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Nota di contenuto	Cover; Title Page; Copyright Page; Table of Contents; Introduction; Acknowledgements; Chapter 1. Principles, Issues and Viewpoints of Traveler Information in a Multimodal Context; 1.1. Introduction; 1.2. A complexity that must be mastered; 1.3. Multimodal information; 1.4. The viatic concept: accompany the traveler; 1.5. Other traveler information-based representative research projects in a multimodal context; 1.5.1. Traveler information and valorization of route time; 1.5.2. Traveler information and personalized accompaniment; 1.5.3. Traveler information and ergonomics 1.5.4. Traveler information and intelligent agents 1.5.5. Traveler information and adjustment to cognitive abilities and the situation of mobility; 1.5.6. Traveler information applied to the bicycle mode; 1.6. Viewpoints; 1.7. Bibliography; Chapter 2. User Needs Analysis Methodology for the Design of Traveler Information Systems; 2.1. Introduction; 2.2. Traveler information: a pluridisciplinary matter; 2.3. The example of the P@ss-ITS project; 2.4. RAMSES methodology for the collection, analysis and modeling of user needs; 2.4.1. Information flows in RAMSES

2.4.2. Generic diagram of information flow
2.4.3. The steps in RAMSES;
2.5. RAMSES in the context of the P@ss-ITS project; 2.5.1. The preparation of collections; 2.5.2. The methodology of data collection; 2.5.3. The analysis of collections; 2.5.4. The definition and evaluation of new services; 2.5.5. Modeling and specification based on P@ss-ITS data; 2.5.6. MASSIV; 2.6. Conclusion; 2.7. Bibliography; Chapter 3. A Generic Method for Personalizing Interactive Systems: Application to Traveler Information; 3.1. Introduction
3.2. Personalization in HCI: examples of existing approaches, at the origin of the approach proposed
3.3. PerMet: method for the development of personalized information systems; 3.3.1. Analysis of the service; 3.3.2. Design of the service; 3.3.3. Implementation of the service; 3.3.4. Analysis of agents; 3.3.5. Design of agent behaviors; 3.3.6. Implementation of agent behaviors; 3.3.7. Integration; 3.3.8. Evaluations; 3.4. PerSyst: personalization system supporting the PerMet method; 3.4.1. General architecture and design of PerSyst; 3.4.2. The coordination agent; 3.4.3. The communication agent
3.4.4. Administration agent
3.5. Application to the public transport of people: itinerary search; 3.5.1. Scenario; 3.5.2. Analysis of the personalized transport service; 3.5.3. Design of the personalized service; 3.5.4. Implementation of the personalized service; 3.5.5. Analysis of constitutive agents of the personalized system; 3.5.6. Design of agent behaviors; 3.5.7. Implementation of the agent behaviors; 3.5.8. Integration; 3.5.9. Evaluations; 3.6. Discussion about the possibility of generalization relative to personalization; 3.7. Conclusion; 3.8. Bibliography
Chapter 4. A Formal Framework for Design and Validation of Multimodal Interactive Systems in Transport Domain

Sommario/riassunto

The human-computer interactions are more and more present in our everyday life, and lead to many conceptual and methodological problems for the designers and evaluators of interactive systems. This book is about Human-Computer Interaction in Transport domain, in which the traveler becomes a user of information systems, particularly before and during the travel(s). This book will focus on traveler information and personalized systems, using a human-centered design approach.

2. Record Nr.	UNINA9910484973803321
Titolo	DNA Computing : 10th International Workshop on DNA Computing, DNA10, Milan, Italy, June 7-10, 2004, Revised Selected Papers // edited by Claudio Ferretti, Giancarlo Mauri, Claudio Zandron
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Altri autori (Persone)	FerrettiClaudio <1965-> MauriGian Carlo ZandronClaudio
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Nota di contenuto	Computing by Observing Bio-systems: The Case of Sticker Systems -- DNA-Based Computation Times -- Computing Beyond the Turing Limit Using the H Systems -- Biomolecular Implementation of Computing Devices with Unbounded Memory -- Characterization of Non-crosshybridizing DNA Oligonucleotides Manufactured In Vitro -- Error Free Self-assembly Using Error Prone Tiles -- On the Computational Complexity of P Automata -- A Weighted Insertion-Deletion Stacked Pair Thermodynamic Metric for DNA Codes -- DNA Extraction by XPCR -- A Method of Error Suppression for Self-assembling DNA Tiles -- Using Automated Reasoning Systems on Molecular Computing -- Parallelism in Gene Assembly -- Splicing Systems for Universal Turing Machines -- Application of Mismatch Detection Methods in DNA Computing -- Bond-Free Languages: Formalizations, Maximality and

Construction Methods -- Preventing Undesirable Bonds Between DNA Codewords -- Testing Structure Freeness of Regular Sets of Biomolecular Sequences -- Minimum Basin Algorithm: An Effective Analysis Technique for DNA Energy Landscapes -- Efficient Initial Pool Generation for Weighted Graph Problems Using Parallel Overlap Assembly -- Partial Words for DNA Coding -- Accepting Hybrid Networks of Evolutionary Processors -- Building the Components for a Biomolecular Computer -- Methods for Manipulating DNA Molecules in a Micrometer Scale Using Optical Techniques -- From Cells to Computers: Membrane Computing – A Quick Overview -- The Capacity of DNA for Information Encoding -- Compact Error-Resilient Computational DNA Tiling Assemblies -- Toward “Wet” Implementation of Genetic Algorithm for Protein Engineering -- Programmable Control of Nucleation for Algorithmic Self-assembly -- DNA Hybridization Catalysts and Catalyst Circuits -- Complexity of Self-assembled Shapes.-Aqueous Computing with DNA Hairpin-Based RAM -- A Programmable Molecular Computer in Microreactors -- Combinatorial Aspects of Minimal DNA Expressions -- A Design for Cellular Evolutionary Computation by Using Bacteria -- An Inexpensive LED-Based Fluorometer Used to Study a Hairpin-Based DNA Nanomachine -- Designs of Autonomous Unidirectional Walking DNA Devices -- Design of an Autonomous DNA Nanomechanical Device Capable of Universal Computation and Universal Translational Motion -- A Clocked DNA-Based Replicator -- A Bayesian Algorithm for In Vitro Molecular Evolution of Pattern Classifiers.
