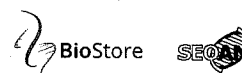


# Feedback

Alignment, MSA



1

Please give us the first 4 characters of your ID: \_\_\_\_\_ . . . . .

2

How would you rate your SeqAn skills concerning the topic addressed in this tutorial before having done it.

☐

No Experience

☐

Basic Skills,  
Few Experience

☐

Ordinary Experience

☐

Much Experience

☐

Extraordinary  
Experience

3

What was your motivation to do this tutorial? How helpful was the tutorial for you?

4

Could you have finished this tutorial without help by the SeqAn team?

☐

No

☐

Yes, but only with a  
significant amount of  
more time

☐

Yes, with slightly to  
no more additional  
time

5

Do you think that the documentation web pages ([www.seqan.de](http://www.seqan.de) and [trac.seqan.de](http://trac.seqan.de)) were helpful to solve the exercises of the tutorial?

☐

Hardly

☐

Average

☐

Above Average

☐

Extraordinary

6

What did you particularly like about this tutorial?

7

What did you particularly dislike about this tutorial? What posed the biggest problems?

check correct alphabets instead of ~~it~~ implicitly  
convert them → like DNAB → DNA

# Feedback

Alignment, MSA



1

Please give us the first 4 characters of your ID:

7 i o p . . . . .

2

How would you rate your SeqAn skills concerning the topic addressed in this tutorial before having done it.



No Experience



Basic Skills,  
Few Experience



Ordinary Experience



Much Experience



Extraordinary  
Experience

3

What was your motivation to do this tutorial? How helpful was the tutorial for you?

learning how to use alignment within SeqAn

4

Could you have finished this tutorial without help by the SeqAn team?



No



Yes, but only with a  
significant amount of  
more time



Yes, with slightly to  
no more additional  
time

5

Do you think that the documentation web pages ([www.seqan.de](http://www.seqan.de) and [trac.seqan.de](http://trac.seqan.de)) were helpful to solve the exercises of the tutorial?



Hardly



Average



Above Average



Extraordinary

6

What did you particularly like about this tutorial?

I like the live coding

7

What did you particularly dislike about this tutorial? What posed the biggest problems?

Default values for alphabets should be errors.  
I mean, if a letter doesn't belong to the alphabet it should not  
be automatically converted to a default value, it should abort  
like taking 'sqrt(-1)'. otherwise, user might think he/she  
has a valid sequence and get a wrong result.

# Feedback

## Alignment, MSA



1

Please give us the first

4 characters of your ID: F45U . . . . .

2

How would you rate your SeqAn skills concerning the topic addressed in this tutorial before having done it.



No Experience



Basic Skills,  
Few Experience



Ordinary Experience



Much Experience



Extraordinary  
Experience

3

What was your motivation to do this tutorial? How helpful was the tutorial for you?

Learn

4

Could you have finished this tutorial without help by the SeqAn team?



No



Yes, but only with a  
significant amount of  
more time



Yes, with slightly to  
no more additional  
time

5

Do you think that the documentation web pages ([www.seqan.de](http://www.seqan.de) and [trac.seqan.de](http://trac.seqan.de)) were helpful to solve the exercises of the tutorial?



Hardly



Average



Above Average



Extraordinary

6

What did you particularly like about this tutorial?

Programming!

7

What did you particularly dislike about this tutorial? What posed the biggest problems?

~~That~~ It needs an alphabet checker so it can report strange characters, instead of transforming them in a default character etc. ✗ in case of proteins.

# Feedback

## Alignment, MSA



1

Please give us the first 4 characters of your ID: h u j . . . . .

2

How would you rate your SeqAn skills concerning the topic addressed in this tutorial before having done it.

☐

No Experience

☒

Basic Skills,  
Few Experience

☐

Ordinary Experience

☐

Much Experience

☐

Extraordinary  
Experience

3

What was your motivation to do this tutorial? How helpful was the tutorial for you?

I want to align elements of non-DNA/AA nature

4

Could you have finished this tutorial without help by the SeqAn team?

☐

No

☐

Yes, but only with a  
significant amount of  
more time

☒

Yes, with slightly to  
no more additional  
time

5

Do you think that the documentation web pages ([www.seqan.de](http://www.seqan.de) and [trac.seqan.de](http://trac.seqan.de)) were helpful to solve the exercises of the tutorial?

☐

Hardly

☐

Average

☒

Above Average

☐

Extraordinary

6

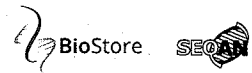
What did you particularly like about this tutorial?

7

What did you particularly dislike about this tutorial? What posed the biggest problems?

# Feedback

## Alignment, MSA



1

Please give us the first

4 characters of your ID: y407 . . . . .

2

How would you rate your SeqAn skills concerning the topic addressed in this tutorial before having done it.

☐

No Experience

☐

Basic Skills,  
Few Experience

☒

Ordinary Experience

☐

Much Experience

☐

Extraordinary  
Experience

3

What was your motivation to do this tutorial? How helpful was the tutorial for you?

4

Could you have finished this tutorial without help by the SeqAn team?

☐

No

☒

Yes, but only with a  
significant amount of  
more time

☐

Yes, with slightly to  
no more additional  
time

5

Do you think that the documentation web pages ([www.seqan.de](http://www.seqan.de) and [trac.seqan.de](http://trac.seqan.de)) were helpful to solve the exercises of the tutorial?

☐

Hardly

☐

Average

☒

Above Average

☐

Extraordinary

6

What did you particularly like about this tutorial?

Approach, ~~the~~

7

What did you particularly dislike about this tutorial? What posed the biggest problems?