you using?
What functionality do you miss?

See 11.

What is / would be your preferred way to develop with SeqAn?

- ☐ As a framework (create apps)
- ☒ As a library (include SeqAn headers in own program)

Other

14 Will you use SeqAn in the future?

- ☐ Yes, why? →
- ☒ *maybe*
- ☐ No, why? →

I know now about the functionality, so I can decide better wether to use for feature programs

15 What do / did you study?

Bioinf

16 What is your currently highest degree?

Bachelor

less data collection would be maybe useful. was a bit too much.

Final Survey

1 Please give us the first
4 characters of your ID: JWZr • • • • • • • • • • •

2 What did you particularly **like** in the installation process?

3 What did you particularly **dislike** in the installation process?

4 What did you particularly **like** about SeqAn?

5 What did you particularly **dislike** about SeqAn?

high knowledge of library needed

6 How would you rate the workshop altogether?

☐	☐	☐	☒	☒
Very bad	Bad	Average	Good	Very good

7 How would you rate the organization of the workshop?

☐	☐	☐	☐	☒
Very bad	Bad	Average	Good	Very good

8 How helpful was the assistance by the SeqAn staff?

☐	☐	☐	☒	☐
Hardly helpful	Below averagely helpful	Averagely helpful	Above averagely helpful	Extraordinarily helpful

9 What do you think about the duration of the workshop?

☐	☐	☒	☐	☐
Far too short	Too short	Good	Too long	Far too long

Final Survey

BioStore SEQAN

10 How would you rate the pure online tutorials (not their integration in the workshop)?

○ Very bad   ○ Bad   ○ Average   ⊠ Good   ○ Very good

11 Why did you attend to this workshop?

○ I'm currently working on a project where I'm expected to use SeqAn

⊠ I'm currently working on a project where I think SeqAn does the job

○ I was just curious

Other reason

12 Did the workshop meet your expectations?

V

13 What functionality of SeqAn are you using?
What functionality do you miss?

alignment related

What is / would be your preferred way to develop with SeqAn?

○ As a framework (create apps)

⊠ As a library (include SeqAn headers in own program)

Other

14 Will you use SeqAn in the future?

⊠ Yes, why? →   ○ No, why? →

speed

15 What do / did you study?

Bioinformatics

16 What is your currently highest degree?

M-S.

Final Survey

BioStore SEQAN

1 Please give us the first
4 characters of your ID: *F4su* • • • • • • • • • • •

2 What did you particularly **like** in the installation process?

The installation

3 What did you particularly **dislike** in the installation process?

—

4 What did you particularly **like** about SeqAn?

It's very powerfull and can be usefull for a lot of things.

5 What did you particularly **dislike** about SeqAn?

Nothing

6 How would you rate the workshop altogether?

Very bad	Bad	Average	Good	Very good
☐	☐	☐	☐	☒

7 How would you rate the organization of the workshop?

Very bad	Bad	Average	Good	Very good
☐	☐	☐	☐	☒

8 How helpful was the assistance by the SeqAn staff?

Hardly helpful	Below averagely helpful	Averagely helpful	Above averagely helpful	Extraordinarily helpful
☐	☐	☐	☐	☒

9 What do you think about the duration of the workshop?

Far too short	Too short	Good	Too long	Far too long
☐	☐	☒	☐	☐

Final Survey

BioStore   SEQAN

10 How would you rate the pure online tutorials (not their integration in the workshop)?

☐ Very bad   ☐ Bad   ☐ Average   ☒ Good   ☐ Very good

11 Why did you attend to this workshop?

☐ I'm currently working on a project where I'm expected to use SeqAn

☐ I'm currently working on a project where I think SeqAn does the job

☒ I was just curious

☐ (blank box)

Other reason

12 Did the workshop meet your expectations?

Definitely !

13 What functionality of SeqAn are you using?
What functionality do you miss?

(blank box)

What is / would be your preferred way to develop with SeqAn?

☐ As a framework (create apps)

☒ As a library (include SeqAn headers in own program)

☐ (blank box)   Other

14 Will you use SeqAn in the future?

☒ Yes, why? →   ☐ No, why? →

(blank box)

15 What do / did you study?

Bioinformatics

16 What is your currently highest degree?

Master in Bioinformatics

Final Survey

BioStore SEQAN

1 Please give us the first
4 characters of your ID: _l_ _Uu_ _l_ _u_ • • • • • • • • • • • • •

2 What did you particularly **like** in the installation process?

Installing the new Xcode 4.4.1 ✓

3 What did you particularly **dislike** in the installation process?

problems with my old Xcode (should be documented, maybe)

4 What did you particularly **like** about SeqAn?

modules (concept of different ...)

