

# BiBiServ: Practices and Problems

*WebServices and Workflows on  
the Bielefeld University  
Bioinformatics Server*

# BiBiServ-Basics...

- Bielefeld University Bioinformatics Server
- founded in 1996
- hosts various Bioinformatics Tools developed within several research groups at Bielefeld University

# BiBiServ-Tools

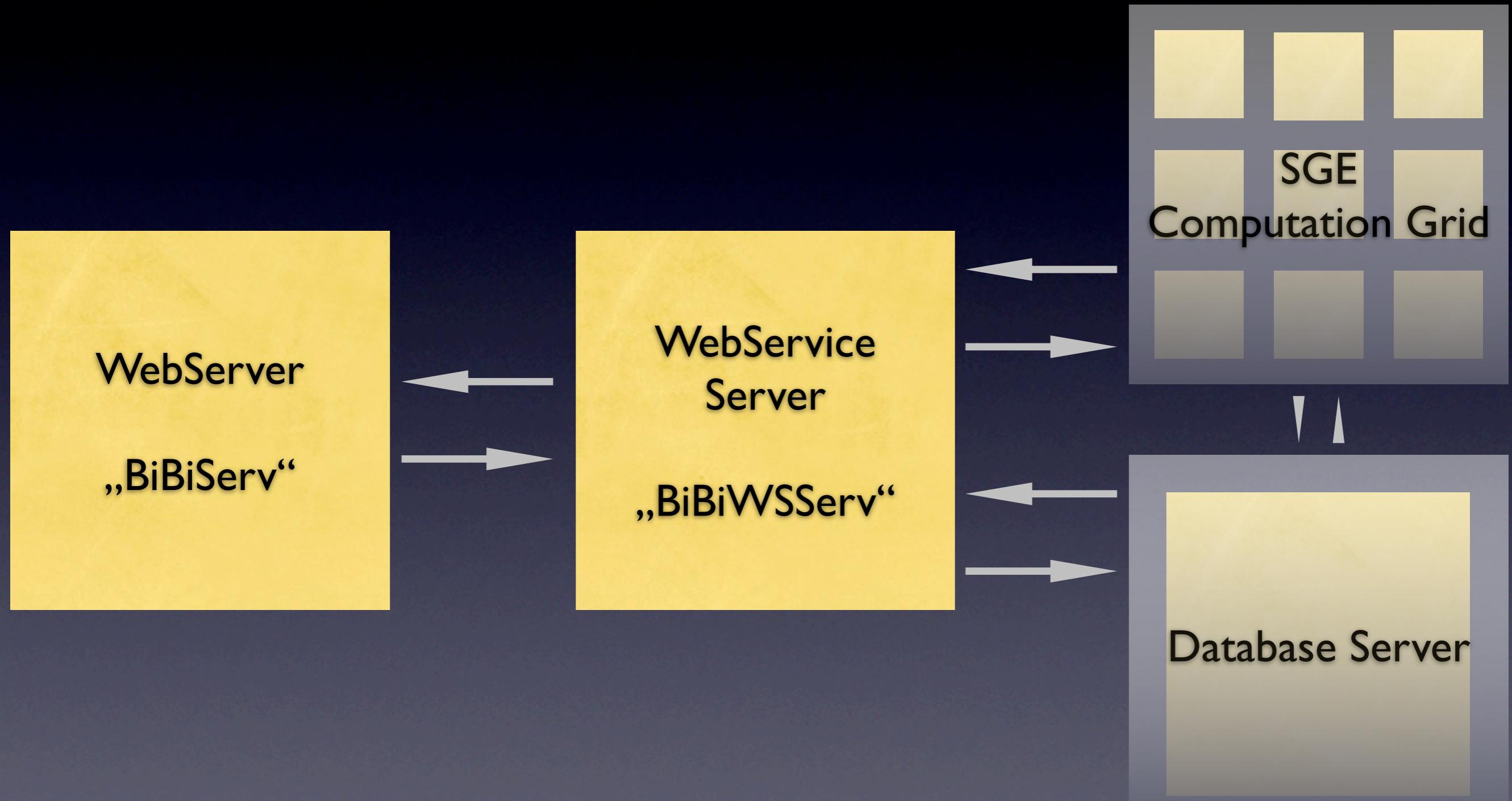
- currently around 30 tools in the areas of:
  - RNA Structure Research
  - Alignment Computation
  - Genome Comparison
  - Primer Design
  - Evolutionary Relationships
  - Miscellaneous Other Applications

