Developments and Applications of Genetic Programming, Offspring Selection, Population Diversity, Variables Impact Analysis, and Virtual Tumor Markers

Stephan M. Winkler

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BEACON
Michigan State University
Stephan Winkler: Optimization of Coefficients of Lists of Polynomials by Evolutionary Algorithms
1989: RISC moves from Linz to Hagenberg

Since then: Development of the Softwarepark Hagenberg now: 800 employed, 1400 students

1993: Start of Upper Austria University of Applied Sciences, School of Informatics, Communication, and Media

Center of Software Competence at Hagenberg

Several companies connected to IT-business
School of ICM, Hagenberg
Departments in Education

Bachelor

Software
- Software Engineering
- Medicine- and Bioinformatics

Systems
- Hardware-Software-Design
- Mobile Computing
- Secure Information Systems

Media
- Media Technology and Design
- Communication and Knowledge Media

Master

Software Engineering

Biomedical Informatics

Information Engineering and -Management

Embedded Systems Design
- Mobile Computing
- Secure Information Systems

Digital Arts
- Interactive Media
- Communication and Knowledge Media

Stephan M. Winkler
Research Group

Heuristic and Evolutionary Algorithms

Research Group

- 4 professors
- 7 PhD students
- Various interns, Master and Bachelor students

Research Focus

- Problem modeling
- Process optimization
- Data-based structure identification
- Supply chain and logistics optimization
- Algorithm development and analysis

Scientific Partners

Industry Partners (excerpt)
HeuristicLab

• Motivation and Goals
  – graphical user interface
  – paradigm independence
  – multiple algorithms and problems
  – large scale experiments and analyses
  – parallelization
  – extensibility, flexibility and reusability
  – visual and interactive algorithm development
  – multiple layers of abstraction

• Facts
  – development of HeuristicLab started in 2002
  – based on Microsoft .NET and C#
  – used in research and education
  – second place at the Microsoft Innovation Award 2009
  – open source (GNU General Public License)
  – version 3.3.0 released on May 18th, 2010
  – latest version 3.3.9 released on October 11th, 2013
Where to get HeuristicLab?

• Download binaries
  – deployed as ZIP archives
  – latest stable version 3.3.9
    • released on October 11th, 2013
  – daily trunk builds
  – http://dev.heuristiclab.com/download

• Check out sources
  – SVN repository
  – HeuristicLab 3.3.9 tag
    • http://dev.heuristiclab.com/svn/hl/core/tags/3.3.9
  – Stable development version
    • http://dev.heuristiclab.com/svn/hl/core/stable

• License
  – GNU General Public License (Version 3)

• System requirements
  – Microsoft .NET Framework 4.0 Full Version
  – enough RAM and CPU power ;)

HeuristicLab Tutorial  http://dev.heuristiclab.com  7
Plugin Architecture
HeuristicLab Demo
Parallel Execution of Experiments

1. start experiment
2. start other optimizers
Symbolic Regression with HeuristicLab

• Parameters
  – problem configuration
  – function set and terminal set
  – model size constraints
  – Evaluation

• Algorithm configuration
  – selection
  – Mutation

• Analysis of results
  – model accuracy
  – model structure and parameters
Symbolic Simplification and Node Impacts
M. Affenzeller, S. Winkler, S. Wagner, A. Beham
Genetic Algorithms and Genetic Programming
Modern Concepts and Practical Applications
CRC Press, 2009

GECCO (EvoSoft)

EuroCAST

APCASE

EMSS
Offspring Selection

Offspring Selection (Child better than fitter parent?)

|POP|

Gender-specific selection (roulette, random)
Crossover
Mutation

Discard child

Yes

No

POP

POP

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Genetic Programming with strict OS

Stephan M. Winkler

Population of Models (Formulas)

Selection of Parents

Offspring Selection

Test (Evaluation) of Models (Formulas)

Data

Generation of new Models / Formulas (Crossover, Mutation, …)
Selection Pressure (t) = Generated Offspring (t) / Successful Offspring (t)
Termination Criterion: SelPres(t) == 100, e.g.
### Genetic Propagation

#### (I) Conventional GP

- $|\text{Pop}| = 1000$;
- Tournament parents selection ($k = 3$);
- Nr. of rounds: 1000

