

Grid-Enabled SEE++

A Grid-Based Medical Decision Support System for the Diagnosis and Treatment of Strabismus

<http://www.risc.uni-linz.ac.at/research/parallel/projects/agrid/>

Károly Bósa,

Wolfgang Schreiner,

Michael Buchberger,

Thomas Kaltofen

Abstract

“Grid-Enabled SEE++” is a software system that deals with the support of diagnosis and treatment of strabismus. Its goal is to adapt and to extend the original SEE++ in several steps and to develop an efficient grid-based tool for “Evidence Based Medicine”, which supports the surgeons to choose the optimal surgery techniques in case of the treatments of certain eye motility disorders. First, we have developed a grid-enabled version of the simulation of a medical examination, by which the pathology of the patient can be estimated. Based on this, we work on a pathology fitting algorithm that attempts to give sufficiently close estimations for the pathological reasons of the disorder. Furthermore, we started to develop a grid-enabled distributed database where both real and simulated pathological cases can be collected, sorted and evaluated for improving both the later pathology fitting calculations and the future medical treatments.

Terminology

- **Strabismus** is the common name given to usually persistent or regularly occurring misalignment of the eyes where eyes point in different directions such that a person may see double images.
- SEE++ is able to simulate a typical medical examination called **Hess-Lancaster test**, from which the reason for the pathological situation of the patient can be estimated.
- The outcome of the Hess-Lancaster test consists of two **Gaze Patterns** of blue points and of red points respectively (see the diagram in the middle of the GUI of SEE++ on Figure 1). The blue points represent the image seen by one eye and the red points the image seen by the simulated other eye; in a pathological situation there is a deviation between the blue and the red points.
- **Pathology Fitting**: It is possible to give the measured gaze pattern of a patient as input. In this case, SEE++ takes some default or estimated eye data and modifies a subset of them until the **calculated gaze pattern of the simulated eye (red points)** matches the **measured gaze pattern (green points)**.