# Used Technologies

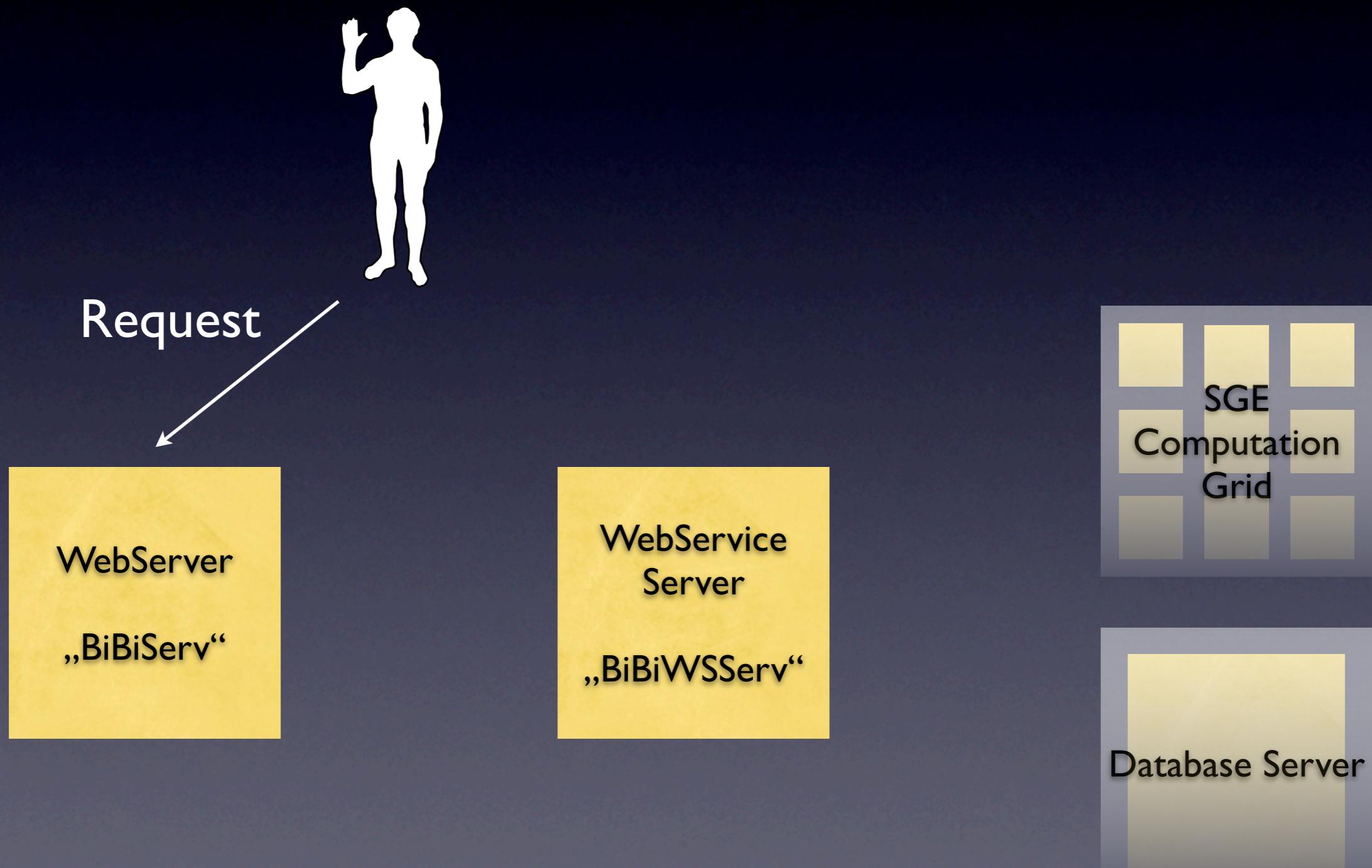
- 1996: HTML/CGI
- 2003: WebServices using XML-RPC
- 2004: WebServices using SOAP / WSDL

