

Kap. 5b

Anwendungen:

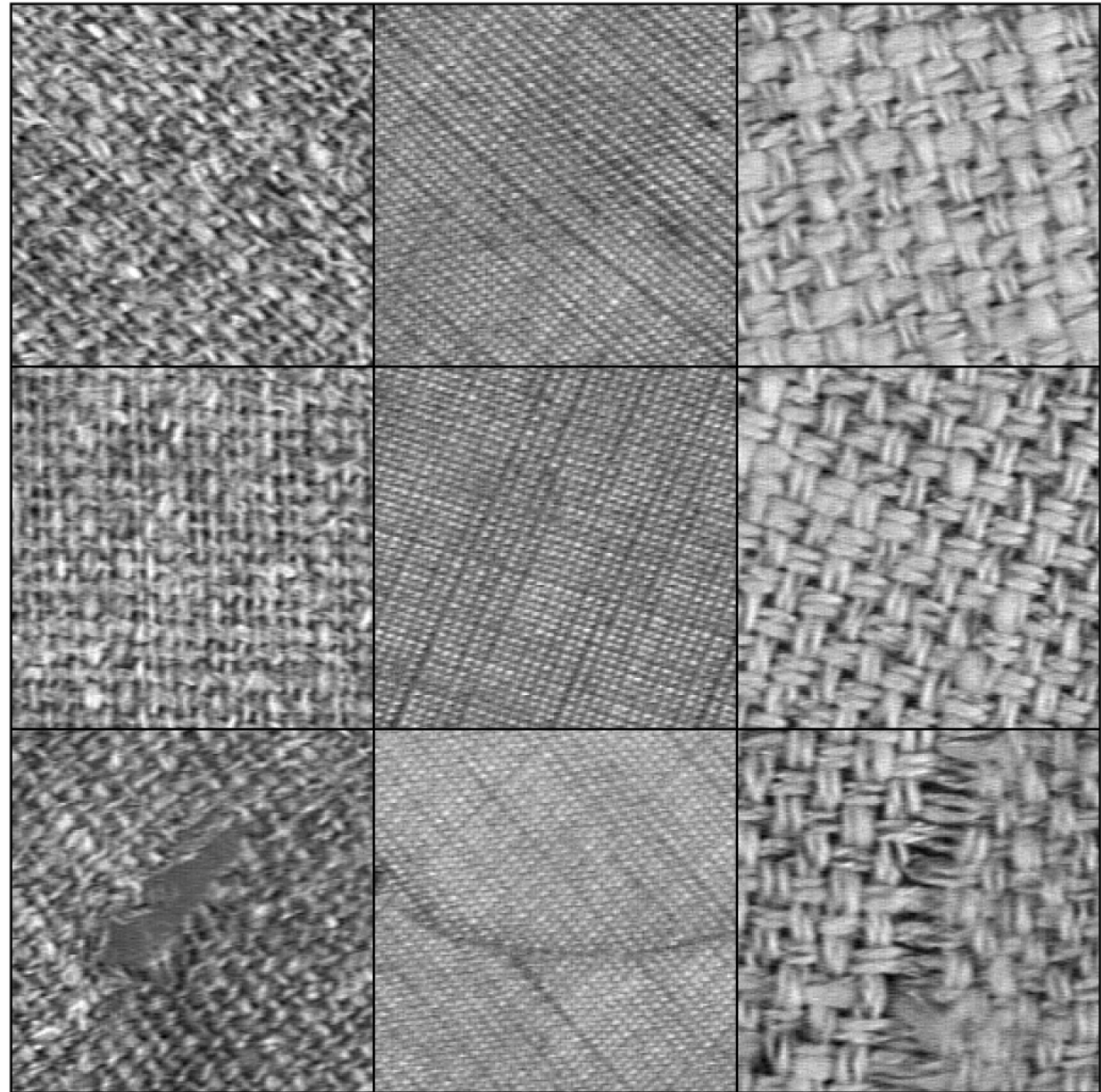
Invarianten über Gruppenmittel

- Sichtprüfungsaufgaben (Textilien)
- Bildsuchmaschinen (query by example) SIMBA und MICHELscope
- Automatische Klassifikation von Blütenpollen
- Suchen in Proteindatenbanken
- Suchen nach Wasserzeichen in alten Drucken

Complexity of Search tasks

- Finding an identical object (pixel by pixel) is trivial !
- Challenge for the future:
Searching in Equivalence classes (up to a very high semantic level) can be very complex and demanding
- Data Bases without an intelligent access and retrieval mechanism is a graveyard for Bits and Bytes!

Visual inspection of textiles with anisotropic texture

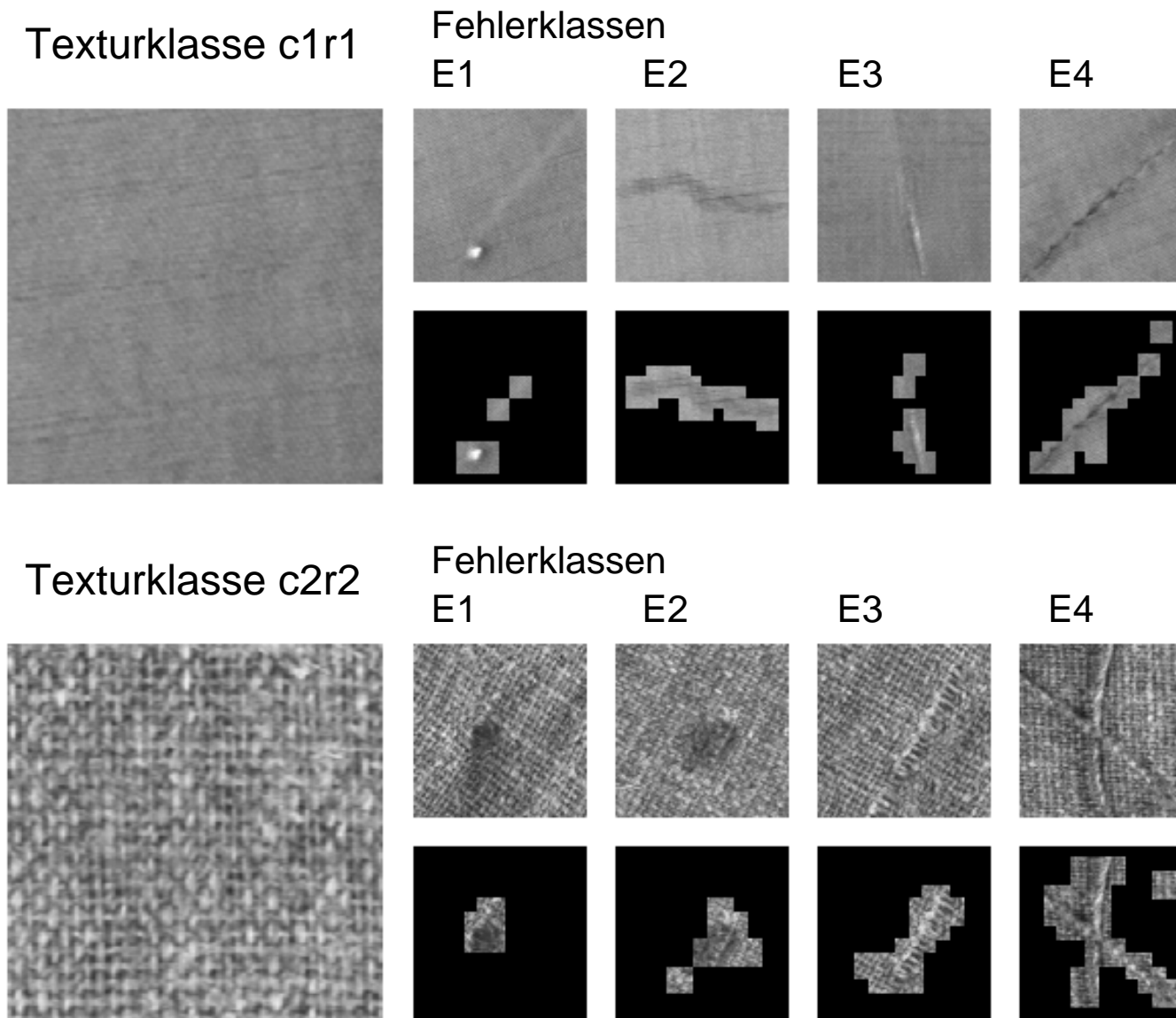


Textildatenbank TILDA

<http://www.informatik.uni-freiburg.de/~lmb/tilda> (ca. 3200 images)