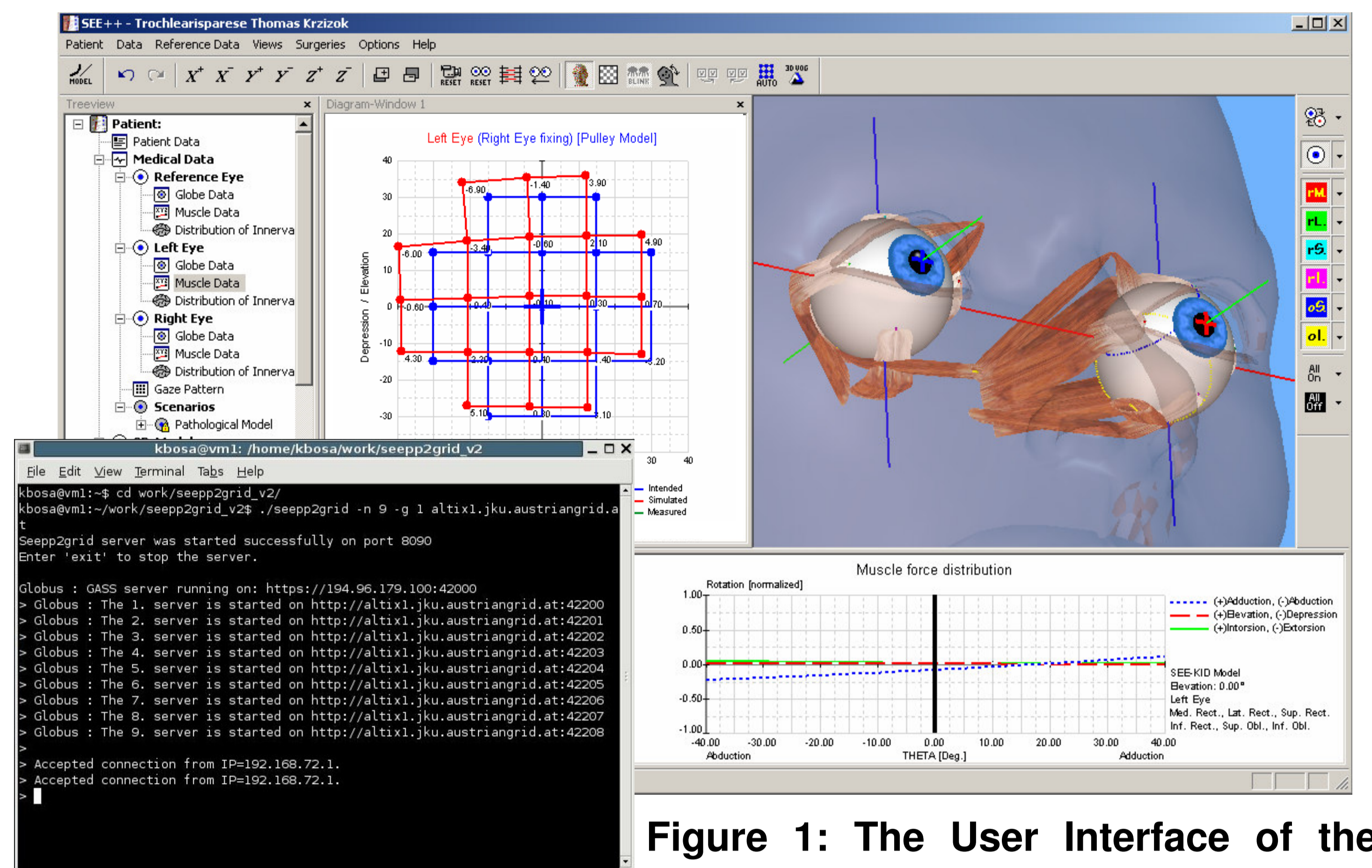


Figure 1: The User Interface of the “SEE++ to Grid Bridge” (in front) and the GUI of the SEE++

