

# Multiple and Extensively Drug Resistant Tuberculosis Data Exploration Portal (MXDR-TB DEPot) Training: Cohort Creation, Visualization, Analysis

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*Eric Engle, Andrei Gabrielian, September 2016, version .2*

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## Introduction

The multiple and extensively drug resistant data exploration portal (MXDR-TB DEPOT) enables users to organize information from tuberculosis resources, including the country-specific TB portals, to help in multi-factor analysis of rare, unusual, atypical, most dangerous MXDR-TB cases. This training document provides sample guided analyses to aid users and provide an initial introduction to the mechanics of using the DEPOT system to create cohorts, visualize and analyze data.

Cohort creation is DEPOT functionality that enables the selection of a subset of patients from the TB Portals data collection using data filters connected with logical operators if needed. The DEPOT can create cohorts for several purposes.

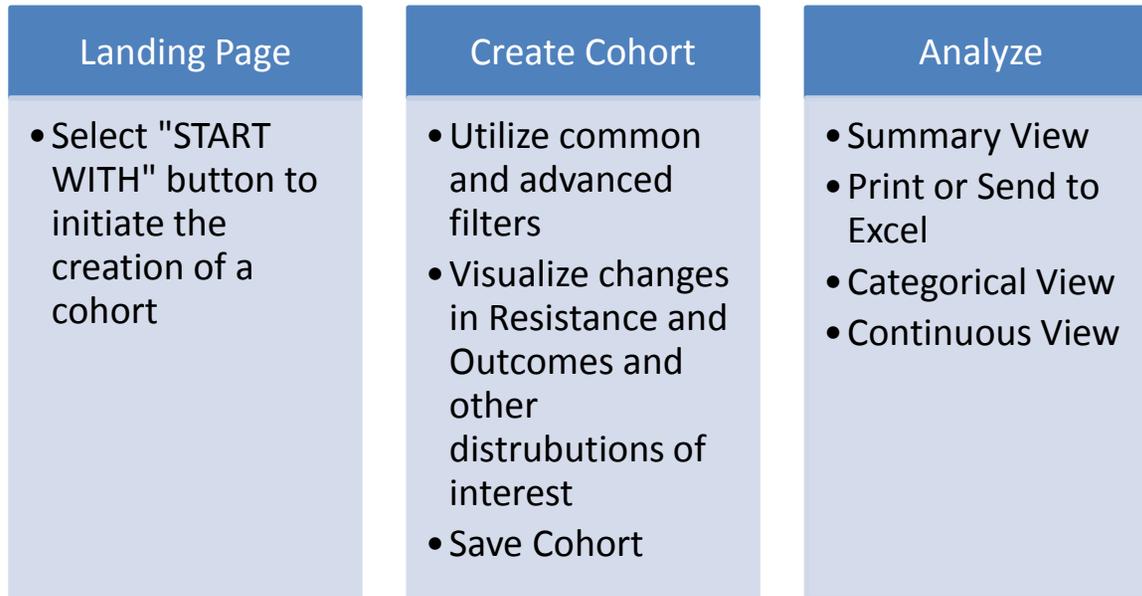
- To discover what is unusual in terms of outcomes and resistance
- To compare any two cohorts out of the collections of patient cases we created
- To visualize the data and conduct statistical analysis to test hypotheses between two cohorts

Outcome and resistance profiles are always visible during the cohort creation process. Through analyze we can determine the variables (also called 'parameters') that best describe the difference between cohorts. This can be any variable we have collected for our TB patients. The DEPOT utilizes all data from TB Portals including clinical data, images and genomic information for the cohort if it is available.

## Process Flow and Activities

### High Level Process Activity Description

The basic process flow used within DEPot is as follows.



## Landing page

The Landing page prompts the user to select their primary area of interest: Clinical Data, CT Scans, Genomic Data, or X-rays. Note that X-rays are currently unique in that because they are not annotated, they can only be utilized by the DEPOT to create a cohort of similar images.

Number	Activity	Visual Result
1	<p>The MXDR-TB DEPOT v1.0 is now live in production. The application can be accessed via the following link:  <a href="https://DEPOT.TBPortals.NIAID.NIH.GOV">https://DEPOT.TBPortals.NIAID.NIH.GOV</a>.</p> <p>We recommend using the Google Chrome browser. If there are any issues with the DEPOT, in addition to a full description of the issue and how it was created, please indicate the browser and operating system in use.</p>	