#### (III) Extended GP

- $|\text{Pop}| = 500$;
- Gender specific parents selection (proportional, random);
- Offspring selection (SuccessRatio = 1, MaxSelPres = 100)
Basis: Structural comparison of structure trees

- Comparison of subtrees
- Analysis of pairs of ascendant – descendant combinations
Comparison of Two Models:

- All pairs of ascendant / descendant combinations in Model1 are compared to all pairs in Model2.
- Similarity of pairs is calculated using penalties for each aspect (node type, coefficients, variable indices, ...).
- Rather „complicated“:
Comparison of Two Models:

- All pairs of ascendant / descendant combinations in Model1 are compared to all pairs in Model2
- Similarity of pairs is calculated using penalties for each aspect (node type, coefficients, variable indices, ...)
- Rather „complicated“
- Multiplicative or additive weighting of penalties; multiplicative weighting is preferred:

\[
\forall i \in \{1, 10\} : p_i = (1 - d_i) \cdot c_i
\]

\[
sim_{tmp}(g_i, g_{i+2}) = \prod_{i=1}^{10} (1 - p_i).
\]

\[
sim_{worst} = \prod_{i=1}^{10} (1 - ((1 - d_i) \cdot c_i)) = \prod_{i=1}^{10} (1 - c_i).
\]

\[
sim(g_i, g_{i+2}) = \frac{\sim_{tmp}(g_i, g_{i+2}) - sim_{worst}}{1 - sim_{worst}}.
\]
Comparison of Two Models:

- All pairs of ascendant / descendant combinations in Model1 are compared to all pairs in Model2
- Similarity of pairs is calculated using penalties for each aspect (node type, coefficients, variable indices, ...)
- Rather “complicated”
- Multiplicative or additive weighting of penalties; multiplicative weighting is preferred

- Mean average of all mutual similarities is then called similarity of models
Genetic Diversity in Single-Population GP:

$$meanSim(m, P) = \frac{1}{|P| - 1} \sum_{m2 \in P, m2 \neq m} sim(m, m2)$$

NO$_x$ Tests, Standard-GP; 2000 Iterations:

NO$_x$ Tests, strict OS; ca. 60 iterations:

Eventually: Selection pressure maximal, genetic diversity = 0
Fine Grained Population Diversity Analysis for Parallel Genetic Programming

Evaluation Based Solutions Similarity

- Sub-trees are evaluated
- Values calculated are compared to values calculated evaluating subtrees of other model

Stephan M. Winkler
- Sub-trees are evaluated
- Values calculated are compared to values calculated evaluating subtrees of other models.
For comparing models M1 and M2, all subtrees in M1 are evaluated as well as all subtrees in M2.

For each subtree $s_t^x$, we look for that subtree $s_t^{x'}$ in the other model that produces values that are most similar to those produced by $s_t^x$ (linear correlation or sum of squared errors).

For each subtree we collect the maximum correlation found in values produced by subtrees of the other model.
Fine Grained Population Diversity Analysis for Parallel Genetic Programming

Structural vs. Evaluation Based Solutions Similarity

• Test Cases:
  - NOx Data Set
    - Measurements taken from a 2 liter 4-cylinder BMW diesel engine at a test bench (simulated vehicle: BMW 320d Sedan); emissions (NOₓ, CO and CO₂, ...) as well as engine parameters were recorded
    - Target: NOₓ emissions, input: only parameters directly measured from the engine's control unit
    - [http://desreg.jku.at/](http://desreg.jku.at/)
  - Thyroid
    - Machine learning benchmark data set containing 21 attributes and 7200 samples
    - Data of patients potentially suffering from hypotiroidism

• Test Scenarios:
  - Standard GP
  - GP with Offspring Selection
  - Population size: 1000
  - Max. tree height: 6, max. tree size: 50
  - Millions of models are compared to each other
  - Structural similarity estimation vs.
  - Evaluation based simulation estimation
Evaluation based similarity calculation consumes a lot more runtime than structural comparison.

The results show that in most cases there is a linear correlation of approximately 0.4 - 0.9 for the results returned by the evaluation based and structural methods; not very surprisingly, this correlation is positive, but not very high. Especially in some cases showing very low evaluation based similarity there can be significantly different results when using structural similarity methods.

