

GeneFisher-P: Variations of GeneFisher as Processes in Bio-jETI

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The GeneFisher web application(s)

GeneFisher (1996): a web application for interactive PCR primer design.

GeneFisher

Institutions: [Bioinformatics Eilsfeld](#)
Authors: [Chris Schleiermacher - Folker Meyer](#)



Primer Design

Primer Parameters

Max. number of primer pairs returned: 8 16 No limit

Set **primer length**: From to bp.

Set **GC content**: From to %.

Set **melting temperature T_m** : From to °C.

Set **Product Size**: From to bp.

Set **primer degeneracy**: fold

Allow multiple **occurrences**: occurrence(s).

3' Clamp Parameters

Set **3' length**: bp.

Set **max. 3' degeneracy**: fold

Set **3' GC content**: From to %

End primer with:
 Adenine Cytosine
 Guanine Thymine

Accept your choice

The GeneFisher web application(s)

GeneFisher2 (2006): AJAX-based reimplementaion of GeneFisher.

The screenshot displays the BiBiServ web application interface. At the top left is the logo for Universität Bielefeld. The main header reads "BiBiServ Bielefeld University Bioinformatics Server". Below the header are three navigation tabs: "Tools", "Education", and "Administration".

On the left side, there is a vertical "Tools" menu with the following categories and links:

- Genome Comparison
 - Checko
 - REPuter
 - more
- Alignments
 - ezg
 - PosSumSearch
 - more
- Primer Design
 - GeneFisher
- RNA Studio
 - RNAcast
 - RNAshapes
 - more
- Evolutionary Relationship
 - ROSE
 - SplitTree
 - more
- Others
 - Xen DB
 - PROdict or
 - more

The main content area is titled "GeneFisher2 - Submission". It contains the following text and form elements:

Enter the sequences of your project in the fields below.
Your input can be single- or multiple-, aligned- or unaligned-, nucleotide- or aminoacid-sequences in [FASTA](#) format.

Click here for [example DNA](#) or [example aminoacid sequences](#), here you can [remove](#) our example.

sequence upload:

paste files in here:

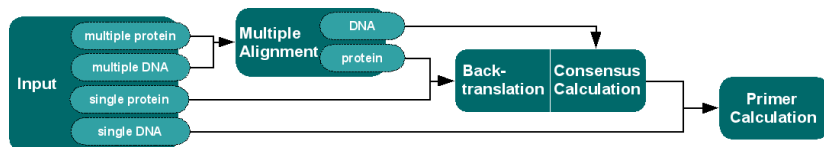
On the right side, there is a green box with the following links:

- Welcome
- Submission
- References
- Manual
- Contact

At the bottom right of the page, the date "Mon May 21 17:18:42 200" is displayed.

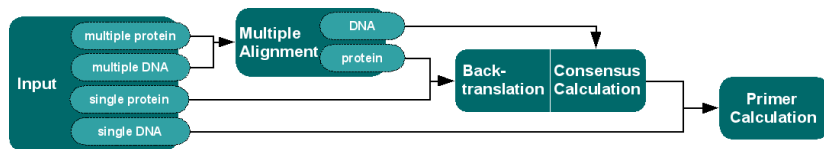
GeneFisher: Process and Components

GeneFisher logical process:



GeneFisher: Process and Components

GeneFisher logical process:



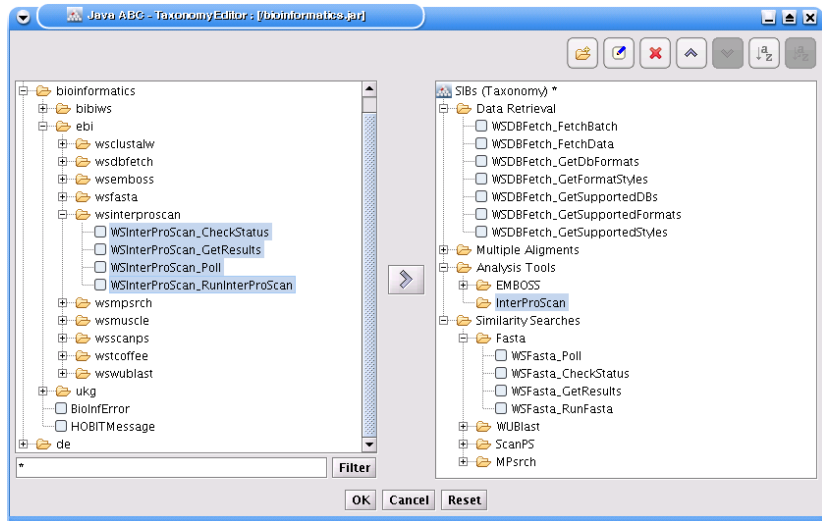
(SIBs for) the required services at BiBiServ:



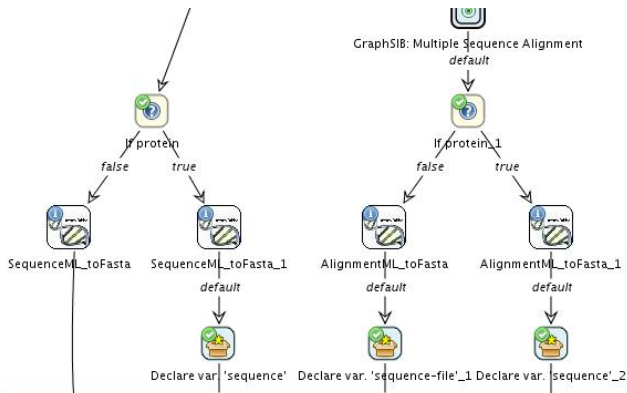
GeneFisher-P: Basic Version

[external]

GeneFisher-P: Component Taxonomies



GeneFisher-P: Local Checking



LocalChecker - Info Window (all results)

Results:

Description	SIB	
SIB branch "error" is neither assigned to an edge nor used as a model branch	SequenceML_toFasta	bioinform
SIB branch "error" is neither assigned to an edge nor used as a model branch	AlignmentML_toFasta	bioinform
SIB branch "error" is neither assigned to an edge nor used as a model branch	AlignmentML_toFasta_1	bioinform
SIB branch "error" is neither assigned to an edge nor used as a model branch	SequenceML_toFasta_1	bioinform
SIB branch "default" is neither assigned to an edge nor used as a model branch	Exit Workflow	de.meta
SIB branch "error" is neither assigned to an edge nor used as a model branch	Exit Workflow	de.meta

GeneFisher-P: Model Checking (1)

Current atomic propositions:

errormessage_3 = [error]

errormessage_4 = [error]

Read Sequence(s) = []

BioDOM.Fasta2SequenceML = [remote]

Select Input File = [inputselection]

Single or Multiple Sequences? = []

Nucleic Acid or Protein? = []

Sequences OK? = []

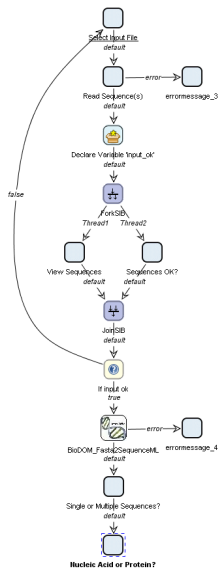
If input ok = [inputcheck]

ForkSIB = []

JoinSIB = []

Declare Variable 'input_ok' = []

View Sequences = []



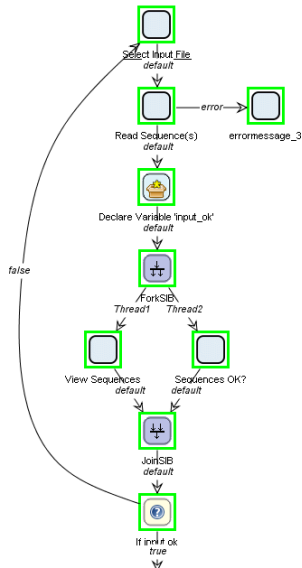
GeneFisher-P: Model Checking (2)

Natural language:

"No remote service is invoked before the input is checked."

Comutation Tree Logic (CTL):
 $AWU(\neg remote, inputcheck)$

(On all paths it is the case that *remote* does not hold until *inputcheck* does.)



GeneFisher-P: Execution

Flowchart steps:

- Read Sequence(s) default
- error → errorMessage_3
- Declare Variable 'input_ok' default
- forkSIB (splits into Thread1 and Thread2)
- Thread1: View Sequences
- Thread2: Sequences OK?

Execution [GeneFisher] window details:

Thread	SIB	Branch
GeneFisher. 2	Declare variable 's...	default
GeneFisher. 2	Declare variable 'n...	default
GeneFisher. 2	Declare variable 't...	default
GeneFisher. 2. Gra...	Select Input File	default
GeneFisher. 2. Gra...	Read Sequence(s)	default
GeneFisher. 2. Gra...	Declare Variable 'i...	default
GeneFisher. 2. Gra...	ForkSIB	
Input Validation. Fo...	View Sequences	error

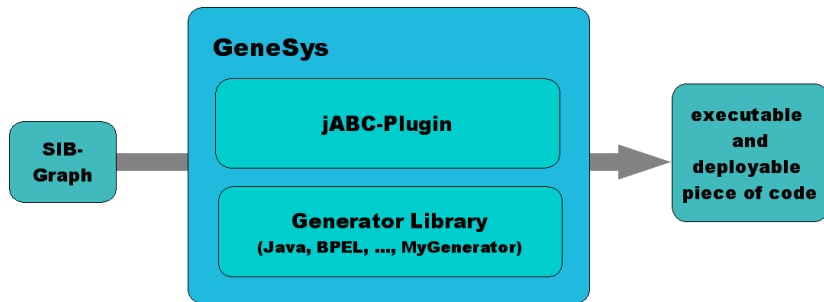
Dialog box: Please check your input. Are your input sequences alright?