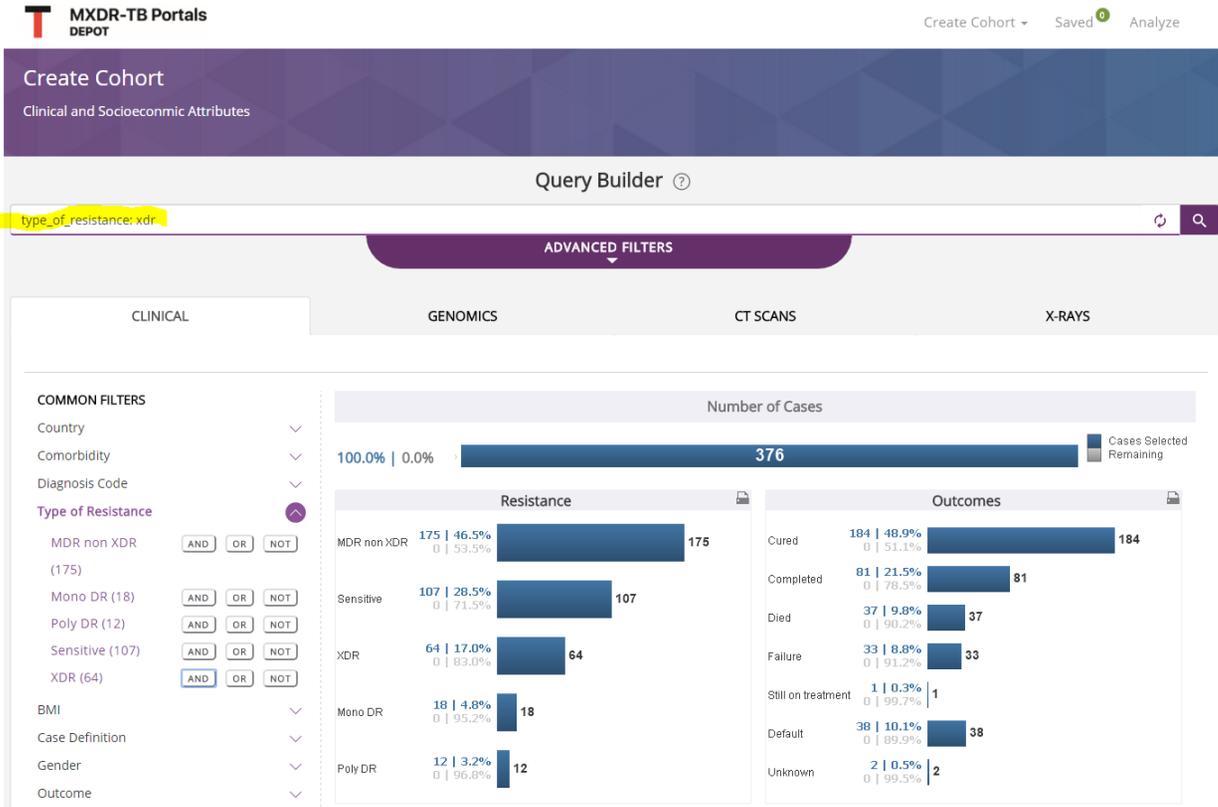
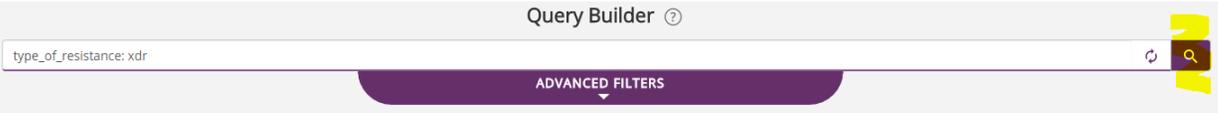
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2	<p>Select "START WITH CLINICAL DATA".</p> <p>From this visualization page we can observe the following elements:</p> <p><b>Query Builder</b> textual bar and <b>ADVANCED FILTERS</b> drawer</p> <p>CLINICAL tab containing the common clinical filters and common clinical data elements</p> <p>GENOMICS tab for visualizing these data</p> <p>CT SCANS tab to visualize the annotation related filters and patient case CT images</p> <p>X-RAYS tab to view patient case X-rays</p>	<p><b>COMMON FILTERS</b></p> <ul style="list-style-type: none"> <li>Country</li> <li>Comorbidity</li> <li>Diagnosis Code</li> <li>Type of Resistance</li> <li>BMI</li> <li>Case Definition</li> <li>Gender</li> <li>Outcome</li> </ul> <p><b>Number of Cases</b></p> <table border="1"> <tr> <td>100.0%</td> <td>0.0%</td> <td>376</td> </tr> </table> <p><b>Resistance</b></p> <table border="1"> <thead> <tr> <th>Resistance Type</th> <th>Count</th> <th>Percentage</th> </tr> </thead> <tbody> <tr> <td>MDR non XDR</td> <td>175</td> <td>46.5%</td> </tr> <tr> <td>Sensitive</td> <td>107</td> <td>28.5%</td> </tr> <tr> <td>XDR</td> <td>64</td> <td>17.0%</td> </tr> <tr> <td>Mono DR</td> <td>18</td> <td>4.8%</td> </tr> <tr> <td>Poly DR</td> <td>12</td> <td>3.2%</td> </tr> </tbody> </table> <p><b>Outcomes</b></p> <table border="1"> <thead> <tr> <th>Outcome</th> <th>Count</th> <th>Percentage</th> </tr> </thead> <tbody> <tr> <td>Cured</td> <td>184</td> <td>48.9%</td> </tr> <tr> <td>Completed</td> <td>81</td> <td>21.5%</td> </tr> <tr> <td>Died</td> <td>37</td> <td>9.8%</td> </tr> <tr> <td>Failure</td> <td>33</td> <td>8.8%</td> </tr> <tr> <td>Still on treatment</td> <td>1</td> <td>0.3%</td> </tr> <tr> <td>Default</td> <td>30</td> <td>10.1%</td> </tr> <tr> <td>Unknown</td> <td>2</td> <td>0.5%</td> </tr> </tbody> </table>	100.0%	0.0%	376	Resistance Type	Count	Percentage	MDR non XDR	175	46.5%	Sensitive	107	28.5%	XDR	64	17.0%	Mono DR	18	4.8%	Poly DR	12	3.2%	Outcome	Count	Percentage	Cured	184	48.9%	Completed	81	21.5%	Died	37	9.8%	Failure	33	8.8%	Still on treatment	1	0.3%	Default	30	10.1%	Unknown	2	0.5%
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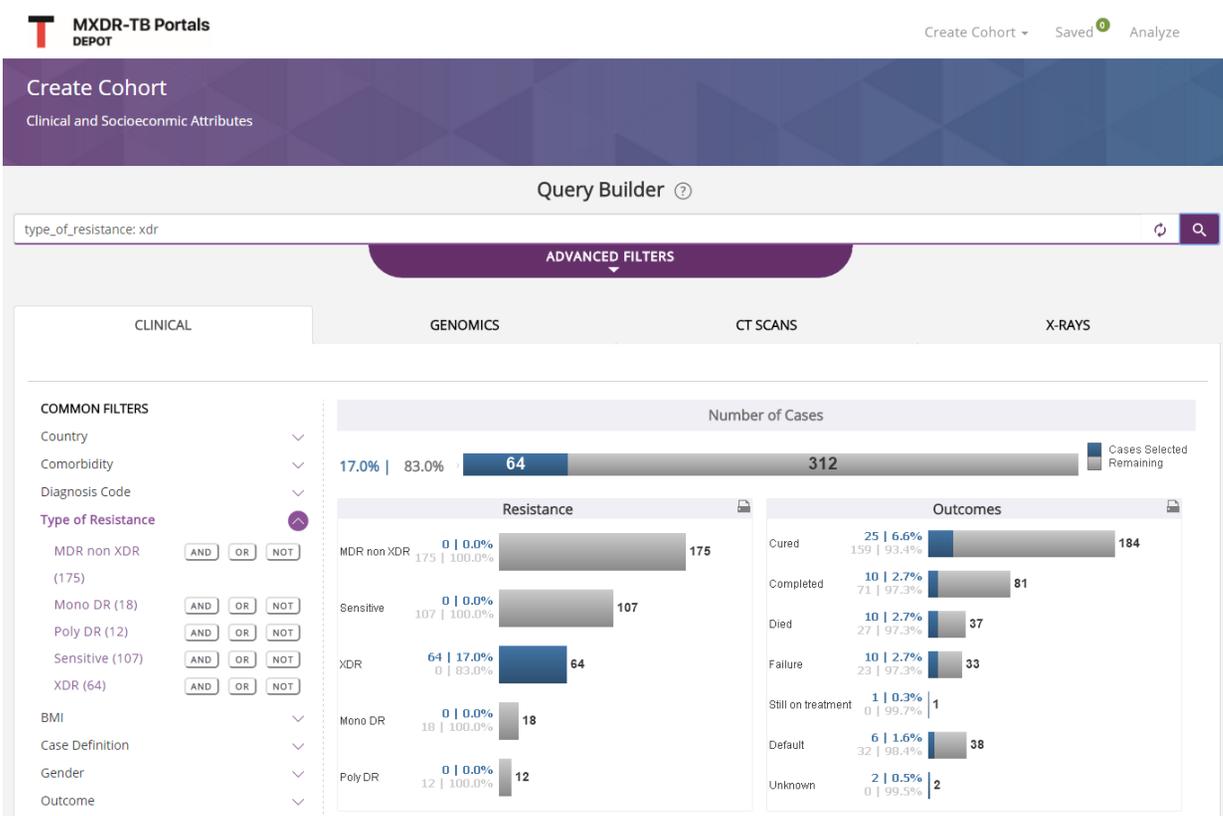
## Cohort Creation