Analyzing these correlations, we see that structural and evaluation based similarity measures give non-redundant information about the similarity of structure trees used in GP; both types of similarity measures should therefore be used for analyzing GP populations and algorithms.
Evolutionary Feature Selection and Parameters Optimization for Machine Learning

- Data mining
- Biomedical domain
- Industrial applications
Variables Impact
Virtual Tumor Markers

Problems: incomplete data, plausibility of prediction, cost of labor test

Parameters of the standard blood examination
Tumor Markers

• Tumor markers are substances found in humans (especially blood and/or body tissues) that can be used as *indicators for certain types of cancer*.

• Elevated tumor marker values themselves are not diagnostic, but rather only suggestive; tumor markers can be used to monitor the result of a treatment (as for example chemotherapy).

• **Research Question**: Do we really need the tumor markers? How good are estimators w/o tumor markers? Which ones are important?
### Virtual Tumor Markers

#### On the Use of Estimated Tumor Marker Classifications in Tumor Diagnosis Prediction

**Modeling Results:**

**Target Breast Cancer Diagnosis, TMs C125, C153, and CEA**

<table>
<thead>
<tr>
<th>Input Data</th>
<th>Average Classification Accuracy</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 Standard Data + TMs</td>
<td>0.78</td>
</tr>
<tr>
<td>1 Standard Data + Virtual TMs</td>
<td>0.72</td>
</tr>
<tr>
<td>1 Standard Data + Virtual TMs</td>
<td>0.79</td>
</tr>
<tr>
<td>1 Standard Data</td>
<td>0.68</td>
</tr>
</tbody>
</table>

- **Base line:** ~54%
- **GP modeling for diagnoses**
- **Models for tumor markers:** SVMs, ANNs, LR, GP
- **II.a:** OR conjunction
- **II.b:** Majority voting

<table>
<thead>
<tr>
<th>Strategy</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>I</td>
<td>0.777 ± 0.104</td>
</tr>
<tr>
<td>II.a</td>
<td>0.713 ± 0.107</td>
</tr>
<tr>
<td>II.b</td>
<td>0.752 ± 0.042</td>
</tr>
<tr>
<td>III</td>
<td>0.699 ± 0.113</td>
</tr>
</tbody>
</table>

S. M. Winkler, M. Affenzeller, G. K. Kronberger, M. Kommenda, S. Wagner, W. Jacak, H. Stekel

*On the Use of Estimated Tumor Marker Classifications in Tumor Diagnosis Prediction - A Case Study for Breast Cancer*

Tumor Markers

Clinical Chemistry 52:3
345–351 (2006)

Minireview

Serum Tumor Markers in Breast Cancer: Are They of Clinical Value?

MICHAEL J. DUFFY

Background: Although multiple serum-based tumor markers have been described for breast cancer, such as CA 15-3, BR 27.29 (CA27.29), carcinoembryonic antigen (CEA), tissue polypeptide antigen, tissue polypeptide specific antigen, and HER-2 (the extracellular domain), the most widely used are CA 15-3 and CEA.

Methods: The literature relevant to serum tumor markers in breast cancer was reviewed. Particular attention was given to systematic reviews, prospective randomized trials, and guidelines issued by expert panels.

For many malignancies, serum tumor markers play an important role in patient management (1–5) (Table 1). In breast cancer, however, the role of serum markers is less well established. The most widely used serum markers in breast cancer are CA 15-3 and carcinoembryonic antigen (CEA). Less widely used markers include BR 27.29 (also known as CA27.29), tissue polypeptide antigen (TPA), tissue polypeptide specific antigen (TPS) and the shed form of HER-2 [Table 2; for a review, see Refs. (6–8)]. The potential uses of serum markers in breast cancer include
Tumor Markers Relevant According to Literature

- Breast Cancer
  - CEA
  - CA 15-3

- Melanoma
  - S100

- Respiratory System Cancer
  - CEA
  - CYFRA (CYFS)

- Carcinoembryonic antigen (CEA) is a glycoprotein involved in cell adhesion. Normally produced during fetal development, usually present in the blood of healthy adults, although levels are raised in heavy smokers.

- CA 15-3 (Carcinoma Antigen 15-3) is a tumor marker for breast cancer. It is derived from MUC1.

- S-100 protein is a family of low molecular weight protein. There are at least 21 different types of S100 proteins.