HTML Interface transformed to  
„just another WebService Client“

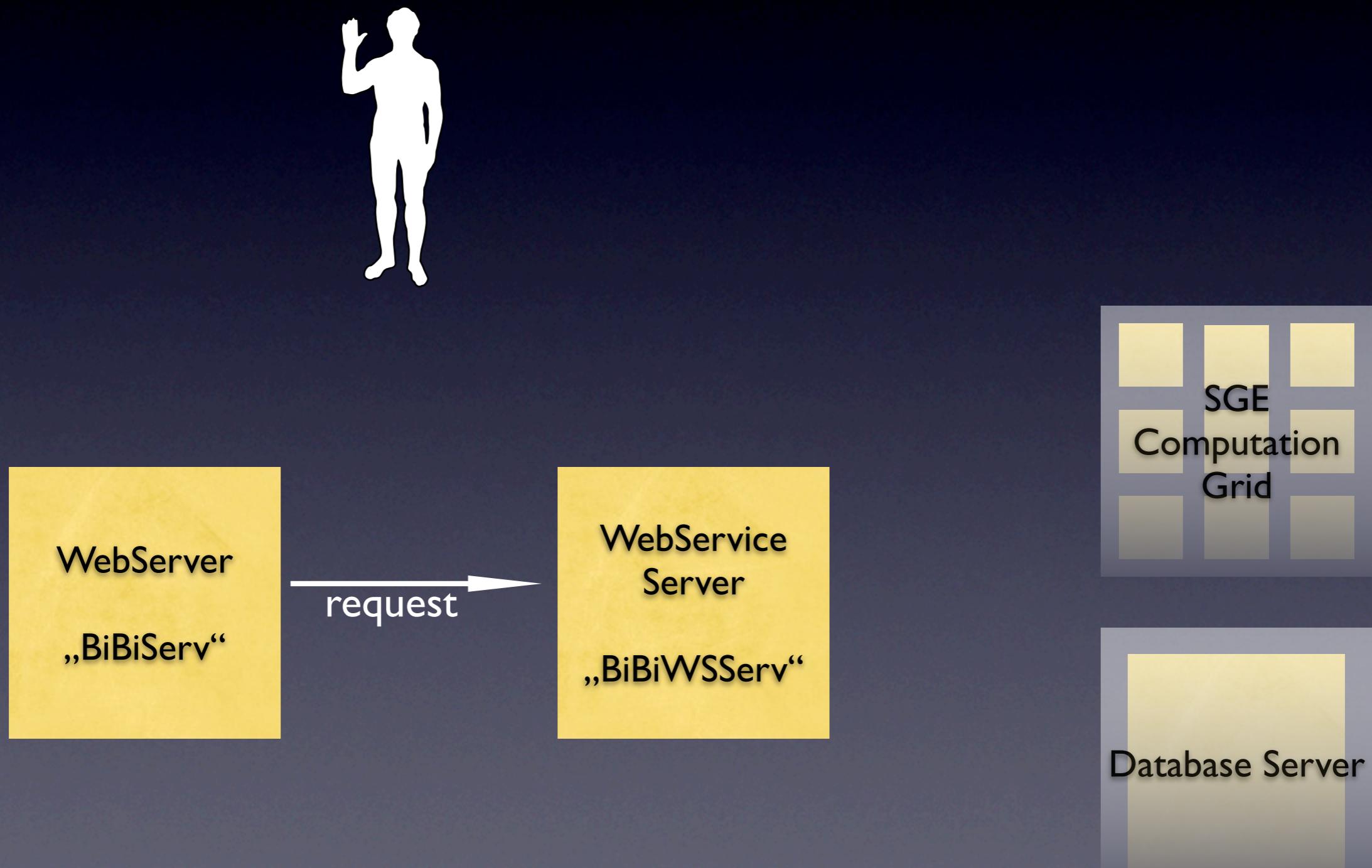
# Architecture



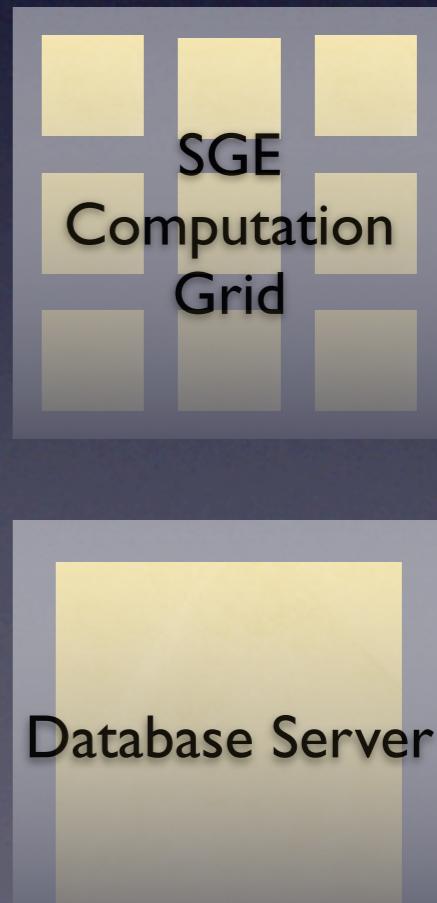
# Usage (HTML Interface)



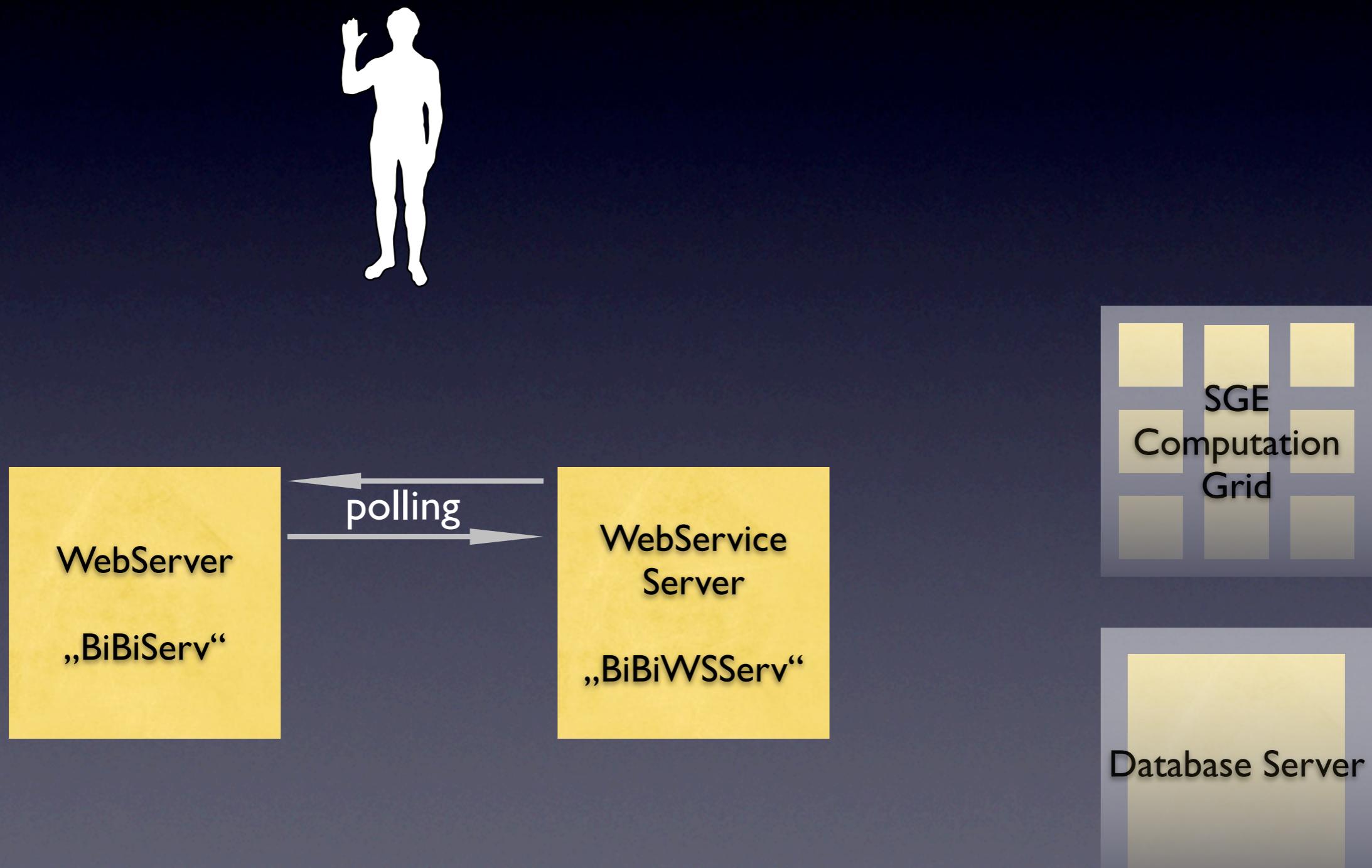
# Usage (HTML Interface)