The Cohort Creation process enables the formation of a group of patients and the exploration of their clinical, imaging, and genomic data using data filters and logical operators.

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1	<p>The Create Cohort page enables the user to define a query. The query aims at selecting a subset of patients from the TB Portals collection using data filters connected with logical operators if needed.</p> <p>Note that this example begins with 376 cases selected. This is the current entire TB Portals collection as of this writing.</p>	<p><b>COMMON FILTERS</b></p> <ul style="list-style-type: none"> <li>Country</li> <li>Comorbidity</li> <li>Diagnosis Code</li> <li>Type of Resistance</li> <li>BMI</li> <li>Case Definition</li> <li>Gender</li> <li>Outcome</li> </ul> <p><b>Number of Cases</b></p> <table border="1"> <tr> <td>100.0%</td> <td>0.0%</td> <td>376</td> </tr> </table> <p><b>Resistance</b></p> <table border="1"> <tr> <td>MDR non XDR</td> <td>175</td> <td>46.5%</td> <td>175</td> </tr> <tr> <td>Sensitive</td> <td>107</td> <td>28.5%</td> <td>107</td> </tr> <tr> <td>XDR</td> <td>64</td> <td>17.0%</td> <td>64</td> </tr> <tr> <td>Mono DR</td> <td>18</td> <td>4.8%</td> <td>18</td> </tr> <tr> <td>Poly DR</td> <td>12</td> <td>3.2%</td> <td>12</td> </tr> </table> <p><b>Outcomes</b></p> <table border="1"> <tr> <td>Cured</td> <td>184</td> <td>48.9%</td> <td>184</td> </tr> <tr> <td>Completed</td> <td>81</td> <td>21.5%</td> <td>81</td> </tr> <tr> <td>Died</td> <td>37</td> <td>9.8%</td> <td>37</td> </tr> <tr> <td>Failure</td> <td>33</td> <td>8.8%</td> <td>33</td> </tr> <tr> <td>Still on treatment</td> <td>1</td> <td>0.3%</td> <td>1</td> </tr> <tr> <td>Default</td> <td>38</td> <td>10.1%</td> <td>38</td> </tr> <tr> <td>Unknown</td> <td>2</td> <td>0.5%</td> <td>2</td> </tr> </table>	100.0%	0.0%	376	MDR non XDR	175	46.5%	175	Sensitive	107	28.5%	107	XDR	64	17.0%	64	Mono DR	18	4.8%	18	Poly DR	12	3.2%	12	Cured	184	48.9%	184	Completed	81	21.5%	81	Died	37	9.8%	37	Failure	33	8.8%	33	Still on treatment	1	0.3%	1	Default	38	10.1%	38	Unknown	2	0.5%	2
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2	In the left hand pane, under the heading Common Filters, Select the drop-down arrow to the right of "Type of Resistance".	<p><b>MXDR-TB Portals DEPOSIT</b> Create Cohort Clinical and Socioeconomic Attributes</p> <p>Query Builder</p> <p>Advanced Filters</p> <p>CLINICAL GENOMICS CT SCANS X-RAYS</p> <p>COMMON FILTERS</p> <ul style="list-style-type: none"> <li>Country</li> <li>Comorbidity</li> <li>Diagnosis Code</li> <li><b>Type of Resistance</b> <ul style="list-style-type: none"> <li>MDR non XDR (175)</li> <li>Mono DR (18)</li> <li>Poly DR (12)</li> <li>Sensitive (107)</li> <li>XDR (64)</li> </ul> </li> <li>BMI</li> <li>Case Definition</li> <li>Gender</li> <li>Outcome</li> </ul> <p>Number of Cases: 376</p> <p>Resistance</p> <table border="1"> <tr><td>MDR non XDR</td><td>175   46.5%</td><td>175</td></tr> <tr><td>Sensitive</td><td>107   28.5%</td><td>107</td></tr> <tr><td>XDR</td><td>64   17.0%</td><td>64</td></tr> <tr><td>Mono DR</td><td>18   4.8%</td><td>18</td></tr> <tr><td>Poly DR</td><td>12   3.2%</td><td>12</td></tr> </table> <p>Outcomes</p> <table border="1"> <tr><td>Cured</td><td>184   48.9%</td><td>184</td></tr> <tr><td>Completed</td><td>81   21.5%</td><td>81</td></tr> <tr><td>Died</td><td>37   9.8%</td><td>37</td></tr> <tr><td>Failure</td><td>33   8.8%</td><td>33</td></tr> <tr><td>Still on treatment</td><td>1   0.3%</td><td>1</td></tr> <tr><td>Default</td><td>38   10.1%</td><td>38</td></tr> <tr><td>Unknown</td><td>2   0.5%</td><td>2</td></tr> </table>	MDR non XDR	175   46.5%	175	Sensitive	107   28.5%	107	XDR	64   17.0%	64	Mono DR	18   4.8%	18	Poly DR	12   3.2%	12	Cured	184   48.9%	184	Completed	81   21.5%	81	Died	37   9.8%	37	Failure	33   8.8%	33	Still on treatment	1   0.3%	1	Default	38   10.1%	38	Unknown	2   0.5%	2
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3	<p>Next to the Type of Resistance value “XDR (64)”, Select the “And” button.</p> <p>Note that the number in parenthesis “64” notes the total number of patients in the TB Portals collection (as of this writing) with a diagnosis of XDR TB.</p> <p>Note also that the Query Builder text box contains the text as shown and highlighted. Also note that the Number of Cases is still equal to 376.</p>	 <p><b>MXDR-TB Portals DEPOSIT</b> Create Cohort Saved Analyze</p> <p>Create Cohort Clinical and Socioeconomic Attributes</p> <p>Query Builder ?</p> <p>type_of_resistance: xdr</p> <p>ADVANCED FILTERS</p> <p>CLINICAL GENOMICS CT SCANS X-RAYS</p> <p>COMMON FILTERS</p> <ul style="list-style-type: none"> <li>Country</li> <li>Comorbidity</li> <li>Diagnosis Code</li> <li>Type of Resistance       <ul style="list-style-type: none"> <li>MDR non XDR (175) [AND] [OR] [NOT]</li> <li>Mono DR (18) [AND] [OR] [NOT]</li> <li>Poly DR (12) [AND] [OR] [NOT]</li> <li>Sensitive (107) [AND] [OR] [NOT]</li> <li>XDR (64) [AND] [OR] [NOT]</li> </ul> </li> <li>BMI</li> <li>Case Definition</li> <li>Gender</li> <li>Outcome</li> </ul> <p>Number of Cases: 100.0%   0.0% 376</p> <table border="1"> <thead> <tr> <th>Resistance</th> <th>Count</th> <th>Percentage</th> </tr> </thead> <tbody> <tr> <td>MDR non XDR</td> <td>175</td> <td>46.5%</td> </tr> <tr> <td>Sensitive</td> <td>107</td> <td>28.5%</td> </tr> <tr> <td>XDR</td> <td>64</td> <td>17.0%</td> </tr> <tr> <td>Mono DR</td> <td>18</td> <td>4.8%</td> </tr> <tr> <td>Poly DR</td> <td>12</td> <td>3.2%</td> </tr> </tbody> </table> <table border="1"> <thead> <tr> <th>Outcomes</th> <th>Count</th> <th>Percentage</th> </tr> </thead> <tbody> <tr> <td>Cured</td> <td>184</td> <td>48.9%</td> </tr> <tr> <td>Completed</td> <td>81</td> <td>21.5%</td> </tr> <tr> <td>Died</td> <td>37</td> <td>9.8%</td> </tr> <tr> <td>Failure</td> <td>33</td> <td>8.8%</td> </tr> <tr> <td>Still on treatment</td> <td>1</td> <td>0.3%</td> </tr> <tr> <td>Default</td> <td>38</td> <td>10.1%</td> </tr> <tr> <td>Unknown</td> <td>2</td> <td>0.5%</td> </tr> </tbody> </table>	Resistance	Count	Percentage	MDR non XDR	175	46.5%	Sensitive	107	28.5%	XDR	64	17.0%	Mono DR	18	4.8%	Poly DR	12	3.2%	Outcomes	Count	Percentage	Cured	184	48.9%	Completed	81	21.5%	Died	37	9.8%	Failure	33	8.8%	Still on treatment	1	0.3%	Default	38	10.1%	Unknown	2	0.5%
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4	Select the icon, “  ”	 <p>Query Builder ?</p> <p>type_of_resistance: xdr</p> <p>ADVANCED FILTERS</p>																																										