- High concentrations of fragments of cytokeratin 19, which are also called CYFRA 21-1, are found in the lung and in malign lung tumours.
Modeling Results w/o (Relevant) TMs: Test Accuracies (5xCV; OSGA+linReg, $\alpha=0.1$; OSGP)

- Breast Cancer
  - all variables: 81.501 % (±0.726)
  - leave out CEA: 81.493 % (±0.845)
  - leave out C153: 77.140 % (±0.753)
  - leave out all tumor markers: 72.548 % (±1.241)
  (use only standard values)
Modeling Results w/o (Relevant) TMs:
Test Accuracies
(5xCV; OSGA+linReg, $\alpha=0.1$; OSGP)

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**Breast Cancer**

- all variables 81.501 % (±0.726)
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(leave out all tumor markers)

(= use only standard values)
Modeling Results w/o (Relevant) TMs: Test Accuracies
(5xCV; OSGA+linReg, $\alpha=0.1$; OSGP)

**Breast Cancer**

- all variables 81.501 % (±0.726)
- leave out CEA 81.493 % (±0.845)
- leave out C153 77.140 % (±0.753)
- leave out CEA & C153 74.590 % (±1.083)
- leave out all tumor markers 72.548 % (±1.241)

(Use only standard values)
Modeling Results w/o (Relevant) TMs: Test Accuracies (5xCV; OSGA+linReg, OSGP)

- **Melanoma**
  - all variables 74.194 % (±0.844)
  - leave out S100 74.033 % (±0.729)
  - only standard values 74.166 % (±0.634)
Modeling Results w/o (Relevant) TMs: Test Accuracies (5xCV; OSGA+linReg, OSGP)

- **Melanoma**
  - all variables: 74.194% (±0.844)
  - leave out S100: 74.033% (±0.729)
  - leave out all tumor markers: 74.166% (±0.634)
    (use only standard values)
Modeling Results w/o (Relevant) TMs: Test Accuracies (5xCV; OSGA+linReg, OSGP)

- **Respiratory System Cancer**
  - all variables 90.668 (±1.326)
  - leave out CEA 90.720 (±0.655)
  - leave out CYFRA (CYFS) 90.930 (±0.797)
  - leave out all tumor markers 87.950 (±0.531)
  (use only standard values)
Modeling Results w/o (Relevant) TMs: Test Accuracies (5xCV; OSGA+linReg, OSGP)

- **Respiratory System Cancer**
  - all variables \[ 90.668 \pm 1.326 \]
  - leave out CEA \[ 90.720 \pm 0.655 \]
  - leave out CYFRA (CYFS) \[ 90.930 \pm 0.797 \]
  - leave out all tumor markers (use only standard values) \[ 87.950 \pm 0.531 \]
Modeling Results w/o (Relevant) TMs: Test Accuracies (5xCV; OSGA+linReg, OSGP)

- Respiratory System Cancer
  - all variables: 90.668 (±1.326)
  - leave out CEA: 90.720 (±0.655)
  - leave out CYFRA (CYFS): 90.930 (±0.797)
  - leave out all tumor markers: 87.950 (±0.531)

(use only standard values)

incl. CA 19-9
Virtual Tumor Markers
Identification and Classification of Objects and Motions in Microscopy Images of Biological Samples Using Heuristic Algorithms
Identification and Classification of Objects and Motions in Microscopy Images of Biological Samples Using Heuristic Algorithms

Outline

- Introduction
  - Image Analysis
  - Heuristic Algorithms

- Biomedical Research Questions and the Use of Heuristic Algorithms
  - Identification of Patterns in Microscopy Images of Biological Samples Using Evolution Strategies
  - Shape Classification of Endothelial Cells in Cornea
  - Identification of PNH Affected Cells by Classifying Motion Characteristics of Single Molecules
  - Modeling and Prognosis of Bone Development
  - Identification of Strands in Microscopy Images of Myocardal Muscles
General Workflow

- (Fluorescence) microscopy image analysis
- Prediction / recognition of development / state of diseases
- Ongoing research conducted at the Bioinformatics Research Group (BIN) and the Heuristic and Evolutionary Algorithms Laboratory (HEAL)
Heuristic algorithms

- Evolutionary algorithms
  - especially evolution strategies (ES)
  - identification of structures in micro- and nanoscale microscopy images

- Machine learning
  - regression and classification
    - linear regression
    - support vector machines
    - random forests
    - neural networks
    - genetic programming
    - HeuristicLab
  - Identification, classification, and prognosis of dynamics seen in series of microscopy images
Biomedical Research Questions

- Identification of patterns in microscopy images of biological samples
- Classification of endothelial cells in cornea
- Identification of PNH affected cells by classifying motion characteristics of single molecules
- Modeling and prognosis of bone development in amnion tissues
- Identification of strands in microscopy images of myocardal muscles
(1) Identification of patterns in microscopy images of biological samples

Goal: Automatically identify grid structures in images of biological samples labeled by μ-patterning.