Texturdefektdetektion bei Textilstoffen

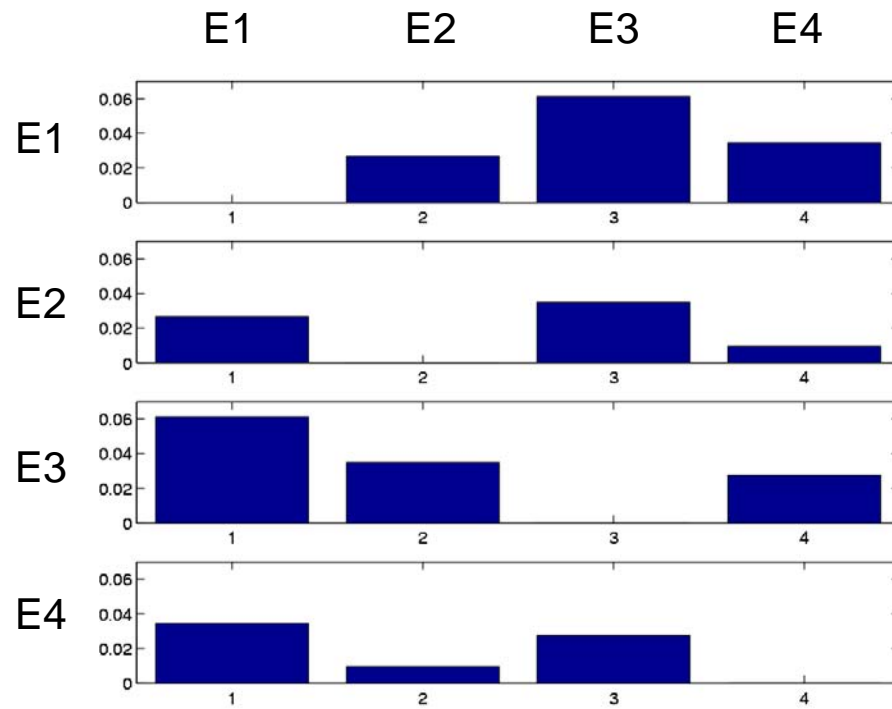
Segmentierung der Defekte



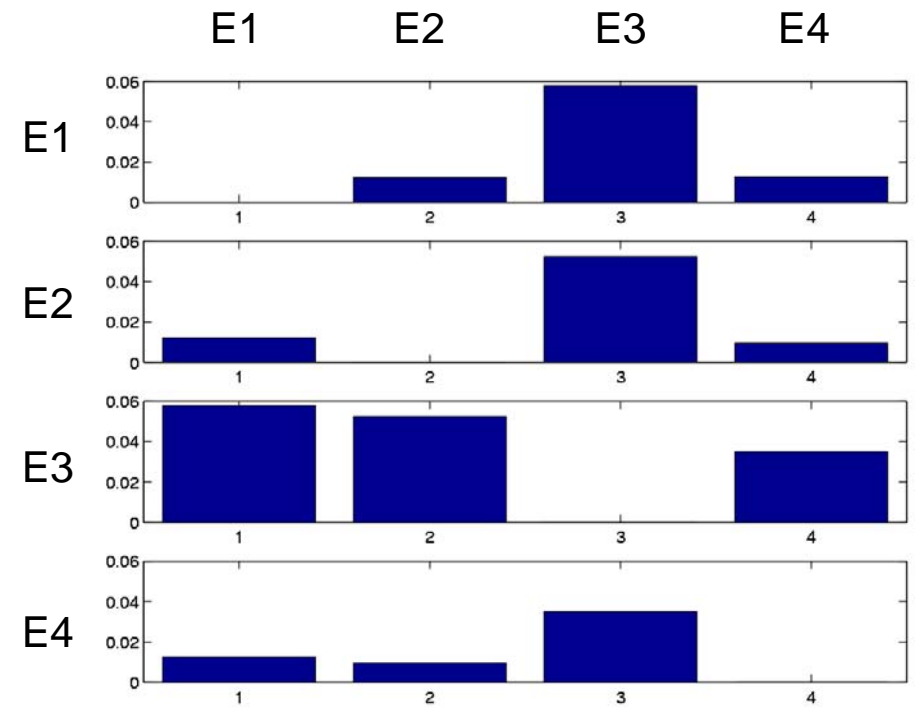
Texturdefektdetektion bei Textilstoffen

Diskriminierung der Defektklassen

Klassendistanzen Texturklasse c1r1

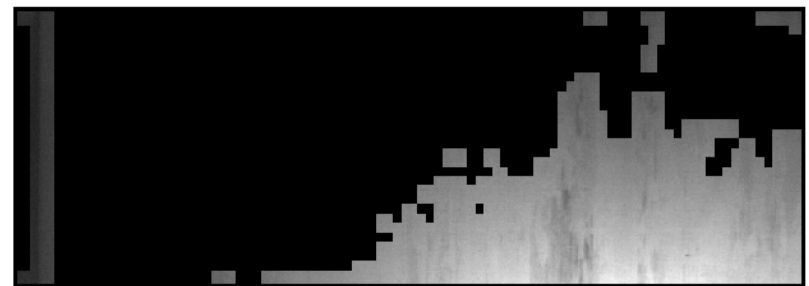
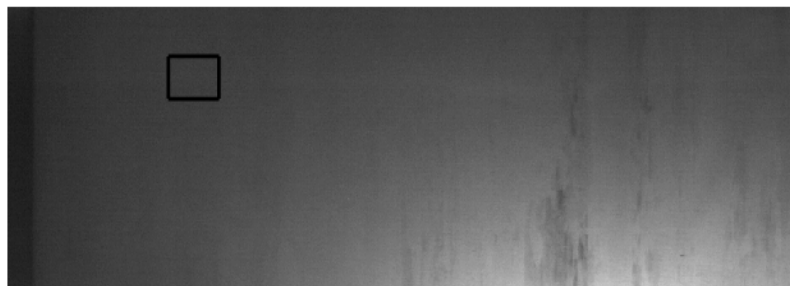
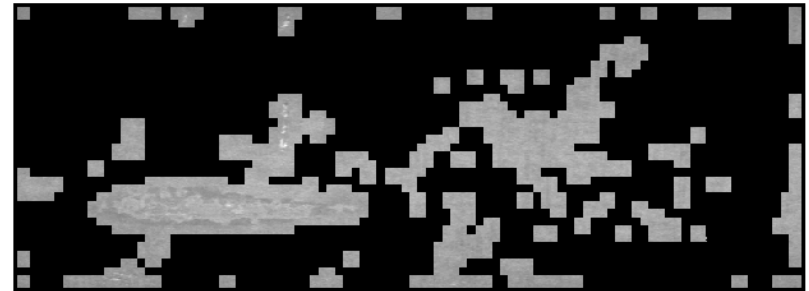
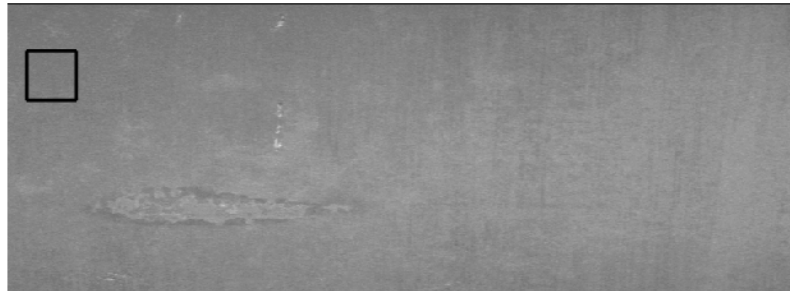
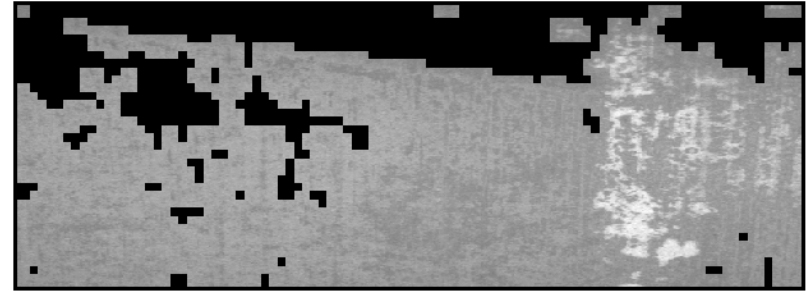
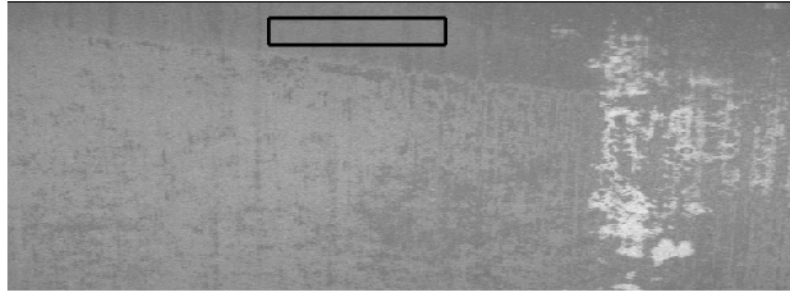


