Automated DOMM Detection in TEM Imagery

By Kyle Dymowski
What is DOMM

• DNA Origami Machines and Mechanisms
Motivation

• Josh Johnson
  – M.S. 2014 Applied Physics
  – Currently working on
    at OSU
Problem Domain

• Transmission electron microscopy
  – Noise related to the process
• Filtering
• Edge Detection
• Normalized Cross Correlation
Assumptions

• Does not need to capture all DOMM in the image.
• All images will be similar.
Previous Works

• Auto-adaptive Algorithm for the Stacking-Level Estimation of Membranes in TEM Images
• TEM Images of Membranoids: A Multiresolution Edge-Detection Approach for Watershed Segmentation
Figure 2 General diagram of the segmentation process with an example on the right column.
Development

- Removing the noise
- Gaussian in nature
Results of Noise Removal

Median Filtering size 10x10

Before

After
Visual Representation, actual images are complemented
Canny Edge Detection

• Must crop out lower 320 pixels to remove information tag of image

150316(5xAuNP Hin S4 16hr RT)-1.tif
Hinge S2 4hrs at 53deg
Cal: 1.153pix/nm
14:37 03/16/15
Microscopist: JJ

100 nm
HV=80kV
Direct Mag: 68000x
CMIF OSU

• This was causing issues for auto thresh of gray levels
• Average Canny edge returned a threshOut of:

\[0.01875, 0.04687\]

Simply multiplying this by a scaler of 2 resulted in images like the following.
Building the Templates

- GIMP 2
Normalized Cross Correlation

- Check image for all rotations at 5 degree increments
- Using a normxcorr2 only returned Correlation coefficients high than .31 were considered.
### Results

<table>
<thead>
<tr>
<th>Image</th>
<th>Found</th>
<th>Actual</th>
<th>Expected</th>
<th>Result</th>
<th>Multiple Identifications</th>
<th>False Positives</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>150316(5xAuNP Hin S4 16hr RT)-1</td>
<td>25</td>
<td>22</td>
<td>28</td>
<td>Good</td>
<td>3</td>
<td>1</td>
<td>Best case for recognition</td>
</tr>
<tr>
<td>150316(5xAuNP Hin S4 16hr RT)-2</td>
<td>20</td>
<td>14</td>
<td>21</td>
<td>Bad</td>
<td>4</td>
<td>2</td>
<td>Mechanisms bunched together</td>
</tr>
<tr>
<td>150316(5xAuNP Hin S4 16hr RT)-3</td>
<td>25</td>
<td>17</td>
<td>21</td>
<td>Good</td>
<td>8</td>
<td>0</td>
<td>N/A</td>
</tr>
<tr>
<td>150316(5xAuNP Hin S4 16hr RT)-4</td>
<td>20</td>
<td>14</td>
<td>19</td>
<td>OK</td>
<td>5</td>
<td>1</td>
<td>Missed some</td>
</tr>
<tr>
<td>150316(5xAuNP Hin S4 16hr RT)-5</td>
<td>18</td>
<td>16</td>
<td>22</td>
<td>Good</td>
<td>3</td>
<td>1</td>
<td>N/A</td>
</tr>
<tr>
<td>150316(5xAuNP Hin S4 16hr RT)-6</td>
<td>10</td>
<td>7</td>
<td>14</td>
<td>Bad</td>
<td>3</td>
<td>0</td>
<td>&quot;Shadow&quot; around mechanisms much darker than other images</td>
</tr>
</tbody>
</table>

72% of the expected mechanisms found
4% were false positives
28 repeated structures
Increasing Results

• Can find a considerable larger amount of mechanisms if correlation coefficient is lowered

• Problems
  – Increase occurrence of finding the same mechanism considerably
  – Increase in finding false positives
Achievements / Further Work

• While only 72% accurate structures are extracted at a fraction of the time.
• Automatic alignment has been achieved within a tolerance of ±5 degrees.
• Second set of images provided were not visually similar.