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5	<p>Note that the Number of Cases, “Cases Selected” shown in the horizontal indicator bar now indicates 64 cases (patients).</p> <p>Correspondingly, notice that the Resistance horizontal bar chart also shows 64 XDR cases. The Outcomes horizontal bar chart also changed. Now it represents the distribution of Outcomes within our chosen group of patients.</p>	 <p>The screenshot displays the MXDR-TB Portals DEPOT Query Builder interface. The search query is 'type_of_resistance: xdr'. The 'Type of Resistance' filter is expanded, showing the following counts: MDR non XDR (175), Mono DR (18), Poly DR (12), Sensitive (107), and XDR (64). The 'Number of Cases' chart shows 64 cases selected (17.0%) out of 312 remaining (83.0%). The 'Resistance' chart shows the distribution of resistance types: MDR non XDR (175), Sensitive (107), XDR (64), Mono DR (18), and Poly DR (12). The 'Outcomes' chart shows the distribution of patient outcomes: Cured (184), Completed (81), Died (37), Failure (33), Still on treatment (1), Default (38), and Unknown (2).</p>

6

In the left hand pane for Common Filters, select the drop-down arrow next to the Outcome field.

Select the "Cured (184), AND" button.

Note: This will add the logical clause to the Query Builder text line. However, it will not automatically execute the query or update the values.