Klassendistanzen Texturklasse c2r2

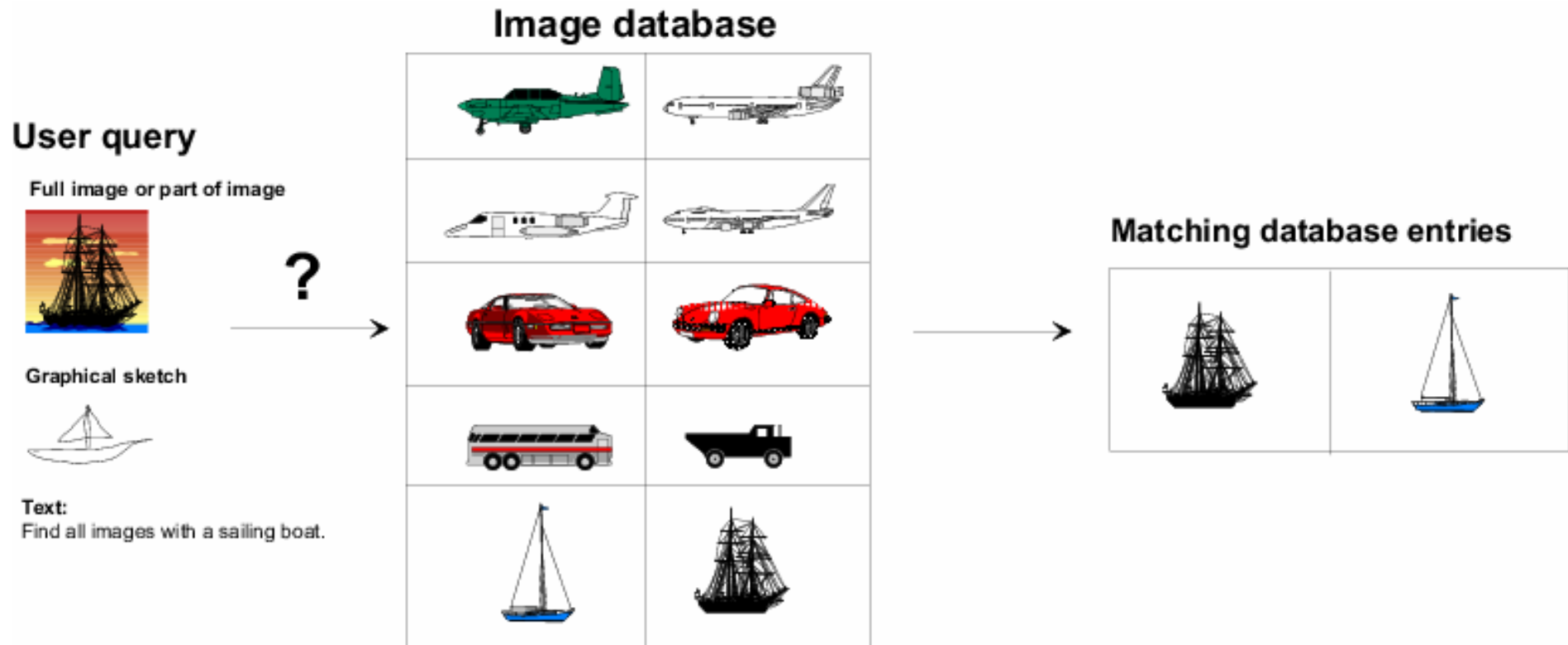


Texturdefektdetektion auf Stahloberflächen

Segmentierung der Defekte



Content based image retrieval



<http://simba.informatik.uni-freiburg.de/>



Query image



0.978



0.828



0.792



0.686



0.674



0.649



0.630



0.595



Query image



0.98



0.82



0.81



0.79



0.78



0.78



0.77



0.76



Query image



0.99



0.79



0.77



0.68



0.68



0.66



0.66



0.66



Query image



0.98



0.82



0.79



0.77



0.74



0.73



0.71



0.71



Query image



0.98



0.79



0.77



0.68



0.68



0.65



0.65



0.63





Query image



0.98



0.80



0.78



0.74



0.70



0.60



0.59



0.57

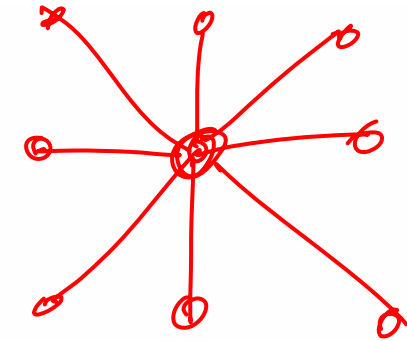
SIMBA – Search IMages By Appearance

COLOR only

*relationale
Kerne*



Search template



96827



63939.4



62383.7



60840.3



59997.4



59316.6



59061



58323.8

SIMBA – Search IMages By Appearance

RELATIONAL only



Search template



87948.7



85491.7



85163



84896.4



84603.2



84379.5



84065.4



83475.7

SIMBA – Search IMages By Appearance

COLOR only



Search template



96689.4



81479.3



77883.8



71489.1



70400.4



67864.2



66298.7



66249.5



SIMBA – Search IMages By Appearance

COLOR+RELATIONAL



Search template



92393.05



81203.6



77685.85



75091.55



71376.85



70761.3







69292.6



68030.95

Experiments

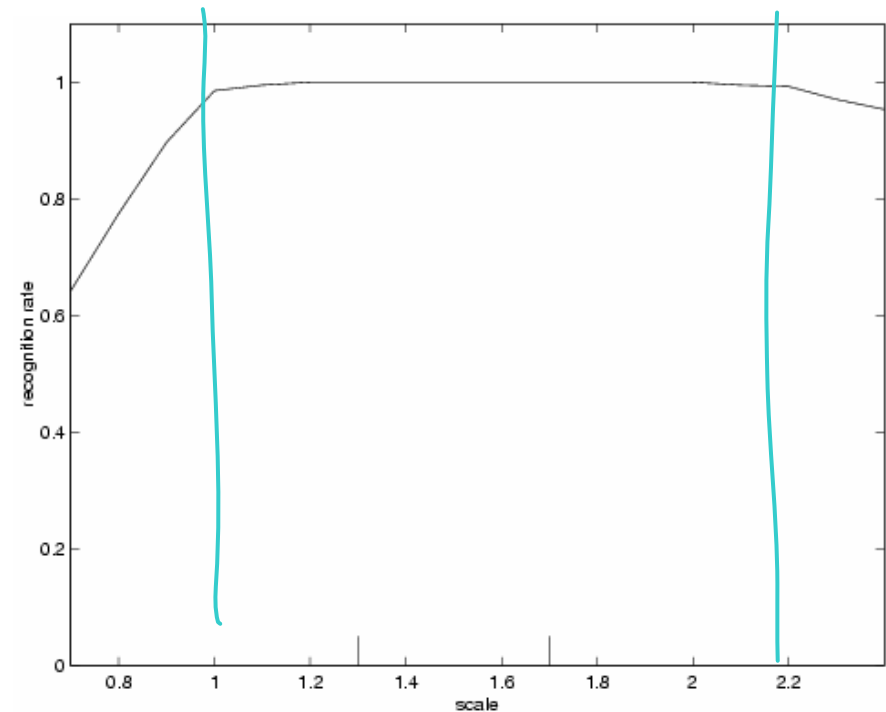


 Search template	 99.95	 99.87	 97.27
	 96.42	 96.02	 95.85
	 95.26	 93.13	 91.60

Robustness to scaling



- Database as before, grayvalue features only
- Kernels $\mathbf{M}(1,0)\mathbf{M}(0,2)$, $\mathbf{M}(2,0)\mathbf{M}(0,4)$
- Images reduced/zoomed (bilinear interpolation) to scales from 0.7 to 2.4
- Database contains scales 1.3 and 1.7 only



→ Good recognition from scale 1 to 2.2, i.e. scale 4.8 in area

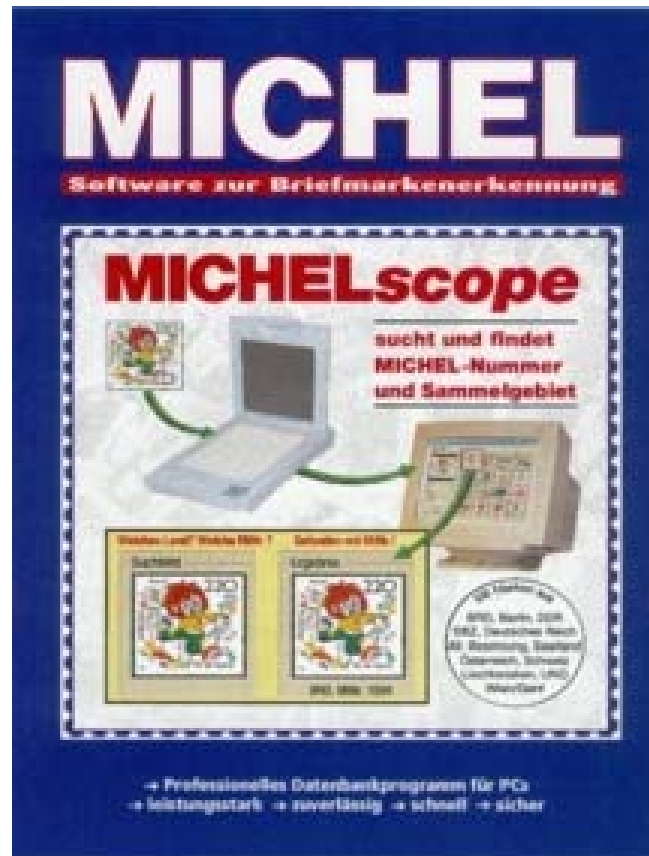
SIMBA

Searching Images by Appearance

<http://simba.informatik.uni-freiburg.de/>

MICHELscope

A search engine for philatelists



Suchbild



Suchmethode

Farbe Textur

Motiv Größe Seitenverhältnis

Datenbank

BRD

Suche starten

Ergebnisse

 Brd0644	 Brd0638	 Brd0732	 Brd0689
 Brd0729	 Brd0636	 Brd0727	 Brd0637
 Brd0645	 Brd0640	 Brd0642	 Brd0635
 Brd0691	 Brd0730	 Brd0639	 Brd0643

