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Autore	Neuhaus Michel
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Note generali	Extended and revised version of the first author's PhD thesis.
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Nota di contenuto	<p>Preface; Contents; 1. Introduction; 2. Graph Matching; 2.1 Graph and Subgraph; 2.2 Exact Graph Matching; 2.3 Error-Tolerant Graph Matching; 3. Graph Edit Distance; 3.1 Definition; 3.2 Edit Cost Functions; 3.2.1 Conditions on Edit Costs; 3.2.2 Examples of Edit Costs; 3.3 Exact Algorithm; 3.4 Efficient Approximate Algorithm; 3.4.1 Algorithm; 3.4.2 Experimental Results; 3.5 Quadratic Programming Algorithm; 3.5.1 Algorithm; 3.5.1.1 Quadratic Programming; 3.5.1.2 Fuzzy Edit Path; 3.5.1.3 Quadratic Programming Edit Path Optimization; 3.5.2 Experimental Results; 3.6 Nearest-Neighbor Classification 3.7 An Application: Data-Level Fusion of Graphs 3.7.1 Fusion of Graphs; 3.7.2 Experimental Results; 4. Kernel Machines; 4.1 Learning Theory; 4.1.1 Empirical Risk Minimization; 4.1.2 Structural Risk Minimization; 4.2 Kernel Functions; 4.2.1 Valid Kernels; 4.2.2 Feature Space Embedding and Kernel Trick; 4.3 Kernel Machines; 4.3.1 Support Vector Machine; 4.3.2 Kernel Principal Component Analysis; 4.3.3 Kernel Fisher Discriminant Analysis; 4.3.4 Using Non-Positive Definite Kernel Functions; 4.4 Nearest-Neighbor Classification Revisited; 5. Graph Kernels; 5.1 Kernel Machines for Graph Matching 5.2 Related Work 5.3 Trivial Similarity Kernel from Edit Distance; 5.4 Kernel from Maximum-Similarity Edit Path; 5.5 Diffusion Kernel from Edit Distance; 5.6 Zero Graph Kernel from Edit Distance; 5.7 Convolution Edit Kernel; 5.8 Local Matching Kernel; 5.9 Random Walk Edit Kernel; 6. Experimental Results; 6.1 Line Drawing and Image Graph Data Sets; 6.1.1 Letter Line Drawing Graphs; 6.1.2 Image Graphs; 6.1.3 Diatom Graphs; 6.2 Fingerprint Graph Data Set; 6.2.1 Biometric Person Authentication; 6.2.2 Fingerprint Classification; 6.2.3 Fingerprint Graphs; 6.3 Molecule Graph Data Set 6.4 Experimental Setup 6.5 Evaluation of Graph Edit Distance; 6.5.1 Letter Graphs; 6.5.2 Image Graphs; 6.5.3 Diatom Graphs; 6.5.4 Fingerprint Graphs; 6.5.5 Molecule Graphs; 6.6 Evaluation of Graph Kernels; 6.6.1 Trivial Similarity Kernel from Edit Distance; 6.6.2 Kernel from Maximum-Similarity Edit Path; 6.6.3 Diffusion Kernel from Edit Distance; 6.6.4 Zero Graph Kernel from Edit Distance; 6.6.5 Convolution Edit Kernel; 6.6.6 Local Matching Kernel; 6.6.7 Random Walk Edit Kernel; 6.7 Summary and Discussion; 7. Conclusions; Appendix A Graph Data Sets; A.1 Letter Data Set; A.2 Image Data Set A.3 Diatom Data Set A.4 Fingerprint Data Set; A.5 Molecule Data Set; Bibliography; Index</p>
Sommario/riassunto	<p>In graph-based structural pattern recognition, the idea is to transform patterns into graphs and perform the analysis and recognition of patterns in the graph domain - commonly referred to as graph matching. A large number of methods for graph matching have been proposed. Graph edit distance, for instance, defines the dissimilarity of two graphs by the amount of distortion that is needed to transform one graph into the other and is considered one of the most flexible methods for error-tolerant graph matching. This book focuses on graph kernel functions that are highly tolerant towards structural</p>