(1) Identification of patterns in microscopy images of biological samples
(1) Identification of patterns in microscopy images of biological samples

- Comparison of
  - **Expected Grid** (grid definition + tolerance)
    with
  - **Binary Image**

\[
N(\text{binary}) = |\{p \mid p \in \text{binary}\}| \quad (1)
\]

\[
P(\text{grid, binary}) = |\{\text{expected}(\text{grid})[p] = \text{binary}[p]\}| \quad (2)
\]

\[
\text{quality(\text{grid, binary})} = \frac{|P(\text{grid, binary})|}{N(\text{binary})} \quad (3)
\]
(1) Identification of patterns in microscopy images of biological samples

- **1/5 success rule (proposed by Rechenberg):**
  - Quotient of successful mutants to all mutants should be about 1/5
  - \( < \frac{1}{5} \rightarrow \text{decrease mutation variance, otherwise increase} \)

- **Mutation operator with implemented self adaption (proposed by Schwefel):**
  - Individual mutation strategy parameter for each solution candidate parameter.

- **Plus vs. Comma Strategy**

Gaussian probability density function

\[ \text{N}(0,1) \]
8 exemplary samples have been selected to be tested with varying ES parameter settings and different downsampling tolerances.

Picture size: 1344 by 1024 pixels
(1) Identification of patterns in microscopy images of biological samples

Improvement during ES process

initial solution quality 0.55

final grid quality 0.72
(2) Classification of endothelial cells in cornea
(2) Classification of endothelial cells in cornea

Goal:
- Find cells
- Identify forms of cells

Approach:
- Fit structures
  - 4 edges
  - 5 edges
  - 6 edges
  - 7 edges
  - 8 edges
- Optimize structures with ES
- Fitness function: How well does structure fit patterns in the image
(2) Classification of endothelial cells in cornea
(2) Classification of endothelial cells in cornea
(3) Identification of PNH affected cells by classifying motion characteristics of single molecules

Find features for motion characteristics of single molecules to distinguish between disease affected (PNH) and healthy cells using machine learning algorithms.

(a) PNH affected blood cells.  
(b) Healthy blood cells.
(3) Identification of PNH affected cells by classifying motion characteristics of single molecules

- Input: Microscopy Images (PNH affected & healthy cells)
  - 1 Microscopy image set = 100 frames
- Detect single molecules (red spots) of blood cells (red circles) in image set
- Build trajectories of single molecules in image set
- Characterize trajectories using a self-defined set of features
- Use features as input for machine learning algorithms

Classification of PNH affected or healthy cells

(3) Identification of PNH affected cells by classifying motion characteristics of single molecules

- Single molecules: fluorescently labeled constituent parts of red blood cells (red spots, images (a), (d)) of the first frame
- Trajectory: path of a single molecule e.g. from frame 1 to frame 100 = motion of a single molecule (images (b) & (c))

(3) Identification of PNH affected cells by classifying motion characteristics of single molecules

- Investigating properties of detected trajectories
- A set of 9 features is defined for distinguishing PNH affect and healthy cells using machine learning algorithms
  
  > the total number of single molecules \((\text{length})\),
  > the average intensity of a trajectory based on the detected single molecules from the detection algorithm \((\text{intensity})\),
  > the average size of hops in a trajectory \((\text{spotDist})\),
  > the variance of the distances between the positions in a trajectory \((\text{varDist})\),
  > the distance of a trajectory \((\text{maxDist})\),
  > the ratio between the sum of the distances in the trajectory and the direction of the trajectory \((\text{distRatio})\),
  > the average motion changes of a trajectory \((\text{motion})\), and
  > the area covered by a trajectory \((\text{polyArea, ellArea})\).
(3) Identification of PNH affected cells by classifying motion characteristics of single molecules

(3) Identification of PNH affected cells by classifying motion characteristics of single molecules

(3) Identification of PNH affected cells by classifying motion characteristics of single molecules