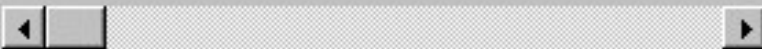
Suchbild



Suchmethode

Farbe

Textur



Motiv

Größe

Seitenverhältnis

Datenbank

BRD

Suche starten

Ergebnisse



Brd0644



Brd0637



Brd0689



Brd0636



Brd1138



Brd0489



Brd0727



Brd0502



Brd0494



Brd0854



Brd0193



Brd0492



Brd0191



Brd0635



Brd0168



Brd0857

Suchbild



Suchmethode

Farbe

Textur



Motiv

Größe

Seitenverhältnis



Datenbank

BRD

Suche starten

Ergebnisse



Brd0523



Brd0485



Brd0538



Brd0232



Brd0408



Brd0409



Brd0486



Brd0447



Brd0540



Brd0164



Brd0449



Brd0266



Brd0386



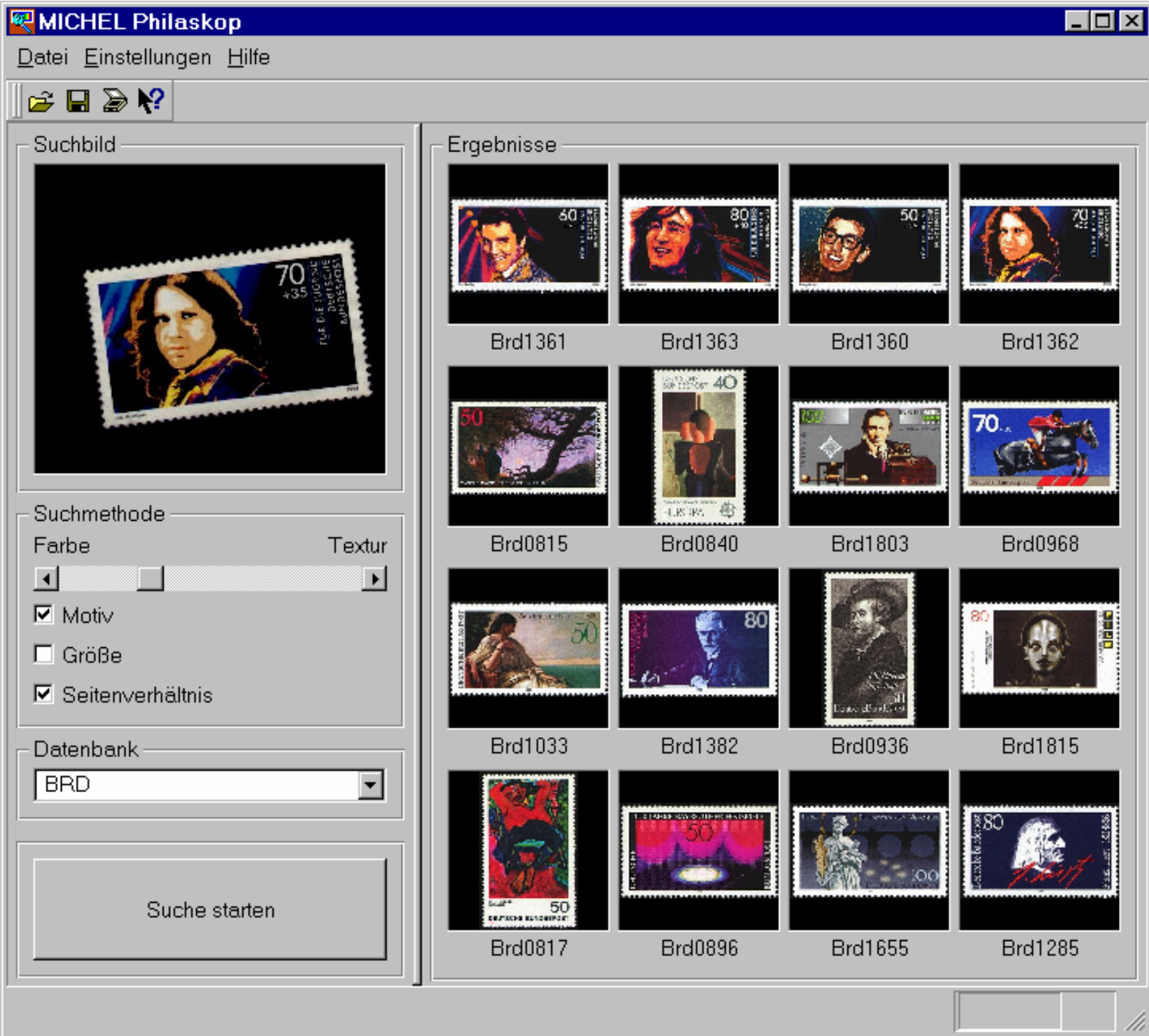
Brd0173

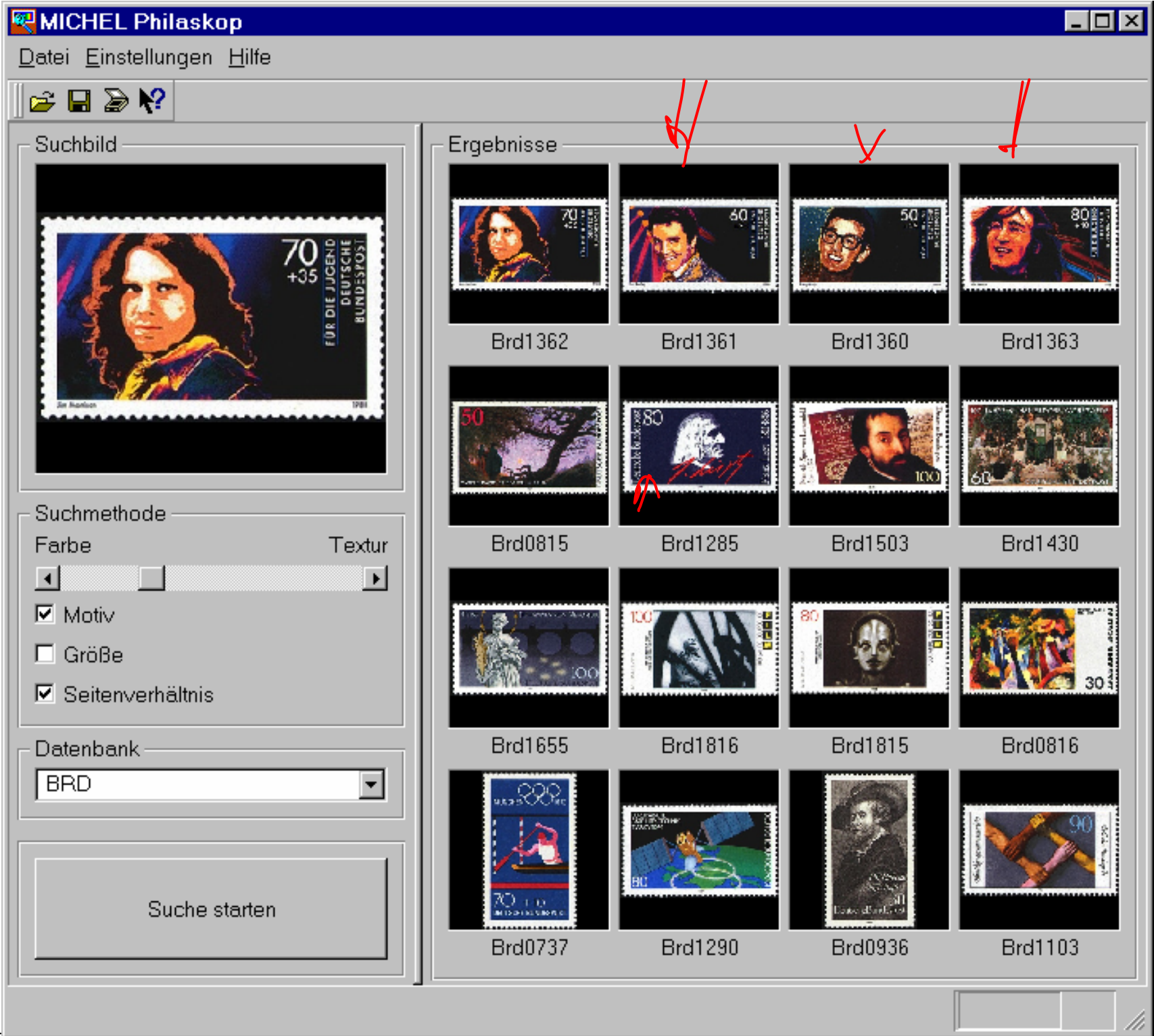


Brd1610



Brd0487





Suchbild



Suchmethode



Farbe

Textur



Motiv

Größe

Seitenverhältnis

Datenbank

BRD

Suche starten

Ergebnisse



Brd0700



Brd0694



Brd0697



Brd0773



Brd0703



Brd0702



Brd0698



Brd0696



X Brd0701



Brd1623



Brd1140



Brd0695 X



Brd1379



Brd1137



Brd0699 X




Brd1038

MICHELphilascope [_] [□] [X]