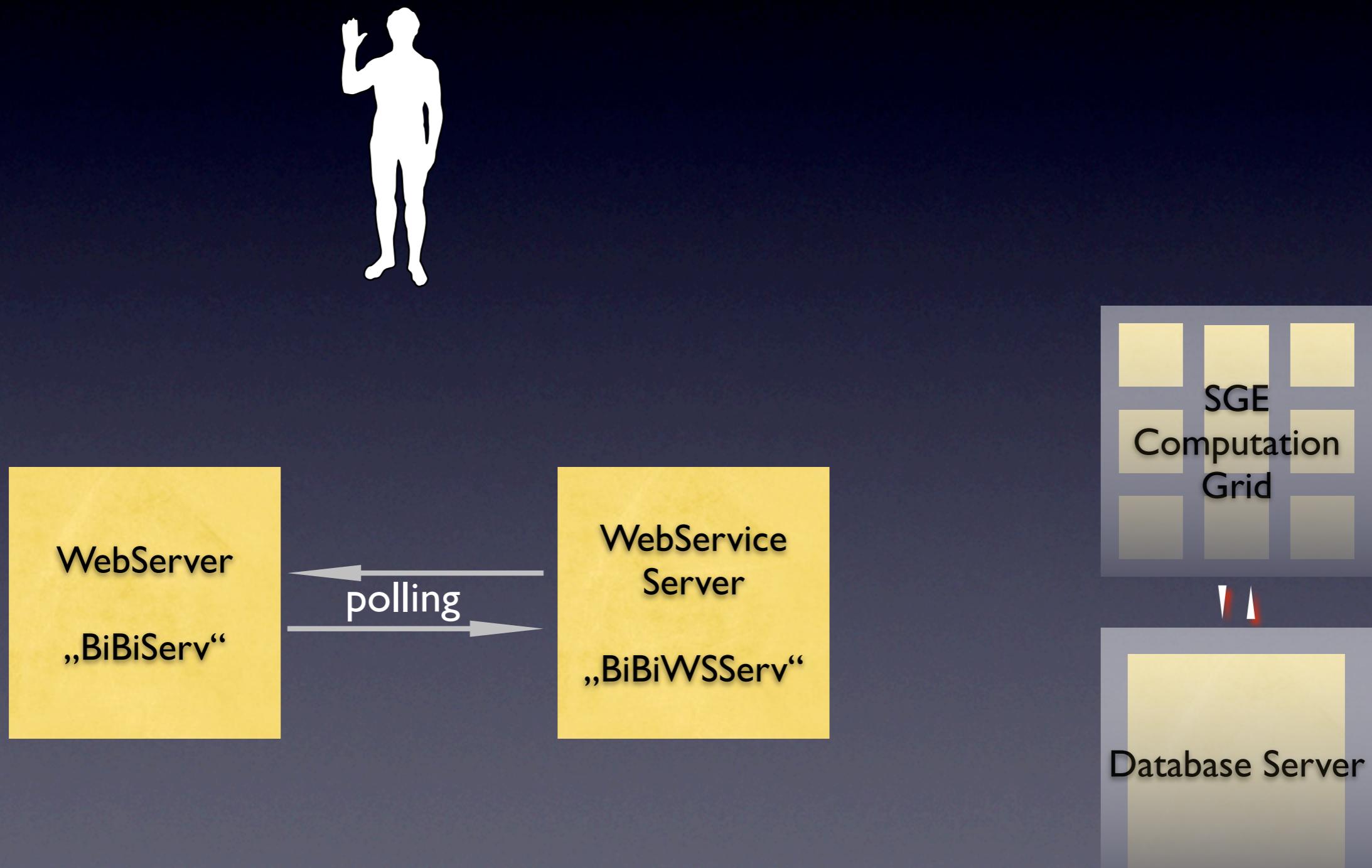
# Usage (HTML Interface)



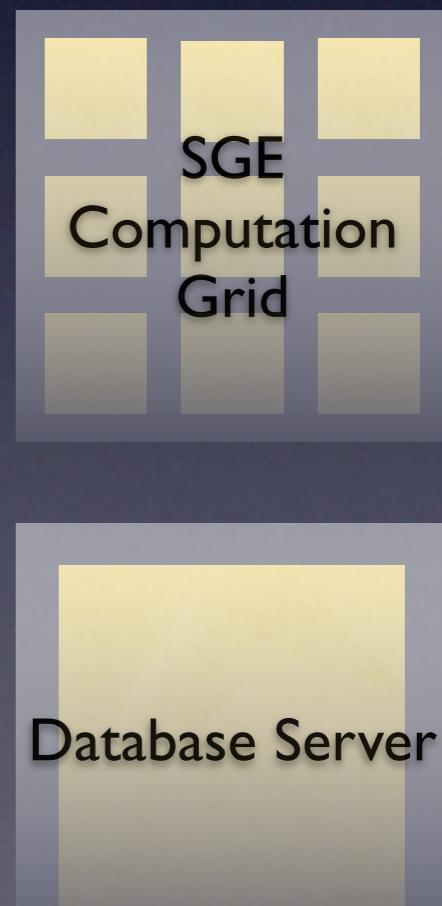
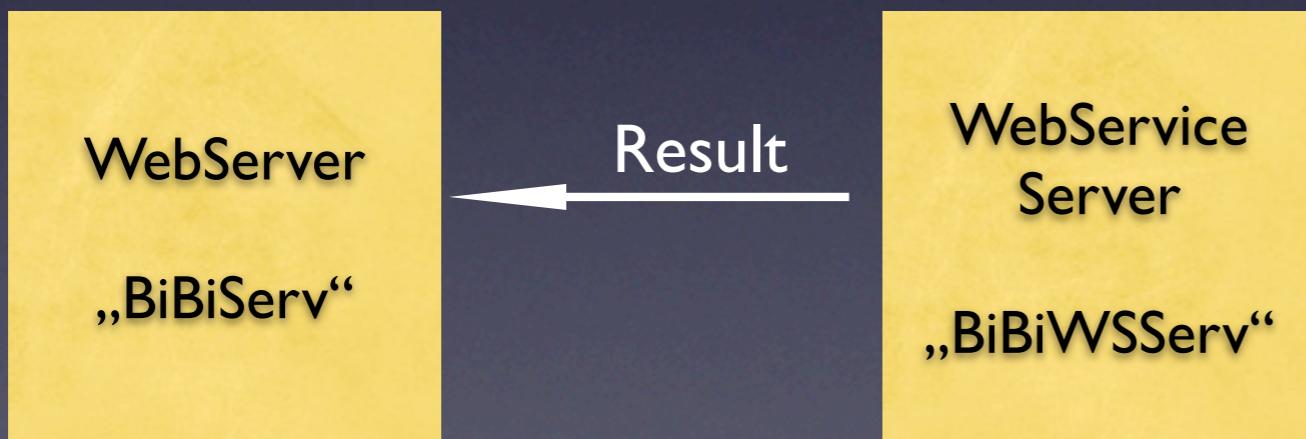
# Usage (HTML Interface)