5 What did you particularly **dislike** about SeqAn?

6 How would you rate the workshop altogether?

☐ Very bad   ☐ Bad   ☐ Average   ☐ Good   ☒ Very good

7 How would you rate the organization of the workshop?

☐ Very bad   ☐ Bad   ☐ Average   ☐ Good   ☒ Very good

8 How helpful was the assistance by the SeqAn staff?

☐ Hardly helpful   ☐ Below averagely helpful   ☐ Averagely helpful   ☒ Above averagely helpful   ☐ Extraordinarily helpful

9 What do you think about the duration of the workshop?

☐ Far too short   ☐ Too short   ☒ Good   ☐ Too long   ☐ Far too long

Final Survey

BioStore   SEQAN

10 How would you rate the pure online tutorials (not their integration in the workshop)?

⬜ Very bad   ⬜ Bad   ⬜ Average   ⬜ Good   ☒ Very good

11 Why did you attend to this workshop?

☒ I'm currently working on a project where I'm expected to use SeqAn

⬜ I'm currently working on a project where I think SeqAn does the job

⬜ I was just curious

⬜ Other reason

12 Did the workshop meet your expectations?

Yes (100%)

13 What functionality of SeqAn are you using?
What functionality do you miss?

Sorry, I'm a beginner (more or less) ☺

What is / would be your preferred way to develop with SeqAn?

☒ As a framework (create apps)

⬜ As a library (include SeqAn headers in own program)

⬜ Other

14 Will you use SeqAn in the future?

☒ Yes, why? →   ⬜ No, why? →

15 What do / did you study?

Bioinformatics

16 What is your currently highest degree?

PhD

Final Survey

BioStore SEQAN

1 Please give us the first
4 characters of your ID: ___ ___ ___ ___ • • • • • • • • • • • •

2 What did you particularly **like** in the installation process?

streamlined

3 What did you particularly **dislike** in the installation process?

4 What did you particularly **like** about SeqAn?

C++ based, variety of algorithms

5 What did you particularly **dislike** about SeqAn?

Not STL -like. Tries to reinvent STL with global functions and it adds a lot o complexity that seems unnecessary

6 How would you rate the workshop altogether?

☐ Very bad   ☐ Bad   ☐ Average   ☑ Good   ☐ Very good

7 How would you rate the organization of the workshop?

☐ Very bad   ☐ Bad   ☐ Average   ☑ Good   ☐ Very good

8 How helpful was the assistance by the SeqAn staff?

☐ Hardly helpful   ☐ Below averagely helpful   ☐ Averagely helpful   ☑ Above averagely helpful   ☐ Extraordinarily helpful

9 What do you think about the duration of the workshop?

☐ Far too short   ☐ Too short   ☑ Good   ☐ Too long   ☐ Far too long

Final Survey

BioStore   SEQ

10 How would you rate the pure online tutorials (not their integration in the workshop)?

○ Very bad   ○ Bad   ○ Average   ☑ Good   ○ Very good

11 Why did you attend to this workshop?

○ I'm currently working on a project where I'm expected to use SeqAn

○ I'm currently working on a project where I think SeqAn does the job

○ I was just curious

To learn about SeqAn

Other reason

12 Did the workshop meet your expectations?

Yes.

13 What functionality of SeqAn are you using?
What functionality do you miss?

Not using yet.

What is / would be your preferred way to develop with SeqAn?

○ As a framework (create apps)

☑ As a library (include SeqAn headers in own program)

Other

14 Will you use SeqAn in the future?

○ Yes, why? →   ○ No, why? →

Not sure yet. Depends on upcoming projects. The STL - non-compliance is a strong road block.

15 What do / did you study?

De novo assembly

16 What is your currently highest degree?

PhD

Final Survey

BioStore SEQ

1 Please give us the first
4 characters of your ID: __ __ __ __   • • • • • • • • • • • •

2 What did you particularly **like** in the installation process?

3 What did you particularly **dislike** in the installation process?

4 What did you particularly **like** about SeqAn?

Free software, standardized + portable code, no java

5 What did you particularly **dislike** about SeqAn?

6 How would you rate the workshop altogether?

☐ Very bad ☐ Bad ☐ Average ☒ Good ☐ Very good

7 How would you rate the organization of the workshop?

☐ Very bad ☐ Bad ☐ Average ☐ Good ☒ Very good

8 How helpful was the assistance by the SeqAn staff?

☐ Hardly helpful ☐ Below averagely helpful ☐ Averagely helpful ☐ Above averagely helpful ☐ Extraordinarily helpful

9 What do you think about the duration of the workshop?

☐ Far too short ☐ Too short ☒ Good ☐ Too long ☐ Far too long

Final Survey

BioStore   SEQAN

10 How would you rate the pure online tutorials (not their integration in the workshop)?

○ Very bad   ○ Bad   ○ Average   ⊠ Good   ○ Very good

11 Why did you attend to this workshop?

⊠ I'm currently working on a project where I'm expected to use SeqAn

○ I'm currently working on a project where I think SeqAn does the job

○ I was just curious

Other reason

12 Did the workshop meet your expectations?

X yes

13 What functionality of SeqAn are you using?
What functionality do you miss?

What is / would be your preferred way to develop with SeqAn?