I. Web Service and WSRF based medical databases for SEE++

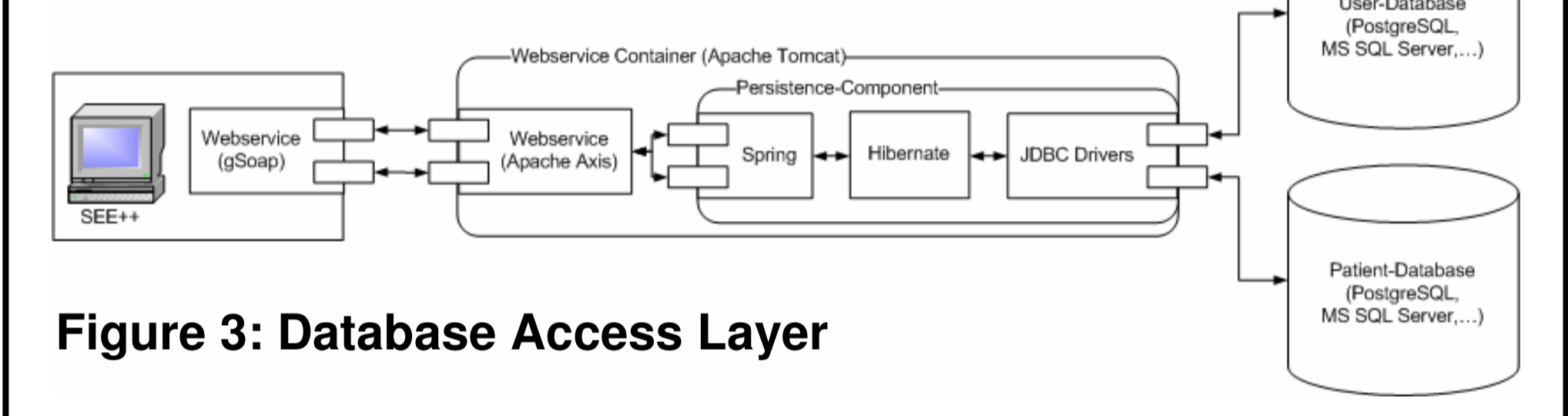


Figure 3: Database Access Layer

II. Grid-Enabled Hess-Lancaster Test. The Speedup is a factor of 14-17.

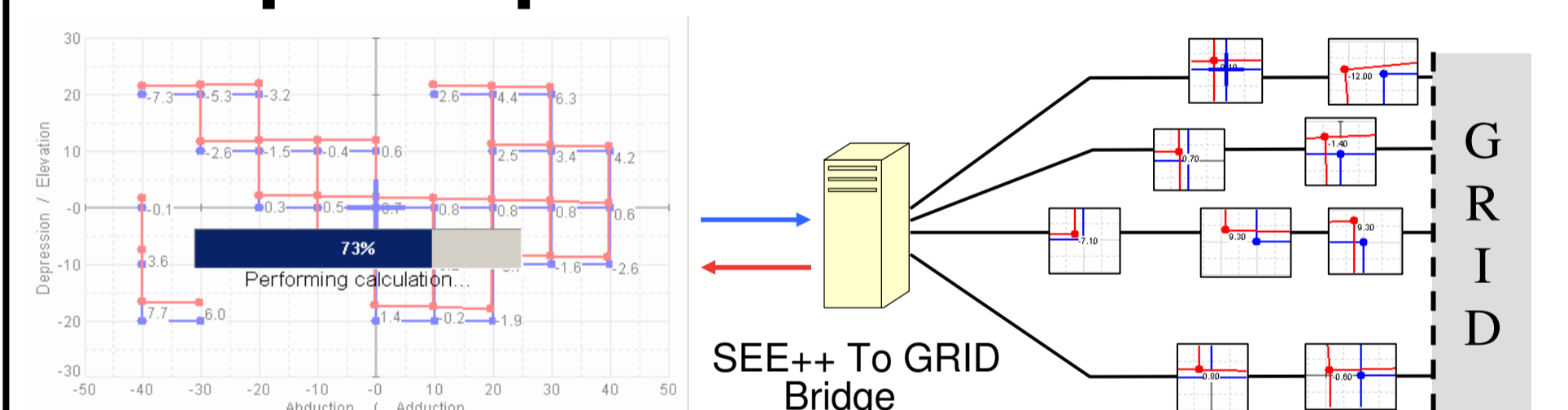


Figure 4: Parallelization of the Gaze Pattern Calculation

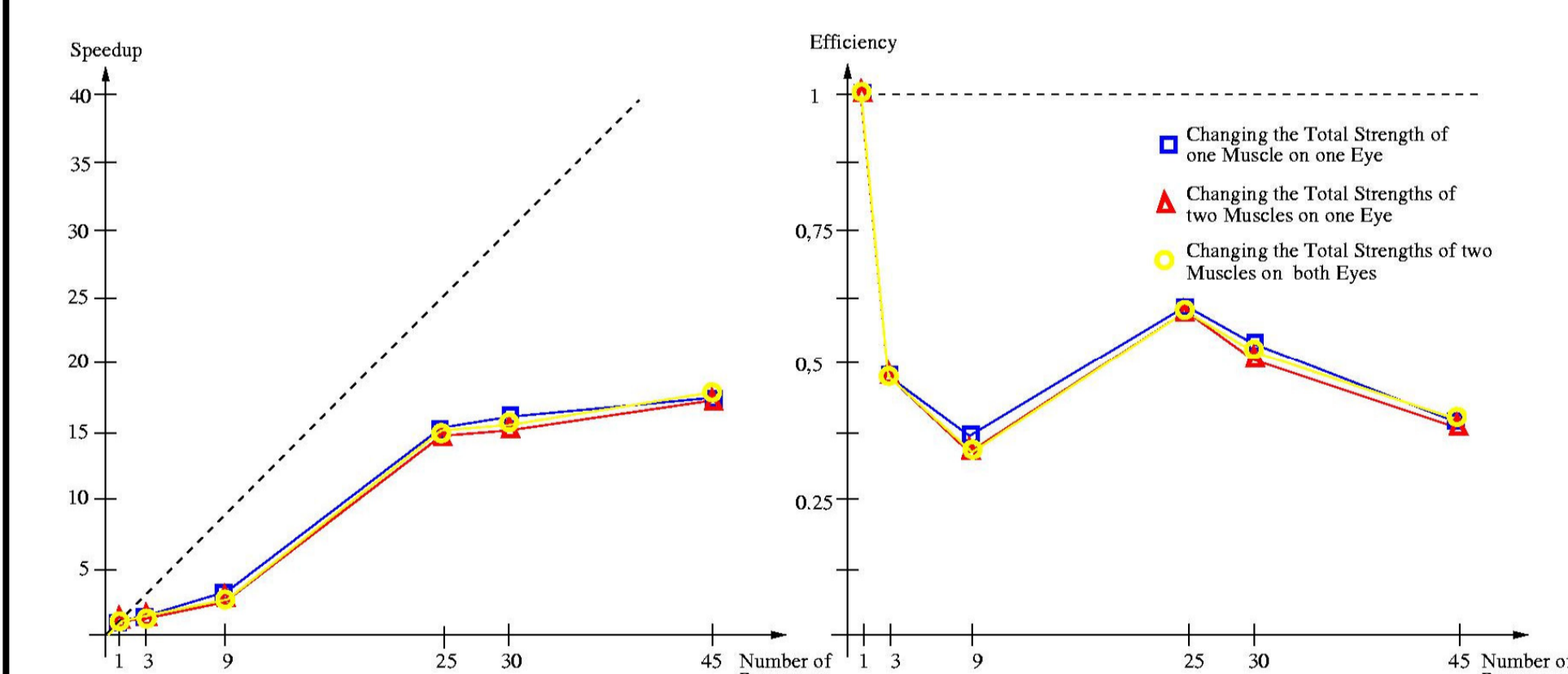


Figure 5: Speedup and Efficiency Diagrams for Gaze Patterns Calculation with 45 points executed on the grid site *altix1.jku.austriangrid.at* (64 Intel Itanium processors 1.4GHz)

Machine Name	altix1.jku.austriangrid.at					altix1.uibk.ac.at			
Number of Processors	1	3	9	25	30	25	30	45	
Changing the Total Strengths of one Muscle on one Eye	25.27s	17.44s	7.58s	1.65s	1.57s	1.43s	1.87s	1.80s	1.71s
Changing the Total Strengths of two Muscles on one Eye	27.18s	18.81s	9.11s	1.82s	1.78s	1.57s	2.01s	1.96s	1.88s
Changing the Total Strengths of two Muscles on both Eyes	28.68s	20.04s	9.80s	1.90s	1.85s	1.59s	2.09s	2.03s	1.92s