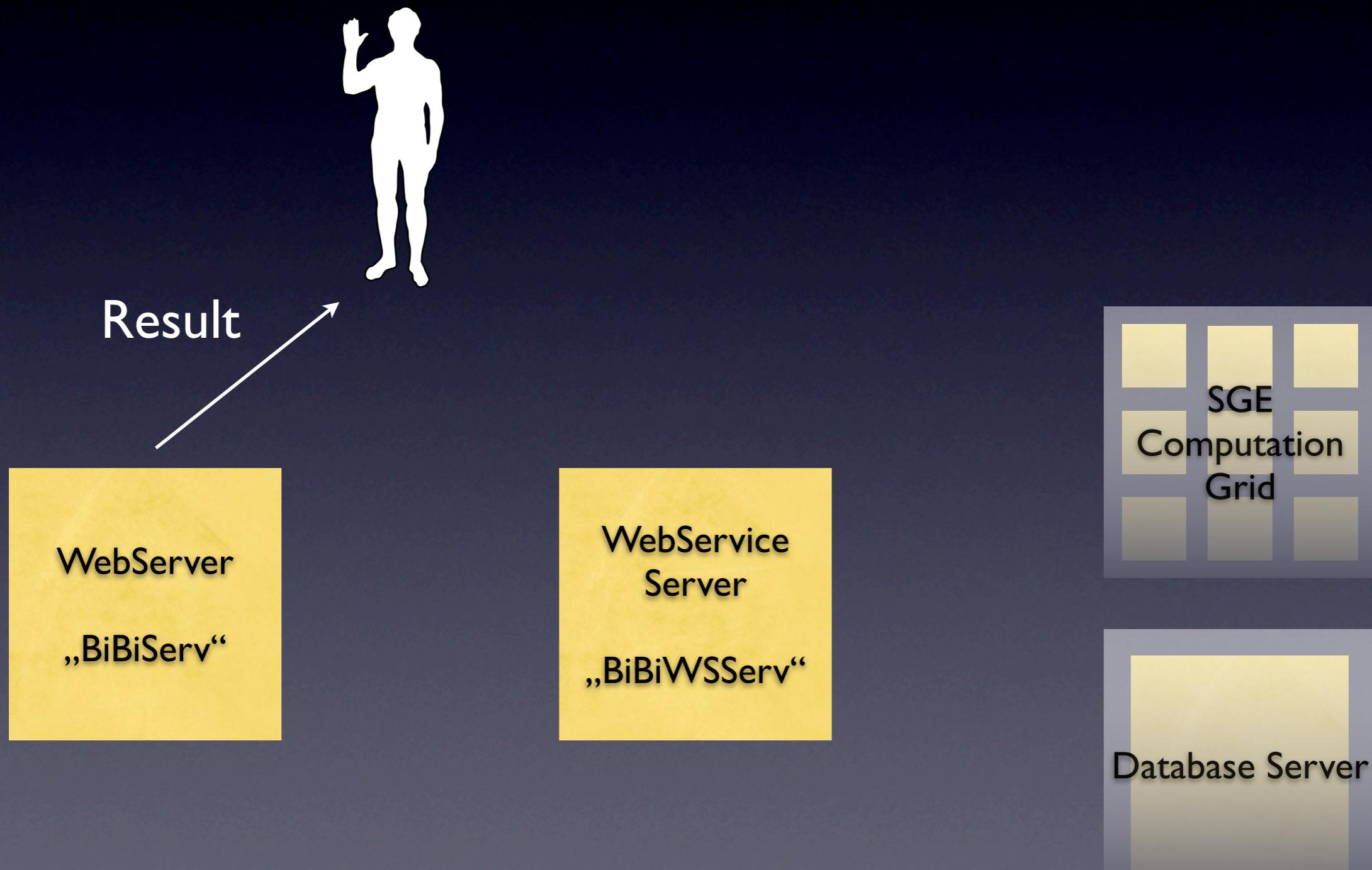
# Usage (HTML Interface)