### COMMON FILTERS

Country ▼

Comorbidity ▼

Diagnosis Code ▼

#### Type of Resistance ▲

MDR non XDR (175) AND OR NOT

Mono DR (18) AND OR NOT

Poly DR (12) AND OR NOT

Sensitive (107) AND OR NOT

XDR (64) AND OR NOT

BMI ▼

Case Definition ▼

Gender ▼

#### Outcome ▲

Completed (81) AND OR NOT

Cured (184) AND OR NOT

Default (38) AND OR NOT

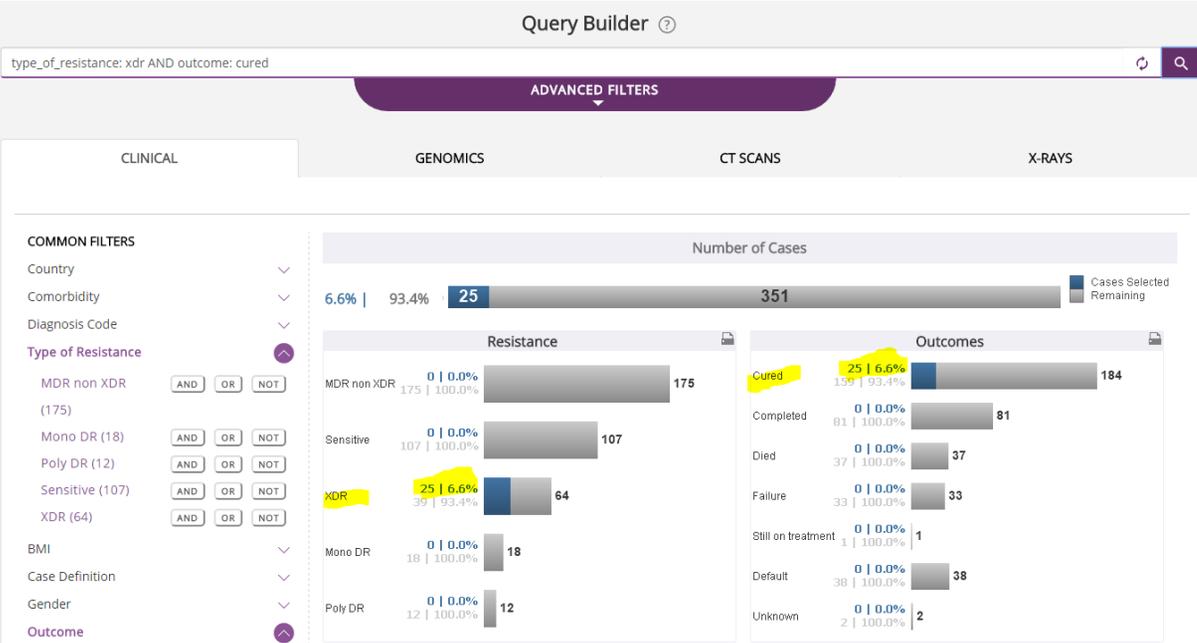
Died (37) AND OR NOT

Failure (33) AND OR NOT

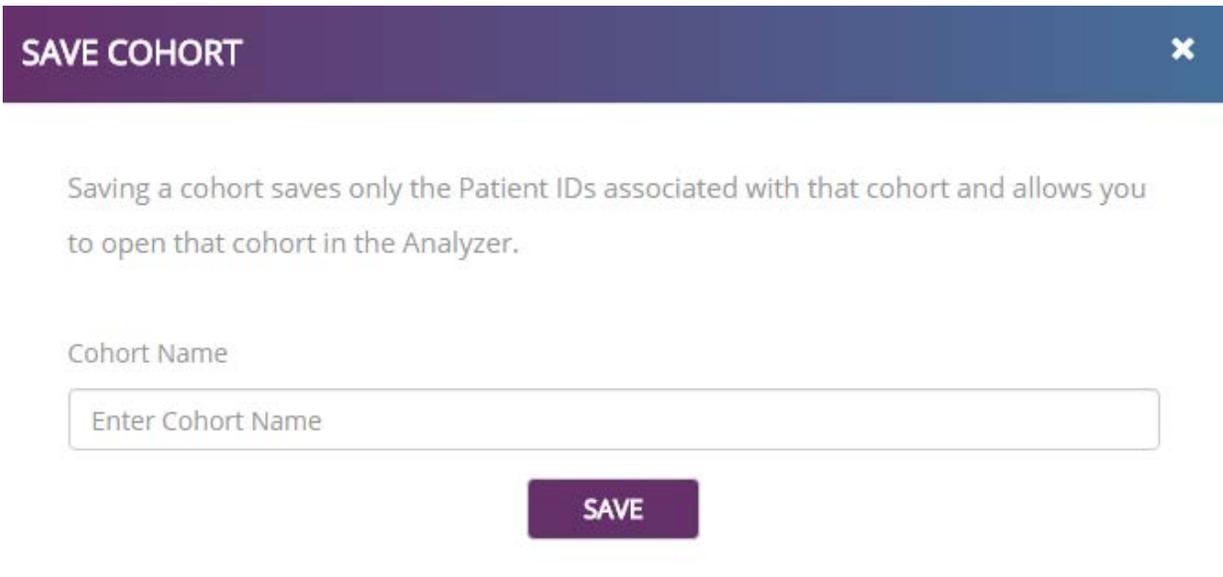
Still on treatment (1) AND OR NOT

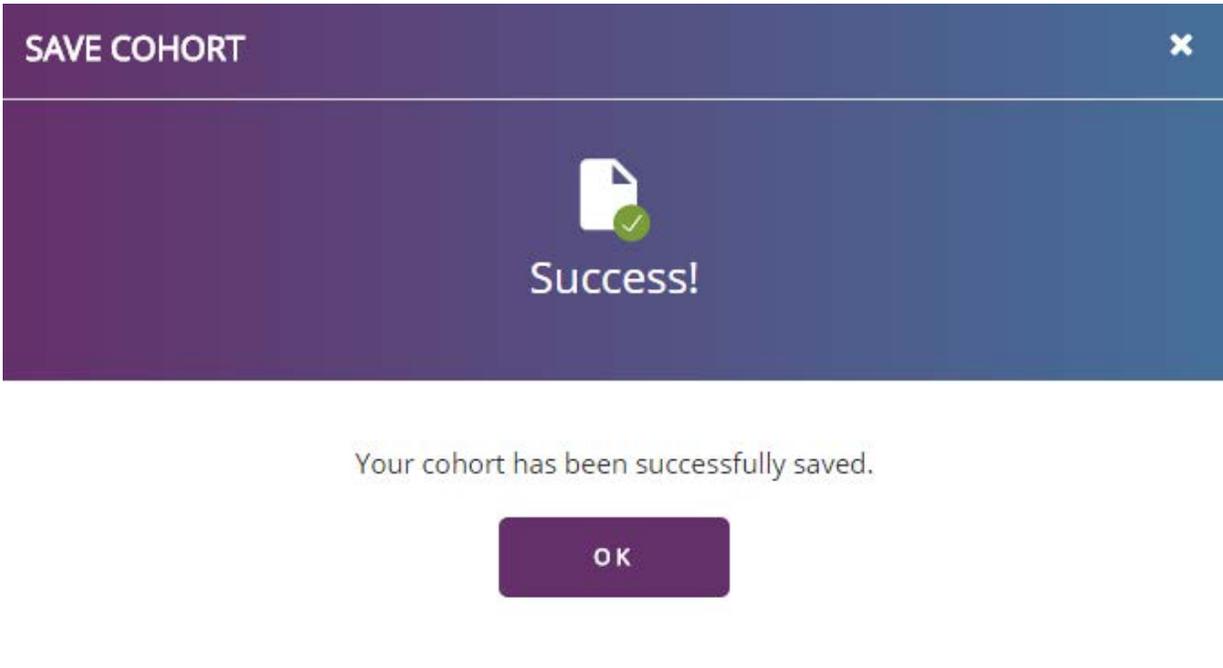
Unknown (2) AND OR NOT

Not Reported (0) AND OR NOT

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7	<p>Select the icon, “  <p>The screenshot shows the 'Query Builder' interface with the search query 'type_of_resistance: xdr AND outcome: cured'. The 'Number of Cases' section shows 25 cases selected (6.6%) out of 351 remaining (93.4%).</p> <p>The 'Resistance' chart shows the following data:</p> <table border="1"> <thead> <tr> <th>Resistance Type</th> <th>Count</th> <th>Percentage</th> </tr> </thead> <tbody> <tr> <td>MDR non XDR</td> <td>175</td> <td>100.0%</td> </tr> <tr> <td>Sensitive</td> <td>107</td> <td>100.0%</td> </tr> <tr> <td>XDR</td> <td>25</td> <td>6.6%</td> </tr> <tr> <td>Mono DR</td> <td>18</td> <td>100.0%</td> </tr> <tr> <td>Poly DR</td> <td>12</td> <td>100.0%</td> </tr> </tbody> </table> <p>The 'Outcomes' chart shows the following data:</p> <table border="1"> <thead> <tr> <th>Outcome</th> <th>Count</th> <th>Percentage</th> </tr> </thead> <tbody> <tr> <td>Cured</td> <td>25</td> <td>6.6%</td> </tr> <tr> <td>Completed</td> <td>81</td> <td>100.0%</td> </tr> <tr> <td>Died</td> <td>37</td> <td>100.0%</td> </tr> <tr> <td>Failure</td> <td>33</td> <td>100.0%</td> </tr> <tr> <td>Still on treatment</td> <td>1</td> <td>100.0%</td> </tr> <tr> <td>Default</td> <td>38</td> <td>100.0%</td> </tr> <tr> <td>Unknown</td> <td>2</td> <td>100.0%</td> </tr> </tbody> </table> </p>	Resistance Type	Count	Percentage	MDR non XDR	175	100.0%	Sensitive	107	100.0%	XDR	25	6.6%	Mono DR	18	100.0%	Poly DR	12	100.0%	Outcome	Count	Percentage	Cured	25	6.6%	Completed	81	100.0%	Died	37	100.0%	Failure	33	100.0%	Still on treatment	1	100.0%	Default	38	100.0%	Unknown	2	100.0%