- Features are used for classifying microscopy images
- 1600 samples
- Training and testing is done (66% - 33%)
- 10-fold cross-validation
- Algorithms are used:
  - Genetic Programming
  - Nearest Neighbour
  - Random Forest
  - Support Vector Machines
(3) Identification of PNH affected cells by classifying motion characteristics of single molecules

<table>
<thead>
<tr>
<th>Algorithm</th>
<th>Parameter Settings</th>
<th>Accuracy Training</th>
<th>Accuracy Test</th>
<th>Sensitivity Test</th>
<th>Specificity Test</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genetic Programming (OSGP)</td>
<td>mutation rate: 15%, tree depth: 10, tree length: 100</td>
<td>86.48%</td>
<td>85.67%</td>
<td>92.99%</td>
<td>78.34%</td>
</tr>
<tr>
<td>Nearest Neighbor</td>
<td>$k$: 10</td>
<td>85.86%</td>
<td>86.17%</td>
<td>82.23%</td>
<td>90.11%</td>
</tr>
<tr>
<td>Random Forest</td>
<td>$t$: 150</td>
<td>91.43%</td>
<td>86.61%</td>
<td>91.99%</td>
<td>81.23%</td>
</tr>
<tr>
<td>Support Vector Machine</td>
<td>RBF kernel, $\nu$: 0.4, $c$: 0.5, $\gamma$: 0.4</td>
<td>86.23%</td>
<td>85.48%</td>
<td>95.24%</td>
<td>75.72%</td>
</tr>
<tr>
<td>Support Vector Machine</td>
<td>poly kernel, $\nu$: 0.4, $c$: 10, $\gamma$: 0.2</td>
<td>86.30%</td>
<td>85.61%</td>
<td>94.24%</td>
<td>76.971%</td>
</tr>
</tbody>
</table>

(4) Modeling and prognosis of bone development in amnion tissues

Von Kossa staining of amniotic membrane under osteogenic conditions on day 0, day 14 and day 28; black regions show positive regions for bone development. 
Source: Red Cross Blood Transfusion Service Linz.
(4) Modeling and prognosis of bone development in amnion tissues

Humane amniotic membrane is the innermost of fetal membranes and a part of the placenta; for research purposes, human placenta is obtained naturally in the course of births.

The viable (i.e., living) amniotic membrane releases a whole array of soluble factors which have a beneficial effect on wound healing after skin lesions. Being able to distinguish between viable and dead regions would be a very important screening opportunity for optimal wound treatment after big skin lesions. Furthermore, amniotic membranes are used in tissue engineering. It has been recently shown that it is possible to differentiate viable amniotic membrane towards the osteogenic tissue (i.e., bone cells).

Current research focuses on developing a machine learning approach that is able to automatically detect these positive areas on the basis of images and can also characterize the mentioned cell development states. An automated prediction of the development of cells using advanced image analysis and machine learning is researched.
(5) Identification of strands in microscopy images of myocardal muscles
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(5) Identification of strands in microscopy images of myocardial muscles

- Application of filters:

- Sobel
- Prewitt
- Kirsch
- Laplace 3x3
- Laplace 5x5
(5) Identification of strands in microscopy images of myocardal muscles

- Alternative approach
  - Define initial lines
  - Choose best
  - Replicate parallel lines
  - Optimize lines by ES

![Image of microscopy software interface showing original and processed images with lines identified](image-url)
(5) Identification of strands in microscopy images of myocardal muscles

- Alternative approach
  - Define initial lines
  - Choose best
  - Replicate parallel lines
  - Optimize lines by ES
Discussion, Acknowledgements

- Ongoing research
  - Object identification
  - Object classification
  - Motion classification
  - Biomedical answers?

- Acknowledgements
  - Research partners at
    - Red Cross Blood Transfusion Service of Upper Austria
    - Olympus Austria
    - Trauma Care Consult
    - Research Centers Hagenberg and Linz of FH OÖ
  - Research Projects
    - *MicroProt* (FH OÖ, basic research programme)
    - *NanoDetect* (FFG, FIT-IT programme)
Identification and Classification of Objects and Motions in Microscopy Images of Biological Samples Using Heuristic Algorithms

Stephan M. Winkler, Susanne Schaller, Daniela Borgmann, Lisa Obritzberger, Viktoria Dorfer, Michael Affenzeller
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