Figure 6: Benchmark Results for Gaze Patterns with 45 points

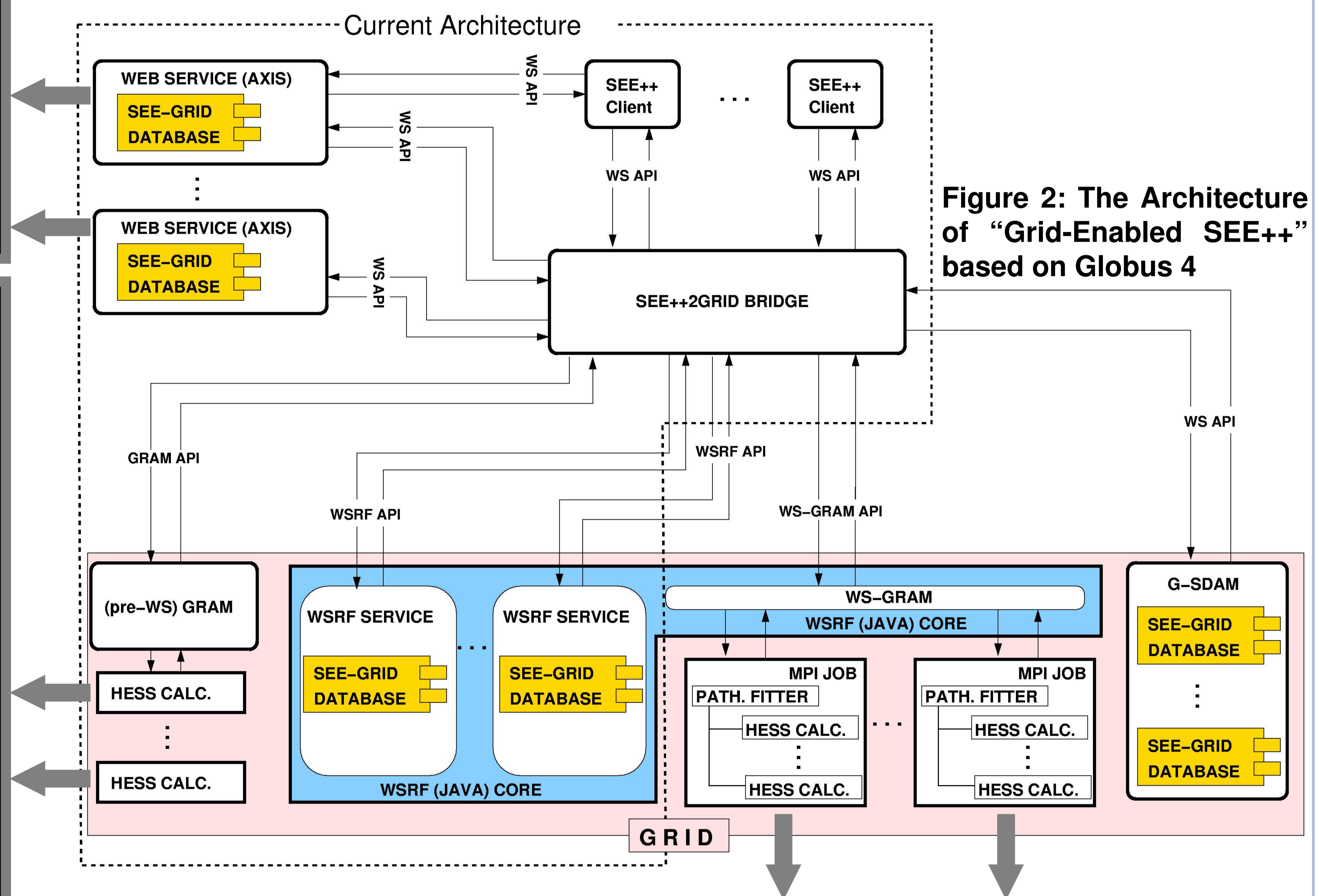


Figure 2: The Architecture of “Grid-Enabled SEE++” based on Globus 4

III. Preliminary Studies with the Pathology Fitting

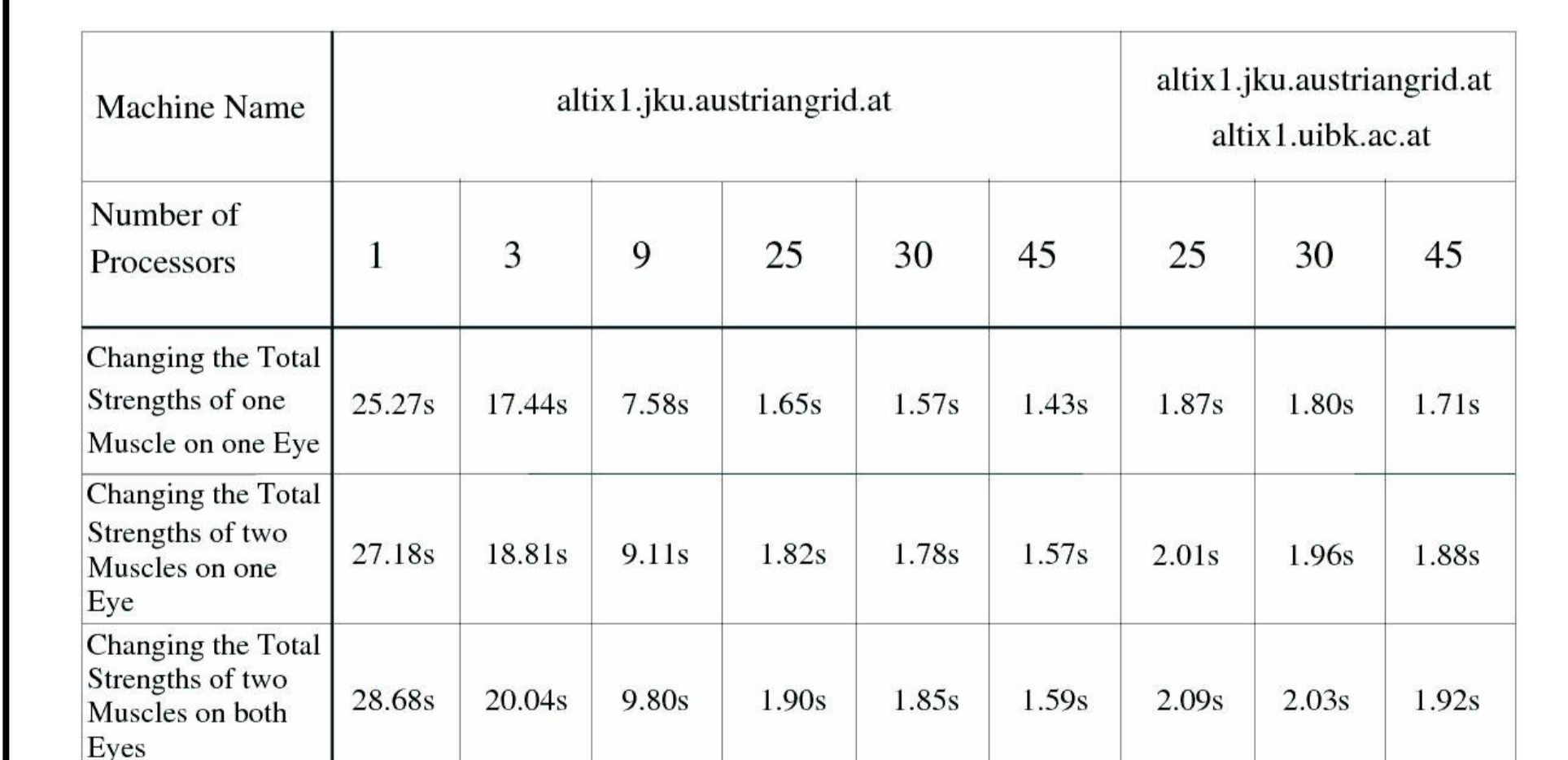


Figure 7: The Outcome of the Pathology Fitting: Intended (blue), Measured (green) and Simulated (red) gaze patterns.

```

/*
Eye : Initial Eye Model
M : Measured Gaze Pattern
H : Heuristic
*/
pathologyFitting(Eye, M, H)
E1 := Eye
C1 := gazePattern(E1)
if C1 matches M return E1

loop
p := nextParameterVariation(H)
if p is equal to NULL return E1
E2 := optimization(p, E1, M)
C2 := gazePattern(E2)
if C2 fits M better than C1
E1 := E2
C1 := C2
if C1 matches M return E1

/*
P : a Type of Eye Model Parameter
E1 : Eye Model
M : Measured Gaze Pattern
*/
optimization(p, E1, M)
v := vector of the p parameter values
on the six eye muscles in E1

loop
C2 := gazePattern(E1, v)
if |M-C2| <= E return E1
v2 := OptimizationStep(v, |M-C2|) /* with Jacobian
and Hessian matrix calculations */
Update parameter p in E1 by v2
v := v2
    
```

Figure 8: A Draft of the Pathology Fitting Algorithm