

BiBiServ – a platform for publication of bioinformatics tools

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BiBiServ – a platform for publication of bioinformatics tools

Overview

- General Information
 - History & Status
 - Statistics
- A story about Persistence ...
- Publishing on BiBiServ
- BiBiServ2

BiBiServ – a platform for publication of bioinformatics tools

General Information – What is BiBiServ ?

- **Bielefeld Bioinformatics Service**
 - Provides a multitude of bioinformatical tools and online education courses for users worldwide via the Bielefeld Bioinformatics Server
- **Bielefeld Bioinformatics Server**
 - A server for online publication of BioInformatical tools for researchers and developers at Bielefeld University
 - Provides online access to the tools functionality
 - Is currently hosting about 40 tools from different application areas, including Alignments, RNA, Genome Comparison, Primer Design and other

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General Information – History & Status (1)

- 1996** Started as part of AG „Praktische Informatik“ in 1996 with a hardware donation of SUN on a single server. BiBiServ serves a collection of loosely coupled bioinformatic tools.
- 2001** Become the self-contained technology platform for the IFB of the CeBiTec, including permanent staff
- 2002** Redesign of the web appearance, unified Corporate Identity
- 2003** Because of a growing number of submissions a small compute grid is integrated into the server structure. Support for xmlrpc based webservice.
- 2004** Member of HOBIT. Support for SOAP based webservice.

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General Information – History & Status (2)

- 2006** Development and Usage of XML specification for common bioinformatic data types to support workflow systems.
- 2007** Ajax support for new/updated tools
- 2009** Start rewriting complete server structure on top of J2EE for next generation BiBiServ (details later in this talk)
- 2010** Integration of Semantic Web Technology (details later in Sven's talk)

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General Information – User Support

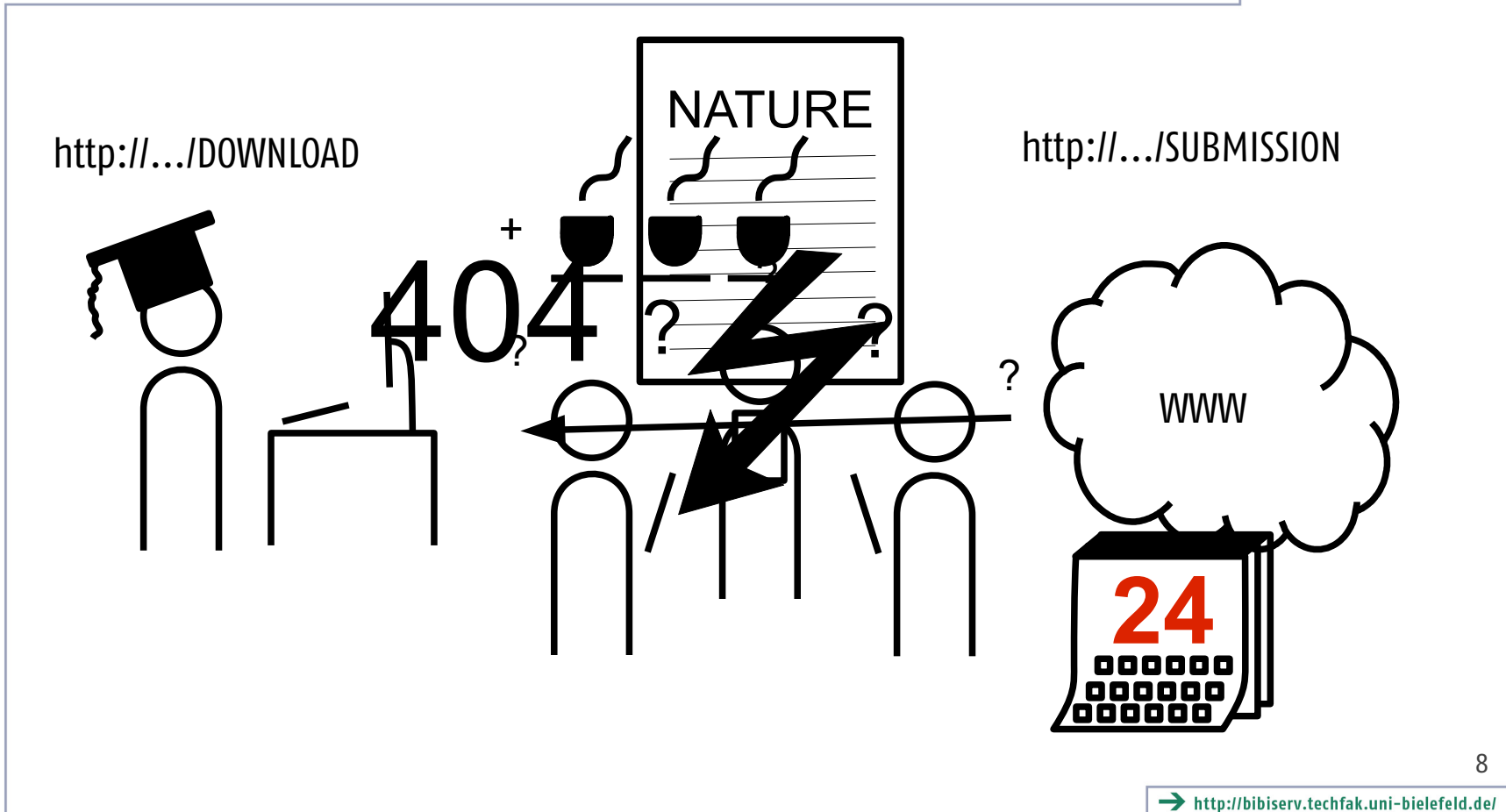
- Easy access to and usage of bioformatical tools via Browser and Web Services (API)
- Choice of different tools with same scope
- Download of binary and/or source version with basic support for usage
- 1st level email support with average reaction times of one day
- Consistent user interface over all tools, allowing for simple re-use of learned access methods