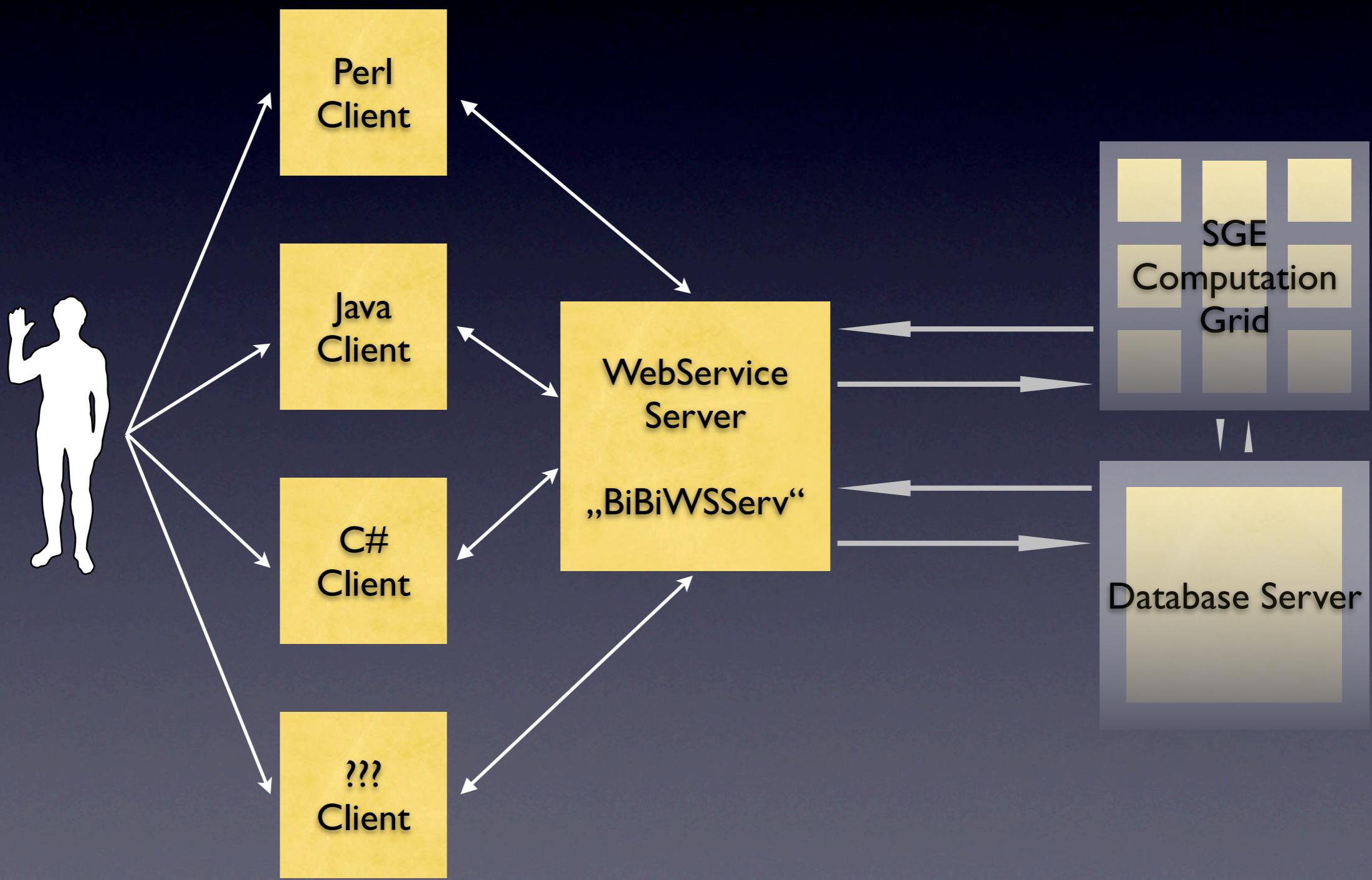
# Usage (HTML Interface)



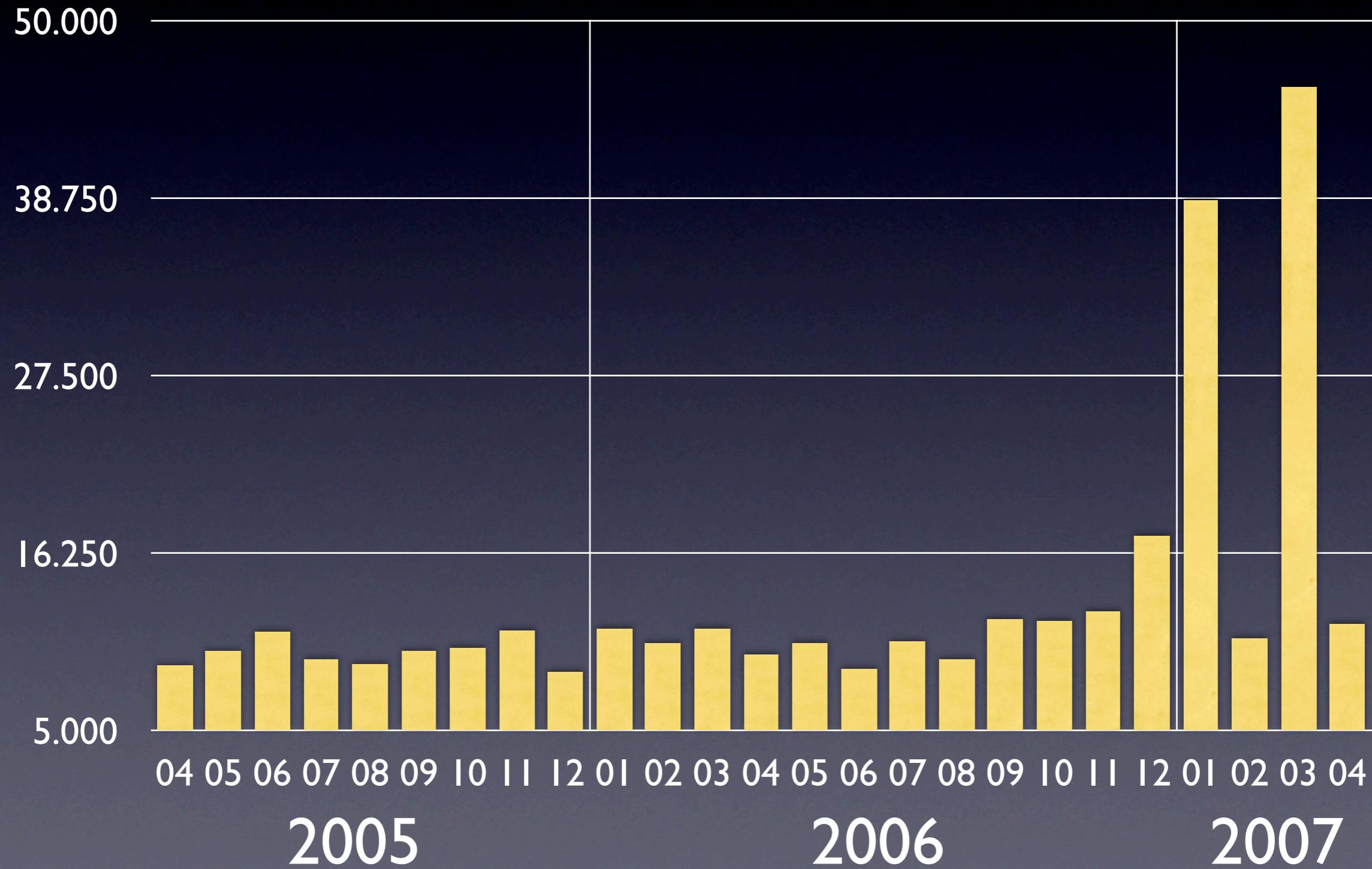
# Usage (HTML Interface)