Datei Einstellungen Hilfe

Suchbild



Suchmethode ↑

Farbe ↔ Textur ↔

Motiv ↔

Größe

















Seitenverhältnis

Datenbank

Deutschland

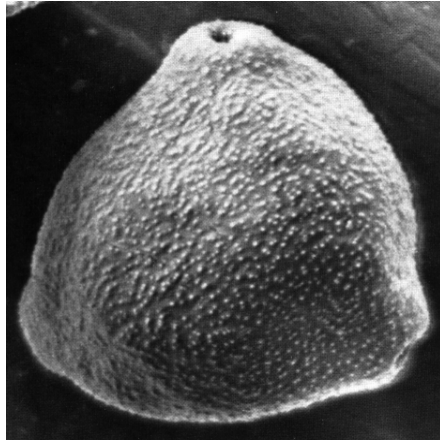
Suche starten

Ergebnisse

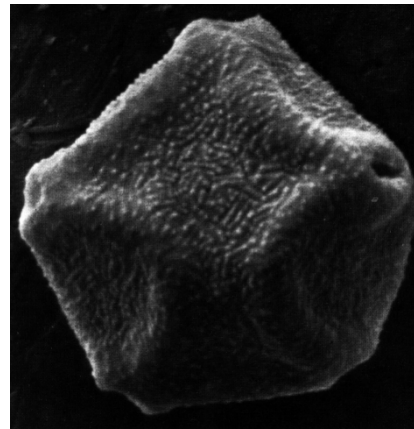
 0509	 0507	 0506	 0510
 0286	 0287	 0290	 0288
 0508	 0289	 0231	 0148
 1143	 0042 ↑	 0032	 0145 ↔

Deutschland Berlin (West) 0042

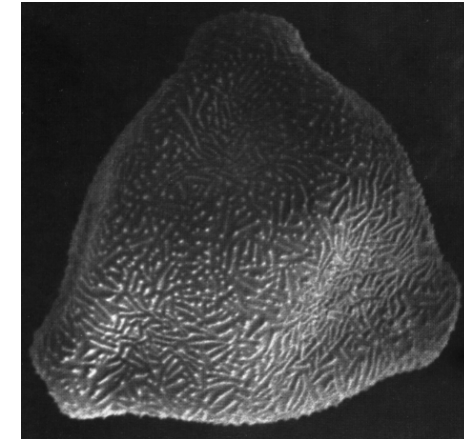
Projekt zur automatischen Erkennung von Blütenpollen - Elektronenmikroskopische Aufnahmen von Pollen



