

Contents

Contents	1
1 Introduction	3
2 E-Science Infrastructures	5
2.1 Introduction to Grid Computing	6
2.2 E-Science Applications	8
2.3 The Grid Programming Environment	9
2.4 Summary and Conclusions	10
3 Eclipse-based Architecture	11
3.1 The Eclipse Rich Client Platform	11
3.1.1 The Workbench, SWT, JFace	12
3.1.2 The Eclipse Plugin Mechanism	13
3.1.3 The Eclipse Extension Mechanism	13
3.2 UNICORE Rich Client	14
3.2.1 URC Plugin Architecture	14
3.2.2 The ServiceBrowser Plugin	15
3.2.3 The GPE4Eclipse Plugin	16
3.3 Summary and Conclusions	18
4 Requirements of Biological Applications in Grids	19
4.1 Biological Background	19
4.2 Computational biology	21
4.3 Biological Sequences and Data Challenges in Grids	22
4.4 Requirement Analysis for Client Support	25
4.5 Related Work	27

<i>CONTENTS</i>	2
4.5.1 UNICORE Clients	27
4.5.2 The g-Eclipse Project	27
4.5.3 Parallel Tools Platform	28
4.5.4 Other Tools in Bioinformatics	29
4.6 Summary and Conclusions	30
5 Design of the Client Support for Biological Applications	31
5.1 Basic Architecture	31
5.2 Sequence Enhancements	34
5.2.1 Sequence Modeling via the GPE-Sequence-Extension	34
5.2.2 Sequence Graphical Interface via the EclipseSequencePlugin	35
5.3 Enabling Database Access	35
5.3.1 Database Browsing via the DatabaseServiceBrowser	35
5.3.2 Database Inputs via the DatabaseServiceBrowser	36
5.4 Summary and Conclusions	36
6 Design Implementation and Evaluation	37
6.1 Implementations of Sequences	37
6.1.1 GPE-Sequence-Extension	37
6.1.2 The EclipseSequencePlugin	39
6.2 Database Access Support	42
6.2.1 OGSA-DAI Integration via the DatabaseServiceBrowser	43
6.2.2 Database File inputs via the DatabaseServiceBrowser	44
6.3 GPE-SWT-Extension	45
6.4 Evaluation Scenario	45
6.4.1 WISDOM Project Use Case	46
6.4.2 The AMBER Sequence	47
6.4.3 Simplified Database Access	48
6.5 Summary and Conclusions	49
7 Summary and Conclusion	51
Bibliography	55
List of Figures	61