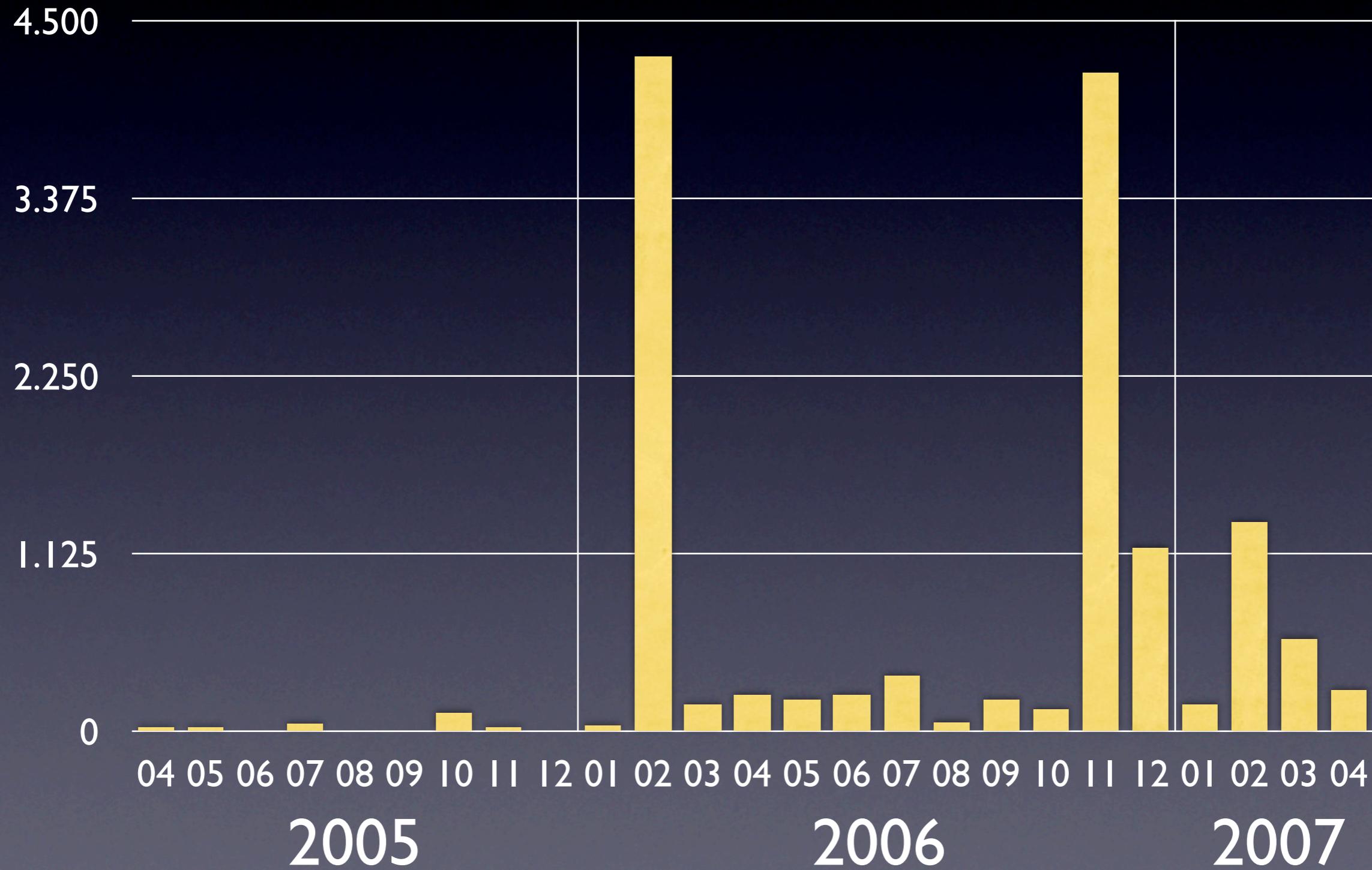
# Usage: other clients



# HTML Interface Usage



# WebService Interface Usage



# HOBIT

- Helmholtz Open BioInformatics Technology
- cooperation of 11 german universities and Helmholtz Institutes as core of a network linking bioinformatics centres together
- Goal: „To connect bioinformatics applications and resources in a uniform way to provide an efficient communication tier for resource access.“
- <http://hobit.sourceforge.net/>