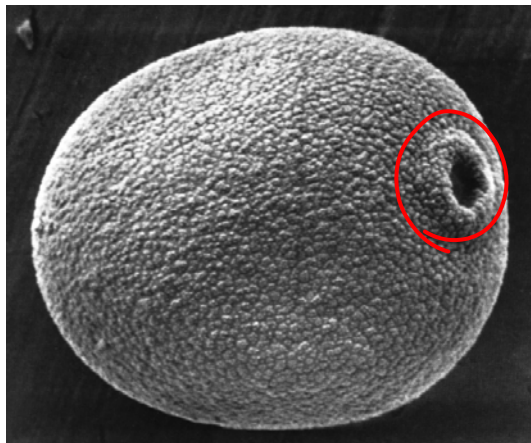
Hasel



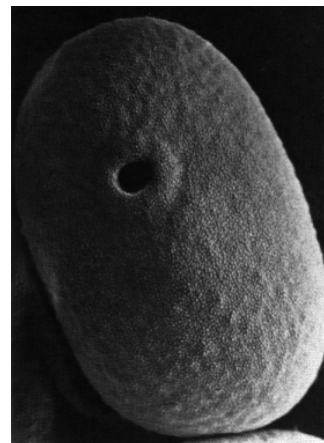
Erle



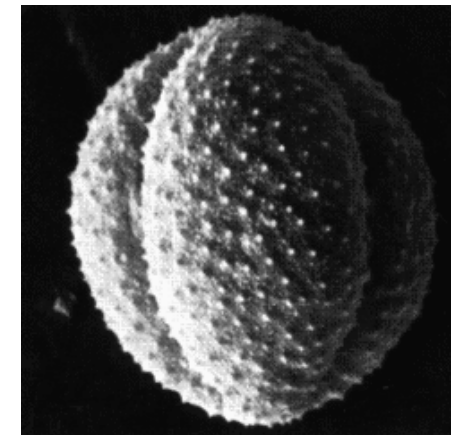
Birke



Gräser



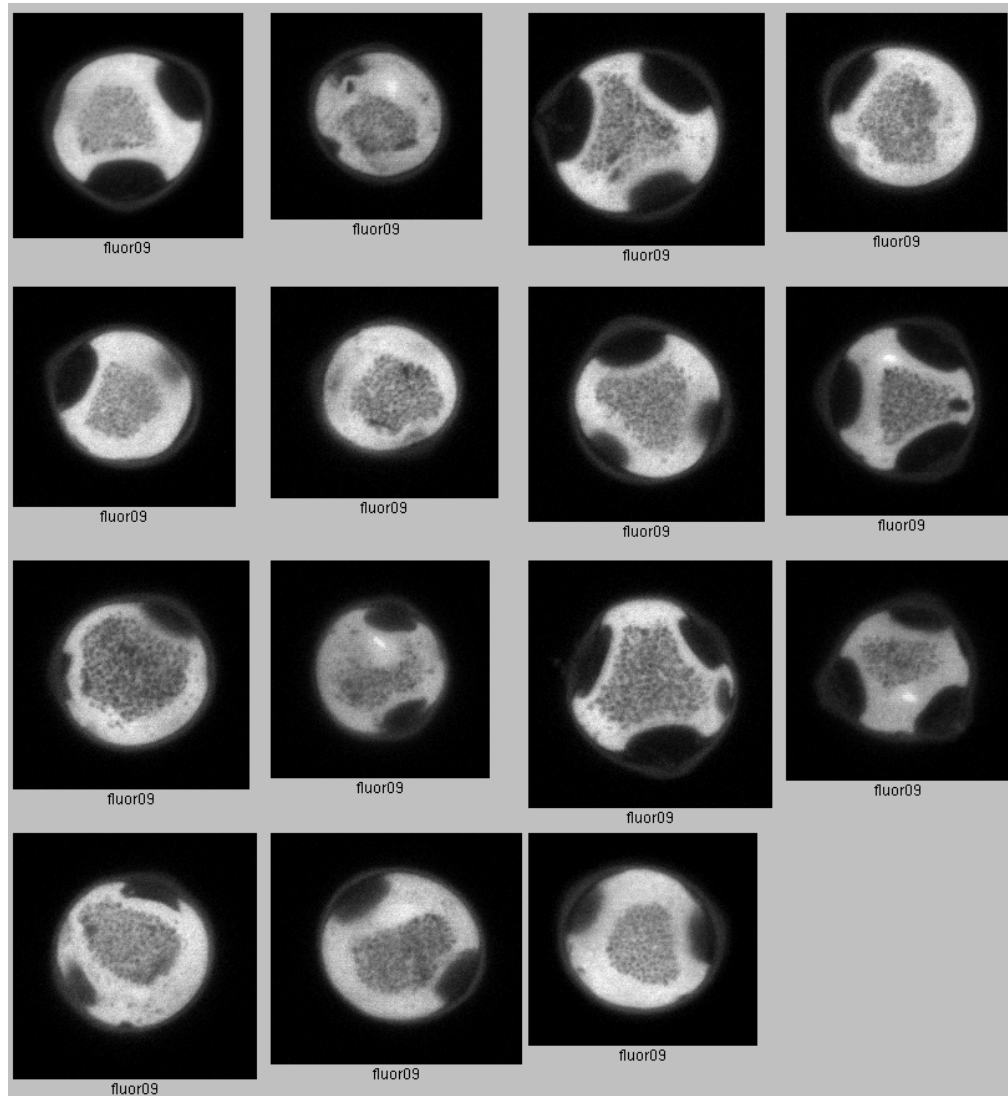
Roggen



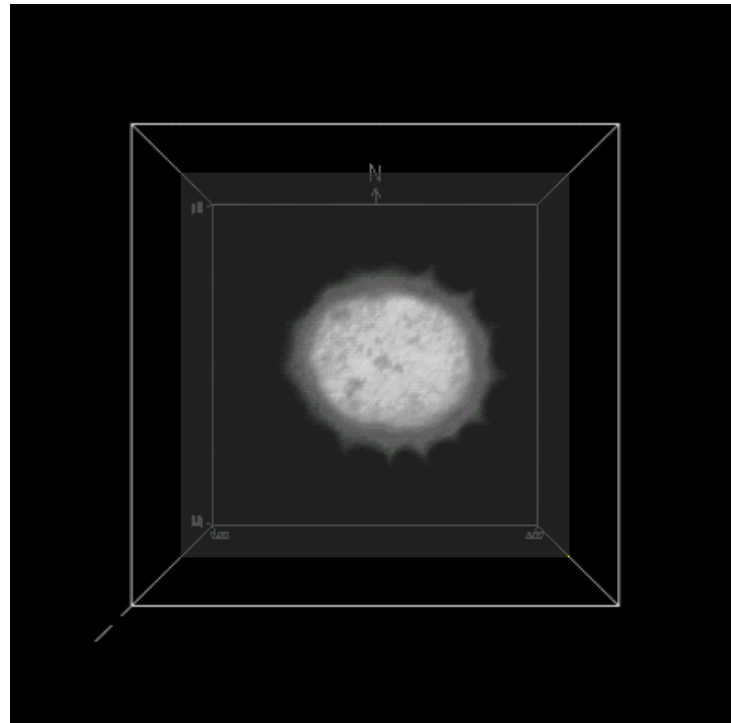
Beifuß

+ 33 further species (not relevant for allergies)

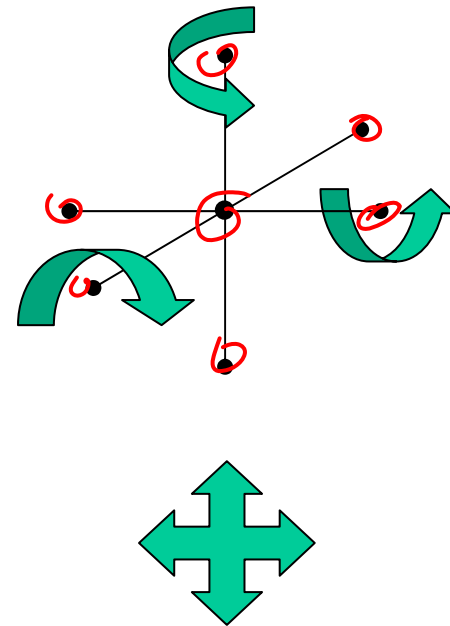
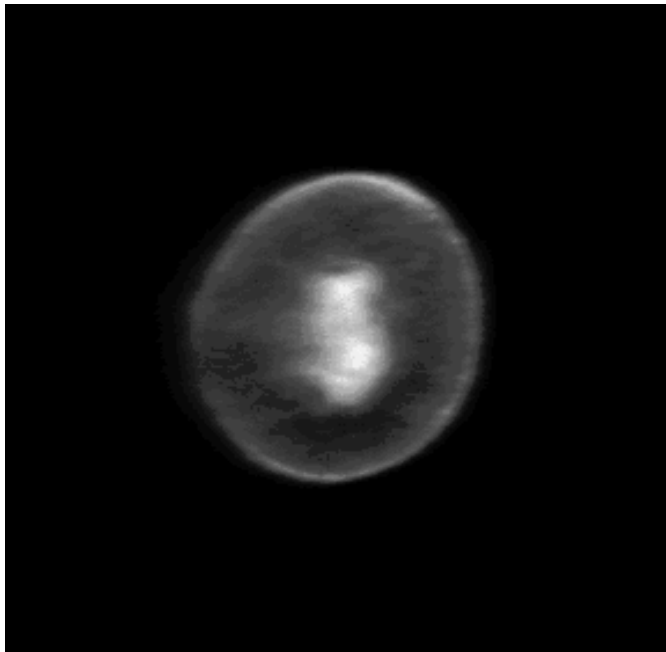
Haselpollen



Gänseblümchen/daisy pollen grain



Eibe/Taxus



Integriere über die 3D Euklidische Bewegung

Reference Data Base Description

- 26 pollen species directly sampled from the plants
 - Correctly assigned species
 - Maybe less variation in size and shape compared to airborne pollen (no different sub-species, no regional variation)
 - No deformation or contamination or agglomeration
- Recording 3D volumes of about 15 samples of each species with a Confocal Laser Scanning Microscope
 - No distortions of the data due to imperfect imaging of a usual microscope

Automated Pollen Recognition in Air Samples by Digital Microscopy

O. Ronneberger, U. Heimann, V. Dietze, E. Schultz

► Motivation

- Time-consuming, but still inaccurate visual pollen counting

► Demand

- Reliable pollen data for pollen forecast

► Approach

- 3D fluorescence imaging (tomography) instead of 2D conventional translucent microscopy
- Image recognition based on general »grey scale invariants«, instead of traditional object specific features

► First results (see table on the right)

- »Grey scale invariants« have characteristic shapes for different pollen species
- Recognition rate of 82% already in a first run

► Outlook

- Employment of digital microscopy for automated particle analysis in general.

Pollen species	Grey Scale Invariants	No.	Mis-classifications
Maple		5	1 (j) → Goose.
Birch		8	3 (r1) → Alder (r3) → Alder (s1) → Alder
Yew		2	-
Alder		10	2 (u3) → Birch (v3) → Birch
Goosefoot		7	-
Horn beam		2	-
Hazel		10	2 (p2) → Goose. (p4) → Alder

Collaborating institutions



Deutscher
Wetter
Dienst



MeteoSchweiz



ALBERT-LUDWIGS-
UNIVERSITY OF FREIBURG

Classification Results using 3D LSM Data

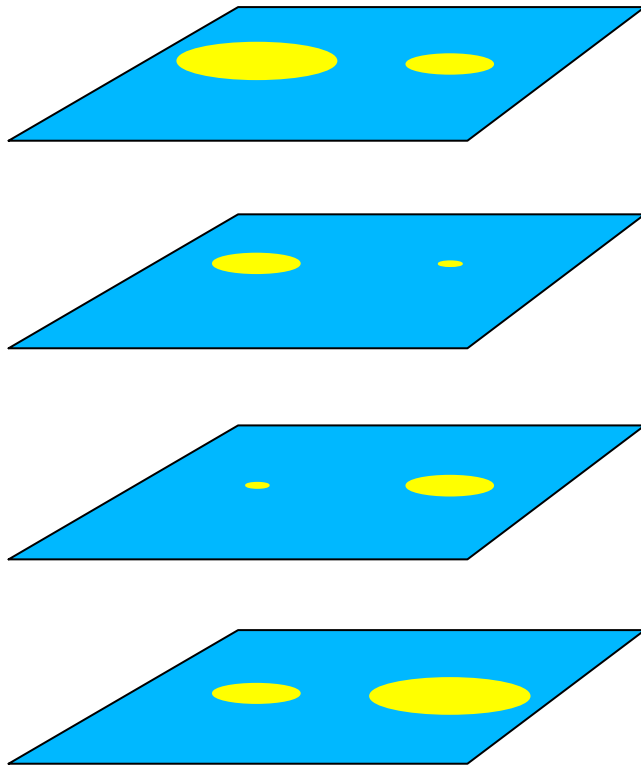
(leave-one-out Classification)

	Correct	Wrong classifications
<i>Artemisia:</i>	13	1 -> <i>Compositae</i> , 1 -> <i>Platanus</i>
<i>Alnus:</i>	15	-
<i>Alnus viridis:</i>	12	-
<i>Betula:</i>	13	2 -> <i>Plantago</i>
<i>Corylus:</i>	13	1 -> <i>Alnus</i>
<i>Gramineae/Poaceae:</i>	15	-
<i>Secale:</i>	11	3 -> <i>Fagus</i> , 1 -> <i>Tilia</i>
Allergolocial irrelevant*:	282	2 -> <i>Gramineae</i>
Total:	97.4%	2.6%

