Lymphoma Diagnosis

Based on Automated analysis of Flow Cytometry Data

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and

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Flow Cytometry

Clustered by SamSPECTRAL

multi-dimensional
Method:  

**Challenge:** Over 200 features with only samples → LASSO

\[
\|Ax - y\|^2 + \lambda \|x\|_1
\]

Result:

<table>
<thead>
<tr>
<th>Actual</th>
<th>type</th>
<th>Total</th>
<th>DLBC</th>
<th>follicular</th>
<th>class_M</th>
<th>SLL</th>
<th>undetermined</th>
<th>misclassified</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>DLBC</td>
<td>28</td>
<td>25 (89%)</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>3 (11%)</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td>follicular</td>
<td>49</td>
<td>2 (4%)</td>
<td>46 (94%)</td>
<td>0</td>
<td>0</td>
<td>1 (2%)</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>class_M</td>
<td>8</td>
<td>2 (4%)</td>
<td>0</td>
<td>5 (63%)</td>
<td>0</td>
<td>1 (12%)</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>SLL</td>
<td>15</td>
<td>0</td>
<td>0</td>
<td>14 (93%)</td>
<td>0</td>
<td>1 (12%)</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>other</td>
<td>20</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>20</td>
<td>-</td>
</tr>
</tbody>
</table>

1 follicular = {FOLL1, FOLL2, FOLL3A, FOLL3B, FSC-FOLL1, FM-FOLL2}
2 class_M = {MALT, MCL, MCLD, MCLM, MCLN, MZLN, MZLS}
3 SLL = {SLL, SLLV}
4 undetermined: Patient did not score high enough in any category
5 Misclassified for a group of diagnosis is the number of patients who are predicted to be in this group incorrectly. Except for DLBC, no patients were misclassified.

**BOLD:** The number of correctly diagnosed patients are bold numbers on the diagonal.