Status: EXECUTING_STEP

```

Human
tctgccctcatcctttctcacagcaatgaatttgc aactggaaccaagtgaaaaacaaattgcctgaattg
ccgctccacaaggtcagagattgtaaatggtcaactactgactttttttttatcccttgactcaagacgctaac
gtgctggtttataaataat
>baboon
tctgccctgtcctttctcacagcaatgaatttgc aactggaaccaagtgaaaaacaaattgcctgaattgactgtatgactgcaactaacagattctt
ccgctccacaaggtcagagattgtaaatggtcaactactgactttttttttatcccttgactcaagacgctaacctcaatttcagaacgtgtttaaacctt
gtgctggtttataaataat
>moLe
tctgccctcctcctttctcacagcaatgaatttgc aactggaaccaagtgaaaaacaaattgcctgaattgactgtatgactgcaactaacagattctt
accgctccacaaggtcagagattgtaaatggtcaactactgactttttttttatcccttgactcaagacgctaacctcaatttcagaacgtgtttaaacctt
    
```

GeneFisher-P: Compilation (1)



GeneFisher-P: Compilation (2)

Edit configuration 'GeneFisher1'

Name: GeneFisher1

Generator: de.metaframe.jabc.genesys.generators.JavaClassExtruder

Description | **Arguments**

- mainClassName: GeneFisher
- model: /home/anna-lena/Desktop/2007-06-10 NetTAB-Material/GeneFisher/GeneFisher.xml
- packageName: de.uni-goe.genefisher
- dependentModels (StrictCollection)
 - [0]: /home/anna-lena/Desktop/2007-06-10 NetTAB-Material/GeneFisher/Multiple_Sequence_Alignment.xml
 - [1]: /home/anna-lena/Desktop/2007-06-10 NetTAB-Material/GeneFisher/Primer_Design.xml
 - [2]: /home/anna-lena/Desktop/2007-06-10 NetTAB-Material/GeneFisher/Input_Validation.xml
 - [3]: /home/anna-lena/Desktop/2007-06-10 NetTAB-Material/GeneFisher/BatCons.xml
- outputFolder: /home/anna-lena/Desktop/2007-06-10 NetTAB-Material/GeneFisher/comp
- apiMode: true

Par. mainClassName (String)

Value GeneFisher

Model model

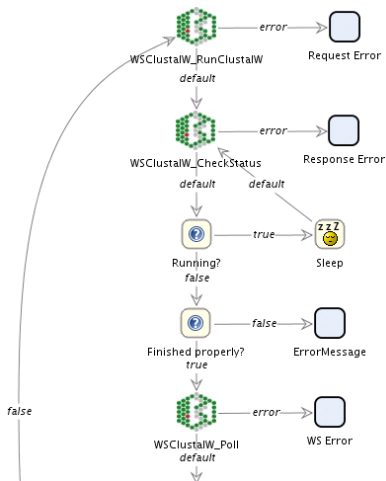
Submodels dependentModels

Please use the two combo boxes on the left to determine which of the arguments displayed in the tree above specify a) the root model from which the generation starts and b) its dependent models (i.e. submodels). All necessary values will then be set for you automatically using the model which is currently active in JABC as well as its submodels.

OK Cancel

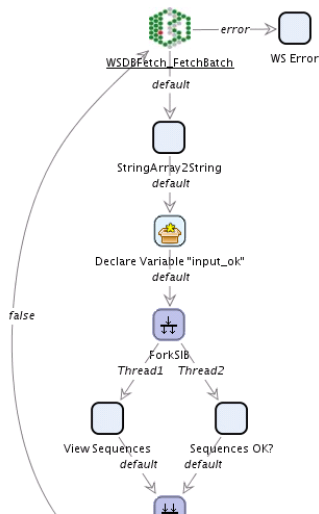
Variations of GeneFisher-P

- **Example 1:**
Using alignment tools from the EBI, e.g. the ClustalW web service.
- **Example 2:**
Data retrieval with the EBI's DBFetch.
- Different levels of interactivity.
- Selection of alignment tools at runtime.
- ...

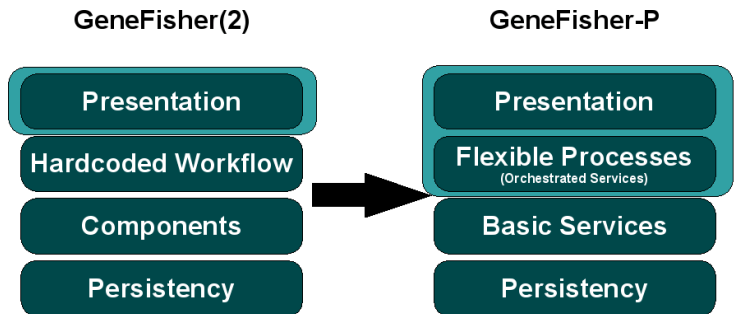


Variations of GeneFisher-P

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Summary



 User Intervention Area

Thanks for your attention!

Questions?