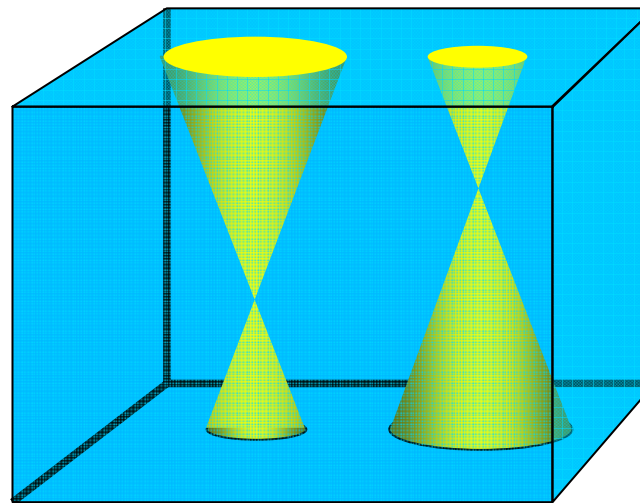
98,7%

* *Acer, Carpinus, Chenopodium, Compositae, Cruciferae, Fagus, Quercus, Aesculus, Juglans, Fraxinus, Plantago, Platanus, Rumex, Populus, Salix, Taxus, Tilia, Ulmus, Urtica*

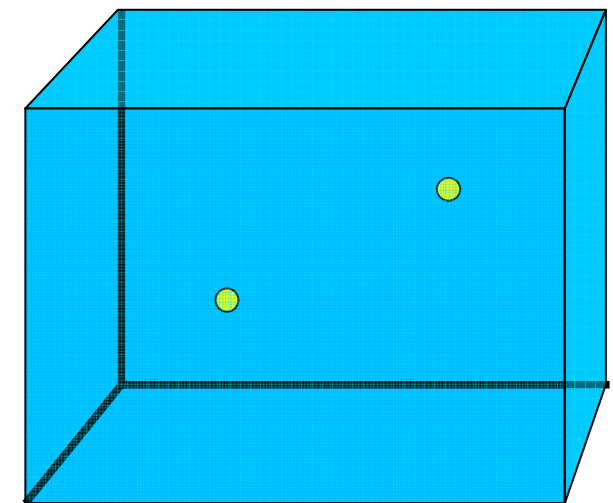
Gewinnung von tomographischen 3D-Daten mit einem normalen Fluoreszenz-Mikroskop



Aufnahme eines
Bildstapels mit einem
normalen Mikroskop

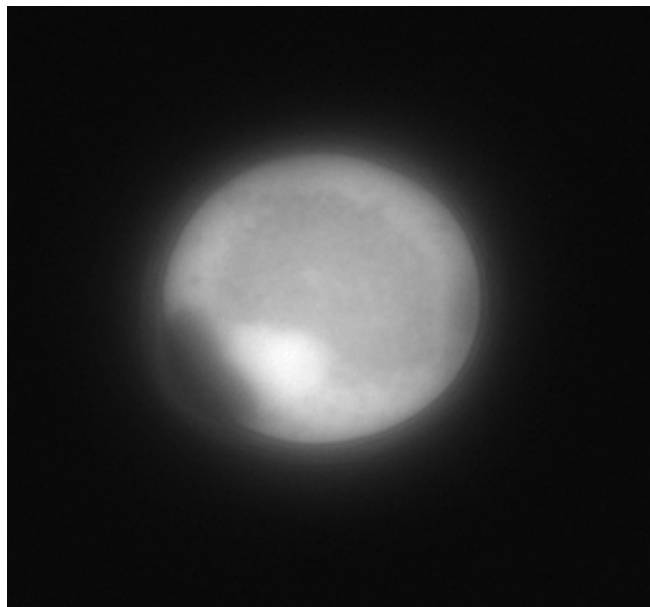


Zusammensetzen der
Bilder im Computer zu
einem Volumen

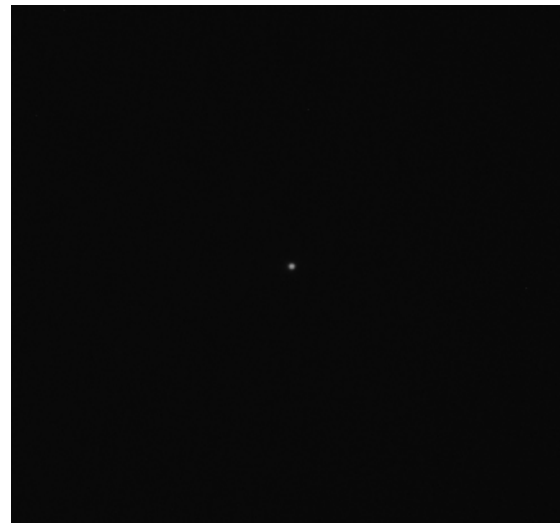


Nach Entfaltung mit der
Punktbildfunktion sind
alle unscharfen
Bereiche entfernt

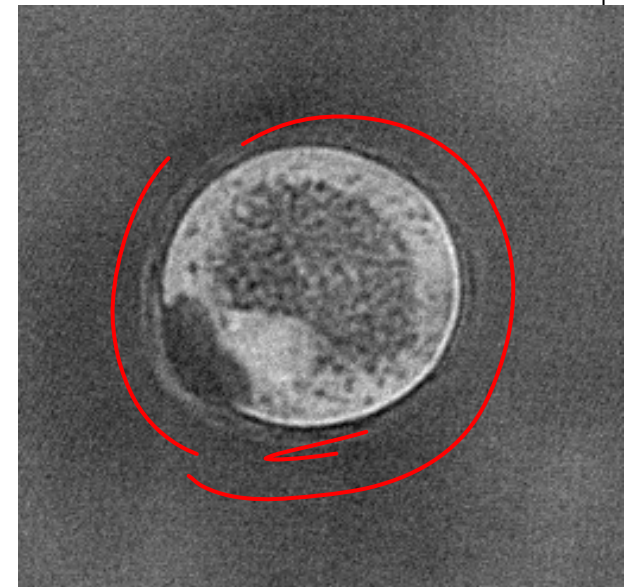
Deconvolution of a Pollen (Hasel/Corylus)



volume



point-spread
function

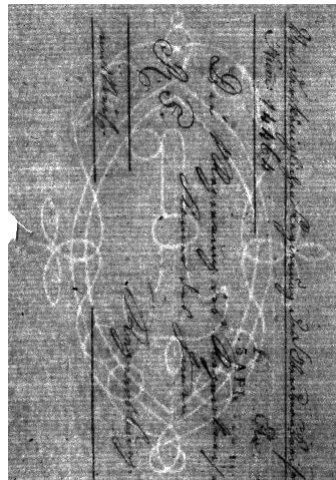


deconvolved volume

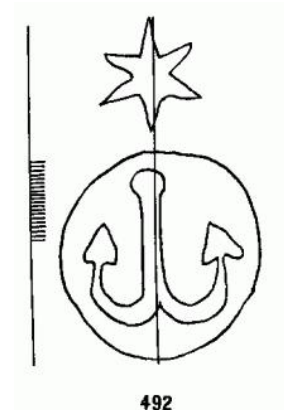
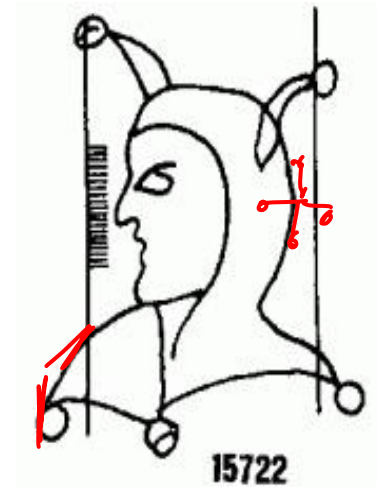
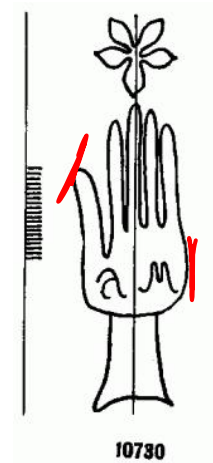


Search Engine for Watermarks in old paper prints (Joint project with Basel Paper Mill, Swiss Museum for Paper, Writing and Printing)

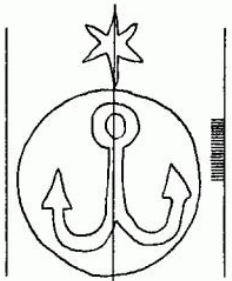
Scanned watermark images
(samples)



After preprocessing
(sample images)



