<table>
<thead>
<tr>
<th>Time</th>
<th>Classroom 1</th>
<th>Classroom 2</th>
<th>Classroom 3</th>
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</thead>
<tbody>
<tr>
<td>09:00 - 10:00 AM</td>
<td>Image and Data Analysis</td>
<td>New Technologies</td>
<td>Phenotypic Screening</td>
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<tr>
<td></td>
<td>Mark Bray (Novartis)</td>
<td>David Andrews (University of Toronto)</td>
<td>Myles Fennel (Sloan Kettering Cancer</td>
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<td></td>
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<td>Center) and Paul Selzer (Novartis)</td>
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<td>10:00 - 10:15 AM</td>
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<tr>
<td>10:15 - 11:15 AM</td>
<td>Assay Types and Assay Development</td>
<td>Systems Biology</td>
<td>t-SNE and Cen-se’ Mapping Methods</td>
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<tr>
<td></td>
<td>Joe Trask (Perkin Elmer)</td>
<td>Steve Haney (President SBI2)</td>
<td>Explained</td>
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<td>Bruce Bagwell (Verity Software house)</td>
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<td>11:15 - 11:30 AM</td>
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<td>11:30 - 12:30 PM</td>
<td>Statistical analysis of screening data</td>
<td>Flow Cytometry and MassSpec CYTOF</td>
<td>CRISPR Technology</td>
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<td></td>
<td>Bartek Rawja, (Purdue University)</td>
<td>David Gebhard (Cytometry Consultant)</td>
<td>Sam Hasson (Amgen)</td>
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<td>Lunch Courses</td>
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<td>12:45 - 2:45 PM</td>
<td>3D Cell Models</td>
<td>Deep Learning</td>
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<td>Paul Johnston (University of Pittsburgh), Daniel LaBarbera (University of Denver), Joe Trask (Perkin Elmer), Judi Wardwell (Insphero), Todd Shelpner (Griffith University), Mary Boutin (NIH/NCATS)</td>
<td>David Egan (Core Life Analytics), Wienan Omta (Core Life Analytics), Sam Cooper (Phenomic AI), Oren Kraus, (Phenomic AI), Juan Caicedo (The Broad Institute)</td>
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<td>Colloquium</td>
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<tr>
<td>3:00 - 6:00 PM</td>
<td>How are Emerging Technologies in Disease models, High content imaging, and Data analytics changing our approach to Drug discovery?</td>
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