# Interoperation Obstacles

- necessary prerequisite:  
common communication protocols &  
common data formats
- most common bioinformatics data formats:
  - tool specific ASCII or binary files  
(but often used for other purposes)
  - no explicit structure
  - no or only implicit semantics  
(e.g. lower vs. upper case letters)
  - not easily extendable

# Hobit Schemas

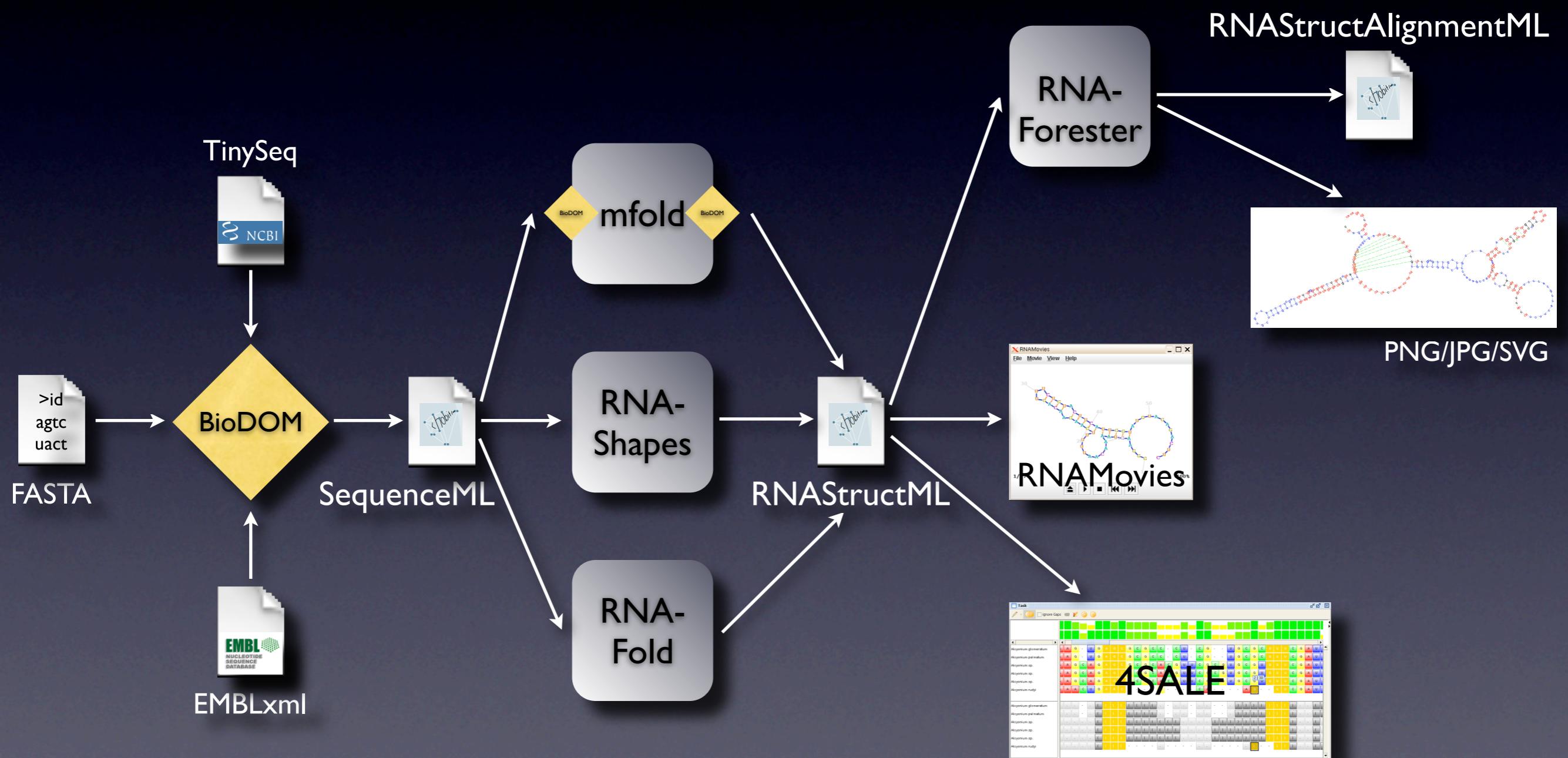
- extendable XML Schema definitions for bioinformatics data
- Basic building blocks for bioinformatical data types
- Several higher-level types:
  - SequenceML
  - AlignmentML
  - RNAStructML
- <http://bioschemas.sourceforge.net/>

# BioDOM

- Java Library for creation of data in HOBIT XML formats + conversion of existing legacy data types
- easy adaptation of existing tools via:
  - BioDOM Library calls
  - usage of BioDOM WebService
- <http://biodom.sourceforge.net/>

# Workflow / Formats

## Example



# BiBiServices as components

- hand-coded workflows
- WSDL-Description -> Taverna, Wildfire
- jABC / Bio-jETI
- Virtual BiBiServ

# The (near) Future

- Better description of services  
(WSDL is mostly OK, but not enough)
- Semantics Layer
- Integration with other Frameworks  
(e.g. BioMoby-S)

# Why we are here...

We are currently looking for generally accepted best practices and open standards for:

- adding a semantic layer
- better service descriptions
- automated tool discovery methods
- component interface requirements for different workflow design tools

# Thanks for your attention :-)!

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