Query Image

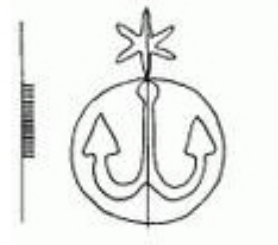


482



482

1.00000



478

0.98446



480

0.98229



471

0.98045



479

0.97986



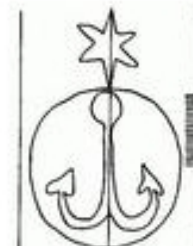
478

0.97949



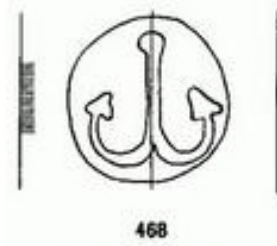
470

0.97924



481

0.97890



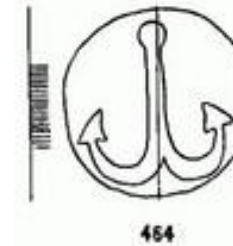
468

0.97787



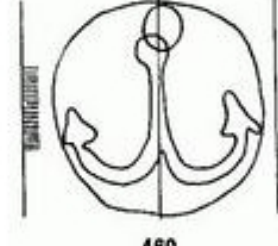
472

0.97580



464

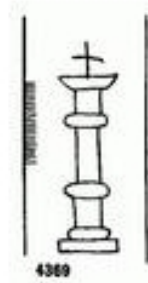
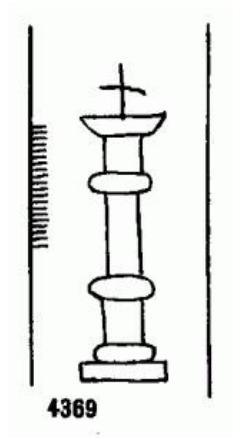
0.97565



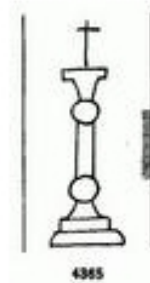
460

0.97326

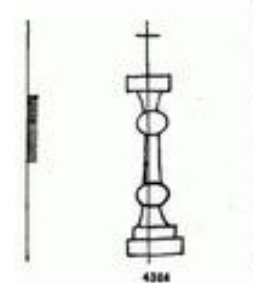
Query Image



1.00000



0.80769



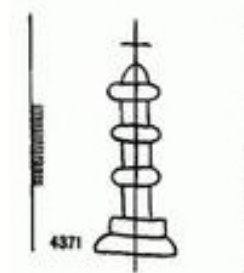
0.80128



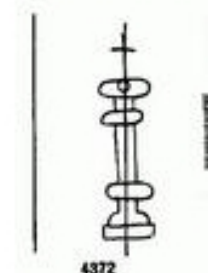
0.78125



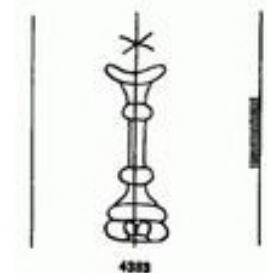
0.77926



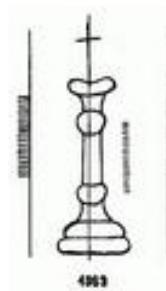
0.77350



0.76923



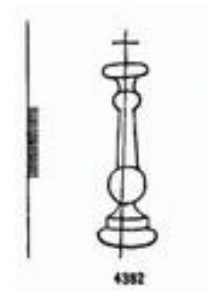
0.72436



0.72192



0.71923

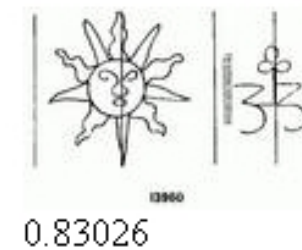
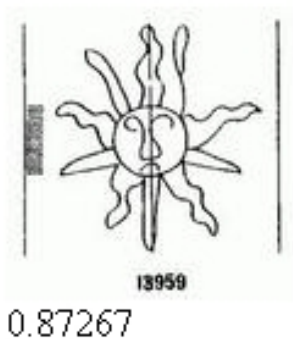
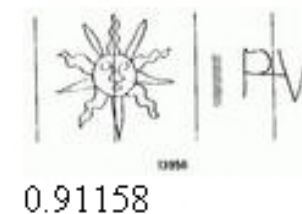
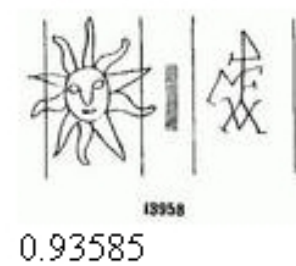
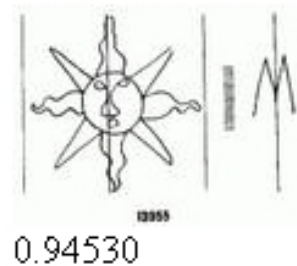
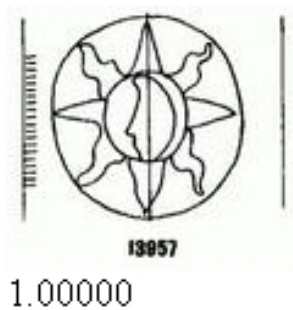


0.71795



0.70964

Query Image



USED FEATURES:

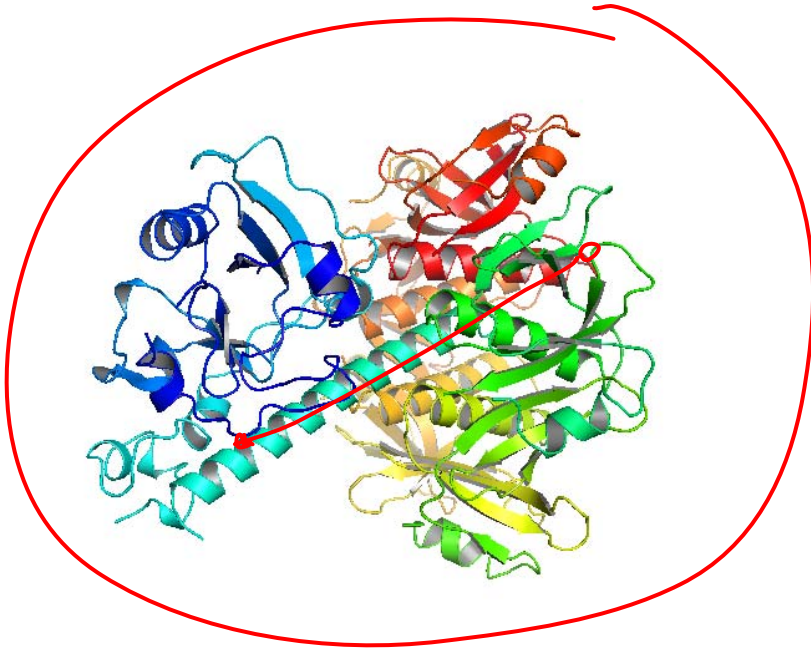


- We encode inter-relational structure knowledge from feature vectors.
- Line segments are grouped by hierarchical clustering.
- Relative spatial arrangements of the grouped line segments are captured in histograms.
- The resulting histogram is robust against illumination changes, rotation, translation and scaling.

Development of a Search Engine for Protein Databases

- There is no canonical way of describing the folding structure of proteins
- This search engines develops space-invariant descriptors for the folding structure of proteins which can be used as index for searching in databases

A Search Engine for Protein Databases based on 3D Folding-Structure



- A Protein is a highly structured 3D object consisting of amino acid chains
- Typical number of amino acids: 100-1000
→ several thousands of atoms
- In the past proteins were compared solely by its amino acid sequence, but different sequence → same 3D-structure → functional behavior

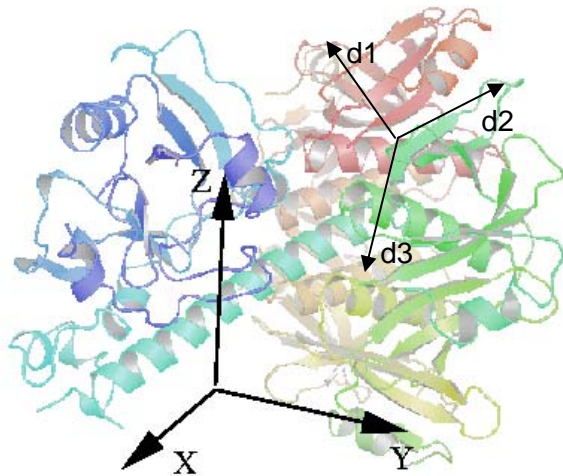
- Growing amount of 3D-macromolecular structural data (currently > 32000 in Brookhaven's PDB)
- need for efficient search and retrieval techniques
 - drug design
 - evolutionary link detection
- current structural search techniques rely on alignment algorithms
→ slow (retrieval times >hour or >day)

A Search Engine for Protein Databases based on 3D Folding-Structure

- Methods known from Content-Based 3D-Shape/Image Retrieval offer numerous fast algorithms
- Search and Classification is feature-based. The features are invariant to the 3D-pose and the numbering of the amino acids.
- *Invariant Protein Features* are numerical quantities that describe global properties of the Protein, for example

F1 = „How often occur two atoms of the Protein within some distance d “

F2 = „Percentage of atoms which are part of a alpha-Helix structure“



Preliminary Results:

Classification Accuracy:

- for SCOP-‘class’ granularity: **99.8%**
- for SCOP-‘fold’ (class alpha): **97.6%**

Retrieval times: less than a second in DB with more than 32000 proteins (>65000 chains)

80%

(1)

Video

“Licht ins Dunkel”

[Licht ins Dunkel\VTS_01_1.avi](#)