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Number	Activity	Visual Result
8	Scroll to the bottom of the page, and select the "SAVE COHORT" button.	<p><b>MXDR-TB Portals DEPOT</b></p> <p>Failure (33) <input type="button" value="AND"/> <input type="button" value="OR"/> <input type="button" value="NOT"/>  Still on <input type="button" value="AND"/> <input type="button" value="OR"/> <input type="button" value="NOT"/>  treatment (1)  Unknown (2) <input type="button" value="AND"/> <input type="button" value="OR"/> <input type="button" value="NOT"/>  Not Reported (0) <input type="button" value="AND"/> <input type="button" value="OR"/> <input type="button" value="NOT"/></p> <p>Female: 15   4.0% (140 total), 125   96.0%</p> <p>Case Definitions: New (6   1.6%, 230 total), Failure (14   3.7%, 61 total), Other (0   0.0%, 7 total), Relapse (4   1.1%, 64 total), Treatment after default (1   0.3%, 14 total)</p> <p>Comorbidity: Diabetes (0   0.0%, 1 total), Hepatic diseases (0   0.0%, 4 total), HIV (1   0.3%, 21 total), Not Reported (23   6.1%, 349 total), Others (1   0.3%, 4 total)</p> <p>Body Mass Index: &lt; 18.5 (7   1.9%, 52 total), 18.5-24.9 (16   4.3%, 257 total), 25-29.9 (2   0.5%, 36 total), 30-over (0   0.0%, 8 total), Not Reported (0   0.0%, 23 total)</p> <p><b>SAVE COHORT →</b> <b>SAVE THE REMAINDER →</b></p> <p>CONNECT: Twitter, YouTube, E-MAIL: depot_support@niaid.nih.gov</p> <p>LINKS: NIAID Website, Privacy Policy, Disclaimer</p> <p>National Institutes of Health (NIH), 9000 Rockville Pike, Bethesda, Maryland 20892. National Institutes of Health...Turning Discovery Into Health®</p> <p>USA.gov NIH</p>

Number	Activity	Visual Result
9	<p>Type in the name of the Cohort... in this example “XDR Cured” and click the “SAVE” button.</p> <p>Note: You can chose any descriptive name of the cohort. Cohorts are currently saved for the length of time when a browser is open – only. When the browser or computer is re-started all saved cohorts are lost.</p>	