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General Information – Statistics

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Persistence (not only) in Bioinformatics



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Persistence (not only) in BioInformatic



GeneFisher2 - Primer calculation

Your Job ID:
bibiserv_1297247726_537

RESULT

manually set primer parameters

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

calculate Primer

Primer Calculation Results

(get more detailed information by clicking in the pairs position)

4 best Pairs (of max. 4)

Pair-ID	Forward Primer	Reverse Primer	Qual.	Prod. Len.	T_m
1	TCTCCACAAGGTCAGAGA	GTTAGCGGCTTGTAGTCA	731	75	



- Tools
 - Genome Comparison
 - RNA Studio
 - Alignment
 - Primer Design
 - GeneFisher submission manual
 - Evolutionary Relationships
 - Others
 - Education
 - Administration

Submission - GeneFisher

Function [currently Single Primer Calculation]

Input

Input 'Input Sequence' (?)
(Consensus)-Sequence. The basis for primer calculation

Select data input method: File Upload | Copy & Paste | Example

Copy & Paste:

```
>singlePrimerTestSequence
tctgctccatccttttctcacagcaatgaatttgcgaatcgaacccaatgaaaaacaaaattoc
ctgaatttacttatatactgcactacacagattctaccctccacaagctcaagattata
aaagtcactactgactttttttttttttccctgactcaagaccctcaactcaatttcagaact
gttttaalaaatgaatgaatgcaatcccttttctgactcttttataataat
```

Input data is valid (Copy & Paste) Detected type is Fasta_DNA_Single

Validate Input Reset

Parameter

Result

Showing 1 of 1 Resulting Primers

Pair Id	PCR Product
1	

Pair ID 1

```
.....|.....|.....|
tctgctccatccttttctcacagcaatgaatttgcgaat
agacggaggtaggaaaagagtgtcgttactttaaactgta
```

2006
(current)

2010
(BiBiServ 2)

BiBiServ
Bielefeld University Bioinformatics Server
GeneFisher2

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Publishing on BiBiServ – Think about

- Resources, Network bandwidth limits
- Theoretical and real runtime consideration
- Tool itself must be runnable within BiBiServ environment
- Kind of publication : online usage (browser, webservice) / download
- Intended User audience
- (OS) License

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Publishing on BiBiServ – Needed informations

- Name, short and long description
- input/output data and format
- Parameter types, restrictions and dependencies (for online usage)
- (explained) example
- (detailed) manual
- Source code (→ long term persistence)
- archives for download (manual, example data)

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Publishing on BiBiServ

**Come early,
Communicate often !**

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Next Generation BiBiServ : BiBiServ 2

- Problems with current server infrastructure
 - Grown structure, outdated server technique
 - Separate structure with different server approaches for web interface and webservice
 - PERL/CGI on webserver side
 - J2EE4 on webserviceserver (=application server) side
 - Tool described within sourcecode
 - Default Template based

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Next Generation BiBiServ : BiBiServ 2

- Upcoming server structure (BiBiServ2)
 - Tooldescription based approach (Wizard guided)
 - Toolspecific Templates (including WI,WS,manual, download area) generated from description
 - Automatic validation/conversion of data formats
 - Increased usability (Interactive WI forms, On-The-Fly validation, Input Descriptions)
 - Secured „MyBiBiServ“ area, user management
 - Statistics about tool usage, resource usage, used parameter, ...
 - Semantic Web techniques (type vs. Format)
 - ...

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Thanks for your attention!