⊠ As a framework (create apps)

○ As a library (include SeqAn headers in own program)

Other

14 Will you use SeqAn in the future?
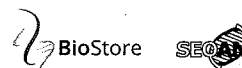
⊠ Yes, why? →

○ No, why? →

15 What do / did you study?

Bioinformatics

16 What is your currently highest degree?

B. Sc.

Final Survey

or similar

A

1 Please give us the first
4 characters of your ID: *R_ps* • • • • • • • • •

2 What did you particularly **like** in the installation process?

had it installed already

3 What did you particularly **dislike** in the installation process?

4 What did you particularly **like** about SeqAn?

The implemented algorithms

5 What did you particularly **dislike** about SeqAn?

Inconsistencies, lack of documentation

6 How would you rate the workshop altogether?

| Very bad | Bad | Average | ☒ Good | Very good |

7 How would you rate the organization of the workshop?

| Very bad | Bad | Average | ☒ Good | Very good |

8 How helpful was the assistance by the SeqAn staff?

| Hardly helpful | Below averagely helpful | Averagely helpful | ☒ Above averagely helpful | Extraordinarily helpful |

9 What do you think about the duration of the workshop?

| Far too short | Too short | ☒ Good | Too long | Far too long |

Final Survey

BioStore SEQAN

10 How would you rate the pure online tutorials (not their integration in the workshop)?

O Very bad   O Bad   O Average   ⊠ Good   O Very good

11 Why did you attend to this workshop?

⊠ I'm currently working on a project where I'm expected to use SeqAn

O I'm currently working on a project where I think SeqAn does the job

O I was just curious

[   ]
Other reason

12 Did the workshop meet your expectations?

yes

13 What functionality of SeqAn are you using?
What functionality do you miss?

Alignment module, I/O, Filtering

What is / would be your preferred way to develop with SeqAn?

⊠ As a framework (create apps)

O As a library (include SeqAn headers in own program)

[   ]
Other

14 Will you use SeqAn in the future?

⊠ Yes, why? →   O No, why? →

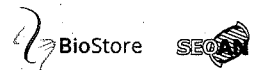*Because it fits to the problems I need to solve*

15 What do / did you study?

Bioinformatics

16 What is your currently highest degree?

MSc

Final Survey

BioStore   SeqAn

1 Please give us the first
4 characters of your ID: _O_ _W_ _4_ _q_ . . . .

2 What did you particularly **like** in the installation process?

3 What did you particularly **dislike** in the installation process?

4 What did you particularly **like** about SeqAn?

Powerful and comprehensive

5 What did you particularly **dislike** about SeqAn?

6 How would you rate the workshop altogether?

☐	☐	☐	☐	☑
Very bad	Bad	Average	Good	Very good

7 How would you rate the organization of the workshop?

☐	☐	☐	☐	☑
Very bad	Bad	Average	Good	Very good

8 How helpful was the assistance by the SeqAn staff?

☐	☐	☐	☐	☑
Hardly helpful	Below averagely helpful	Averagely helpful	Above averagely helpful	Extraordinarily helpful

9 What do you think about the duration of the workshop?

☐	☐	☑	☐	☐
Far too short	Too short	Good	Too long	Far too long

Final Survey

BioStore SE@AN

10 How would you rate the pure online tutorials (not their integration in the workshop)?

O Very bad O Bad O Average ☑ Good O Very good

11 Why did you attend to this workshop?

O I'm currently working on a project where I'm expected to use SeqAn

☑ I'm currently working on a project where I think SeqAn does the job

O I was just curious

Other reason

12 Did the workshop meet your expectations?

Yes

13 What functionality of SeqAn are you using?
What functionality do you miss?

I/O , Align , Interval Tree

What is / would be your preferred way to develop with SeqAn?

O As a framework (create apps)

☑ As a library (include SeqAn headers in own program)

Other

14 Will you use SeqAn in the future?

☑ Yes, why? →   O No, why? →

Good possibilities

15 What do / did you study?

Bio informatics

16 What is your currently highest degree?

MS

tutorials / slides

- consistently use namespaces
- either "using namespace segan" (but not for the first beginner tutorials)
- or always qualify with "segan::" prefix (don't rely on argument dependent lookup)
- never use "::segan::...."