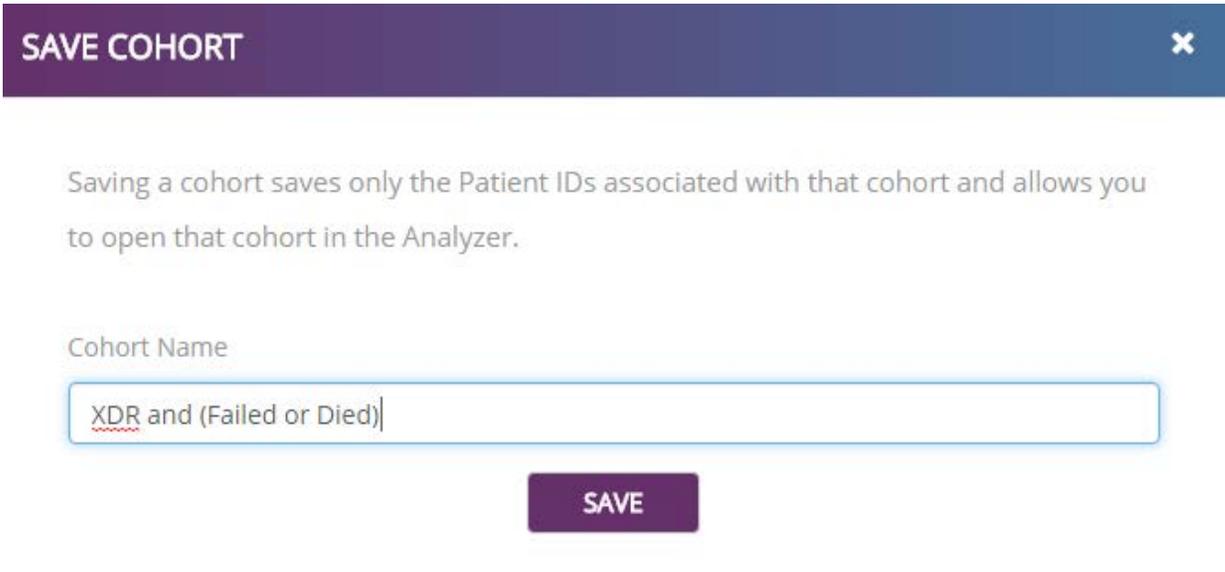
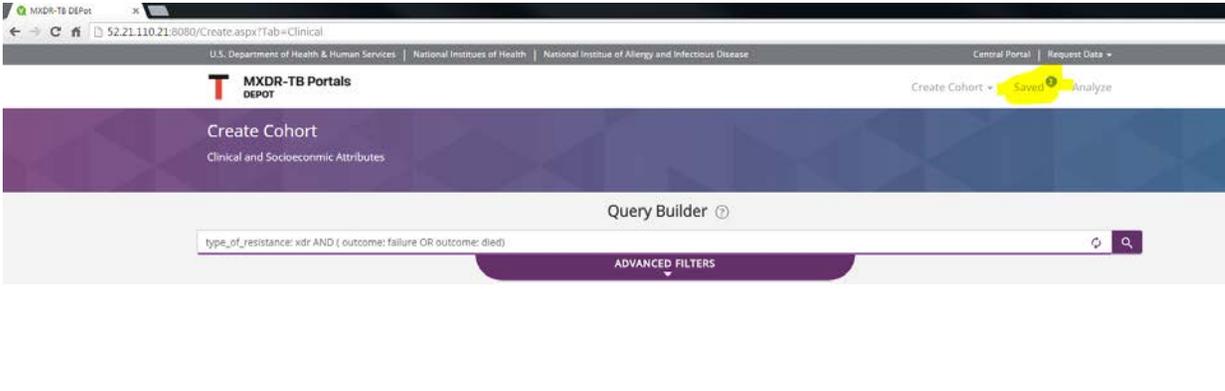
Number	Activity	Visual Result
10	After clicking save the DEPot will inform the user that the save worked successfully. Click, "OK".	 <p>The screenshot shows a modal dialog box with a dark blue header containing the text "SAVE COHORT" and a close button (X). The main content area is white and features a document icon with a green checkmark, the word "Success!" in a large font, the message "Your cohort has been successfully saved." in a smaller font, and a purple "OK" button at the bottom.</p>

Number	Activity	Visual Result																																										
11	<p>The user is returned to Create Cohort screen. Scroll up and you will recognize the query and cohort we just saved. Now we will create another cohort for subsequent comparative analysis.</p> <p>We will start this process by deleting text from the Query Builder text box string.</p>	<p><b>MXDR-TB Portals DEPOIT</b> Create Cohort Clinical and Socioeconomic Attributes</p> <p>Query Builder: type_of_resistance: xdr AND outcome: cured</p> <p>ADVANCED FILTERS</p> <p>CLINICAL GENOMICS CT SCANS X-RAYS</p> <p>COMMON FILTERS: Country, Comorbidity, Diagnosis Code, Type of Resistance, BMI, Case Definition, Gender, Outcome</p> <p>Number of Cases: 351 (25 Selected, 326 Remaining)</p> <table border="1"> <thead> <tr> <th>Resistance</th> <th>Count</th> <th>Percentage</th> </tr> </thead> <tbody> <tr><td>MDR non XDR</td><td>175</td><td>100.0%</td></tr> <tr><td>Sensitive</td><td>107</td><td>100.0%</td></tr> <tr><td>XDR</td><td>25</td><td>6.6%</td></tr> <tr><td>Mono DR</td><td>18</td><td>100.0%</td></tr> <tr><td>Poly DR</td><td>12</td><td>100.0%</td></tr> </tbody> </table> <table border="1"> <thead> <tr> <th>Outcomes</th> <th>Count</th> <th>Percentage</th> </tr> </thead> <tbody> <tr><td>Cured</td><td>184</td><td>52.4%</td></tr> <tr><td>Completed</td><td>81</td><td>23.1%</td></tr> <tr><td>Died</td><td>37</td><td>10.5%</td></tr> <tr><td>Failure</td><td>33</td><td>9.4%</td></tr> <tr><td>Still on treatment</td><td>1</td><td>0.3%</td></tr> <tr><td>Default</td><td>38</td><td>10.8%</td></tr> <tr><td>Unknown</td><td>2</td><td>0.6%</td></tr> </tbody> </table> <p>Gender: A15 (22   5.9%), 317   94.1%, 339</p> <p>Diagnosis: BY (22   5.9%), 317   94.1%, 339</p> <p>Country: BY (22   5.9%), 317   94.1%, 339</p>	Resistance	Count	Percentage	MDR non XDR	175	100.0%	Sensitive	107	100.0%	XDR	25	6.6%	Mono DR	18	100.0%	Poly DR	12	100.0%	Outcomes	Count	Percentage	Cured	184	52.4%	Completed	81	23.1%	Died	37	10.5%	Failure	33	9.4%	Still on treatment	1	0.3%	Default	38	10.8%	Unknown	2	0.6%
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12	<p>Delete the text, "AND outcome: cured" and again execute the query using the icon, "🔍"</p>	<p>Query Builder: type_of_resistance: xdr</p> <p>ADVANCED FILTERS</p>																																										

Number	Activity	Visual Result
13	<p>The query results are updated to the original 64 XDR cases as shown on the right.</p> <p>Note the “Outcome” field in the lower left of the Common Filters left hand pane.</p>	<p>The screenshot shows a 'Query Builder' interface with the search term 'type_of_resistance: xdr'. The 'ADVANCED FILTERS' section is active. The 'COMMON FILTERS' pane on the left includes fields like Country, Comorbidity, Diagnosis Code, Type of Resistance (with 'XDR (64)' selected), BMI, Case Definition, Gender, and Outcome. The main area displays a 'Number of Cases' bar chart showing 64 selected cases (17.0%) out of 312 remaining cases (83.0%). Below this are two sub-charts: 'Resistance' and 'Outcomes'. The 'Resistance' chart shows 64 XDR cases (17.0%) and 107 Sensitive cases (33.0%). The 'Outcomes' chart shows 184 Cured cases (57.5%), 81 Completed cases (25.3%), 37 Died cases (11.4%), 33 Failure cases (10.2%), 1 Still on treatment case (0.3%), 38 Default cases (11.8%), and 2 Unknown cases (0.6%).</p>

Number	Activity	Visual Result
14	<p>If necessary, select the drop-down arrow on the Outcome field in the lower left of the Common Filters pane (the users should still be on the Clinical tab in query builder).</p> <p>First, select the “AND” next to “Failure (33)”, and then select the “OR” next to the “DIED (37)”.</p> <p>The Query Builder text string will appear as shown on the left. However, we are not done yet.</p>	<p>The screenshot shows the 'Outcome' filter section in a query builder. It lists several outcome categories with their respective counts and associated logic buttons (AND, OR, NOT):</p> <ul style="list-style-type: none"> <li>Completed (81)</li> <li>Cured (184)</li> <li>Default (38)</li> <li>Died (37)</li> <li>Failure (33)</li> <li>Still on treatment (1)</li> <li>Unknown (2)</li> <li>Not Reported (0)</li> </ul> <p>The 'AND' button for 'Failure (33)' and the 'OR' button for 'Died (37)' are highlighted in yellow. Below the list, the query string is displayed as: <code>type_of_resistance: xdr AND outcome: failure OR outcome: died</code>. A purple bar at the bottom contains the text 'ADVANCED FILTERS'.</p>

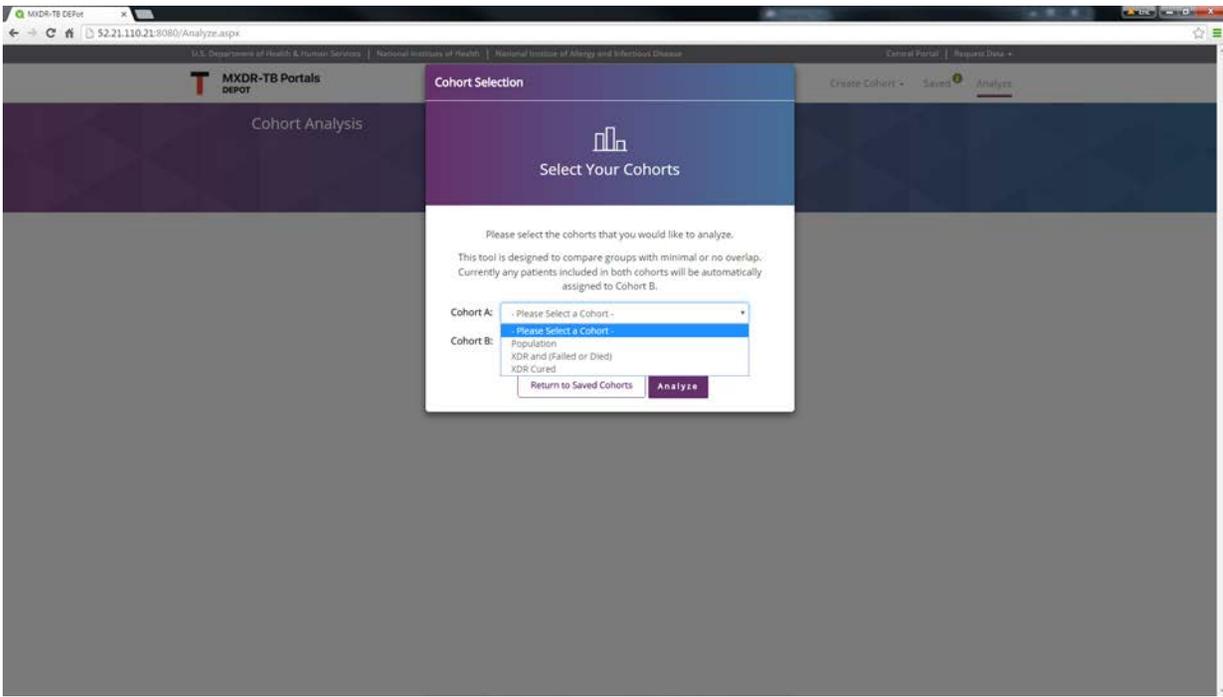
Number	Activity	Visual Result
15	<p>The system permits us to edit the Query Builder text string directly. Here we are adding the left and right parenthesis grouping as shown.</p> <p>Note: The use of parenthesis does change the meaning of the query and the query results.</p>	<p>The screenshot shows the 'Query Builder' interface with the query string: <code>type_of_resistance: xdr AND (outcome: failure OR outcome: died)</code>. The string is enclosed in a light blue box with a search icon on the right. Below the query string is a purple bar labeled 'ADVANCED FILTERS'.</p>
16	<p>Select the icon, “”</p>	<p>The screenshot shows the 'Query Builder' interface with the query string: <code>type_of_resistance: xdr AND ( outcome: failure OR outcome: died)</code>. The search icon on the right side of the query string is highlighted with a yellow box.</p>
17	<p>The results of the query are shown on the right. There are 20 XDR patients found that have an outcome of either died or failure.</p> <p>Note that the query string without the parenthesis would yield 47 total cases. This is the 10 XDR cases that Failed, and 37 total cases that had Died. The parenthesis are important and change the meaning of the query.</p> <p>Also note, the user may type in the entire query string if the field names are values are well understood.</p>	<p>The screenshot shows the 'Query Builder' interface with the query string: <code>type_of_resistance: xdr AND ( outcome: failure OR outcome: died)</code>. Below the query string is a purple bar labeled 'ADVANCED FILTERS'. The main content area is divided into four tabs: CLINICAL, GENOMICS, CT SCANS, and X-RAYS. The 'CLINICAL' tab is active, showing a 'COMMON FILTERS' section on the left and a 'Number of Cases' section on the right. The 'Number of Cases' section shows a bar chart with 356 total cases, 20 cases selected (highlighted in yellow), and 336 cases remaining. The 'Resistance' section shows a bar chart with 175 MDR non XDR, 107 Sensitive, 64 XDR (20 highlighted in yellow), 18 Mono DR, and 12 Poly DR. The 'Outcomes' section shows a bar chart with 184 Cured, 81 Completed, 37 Died (10 highlighted in yellow), 33 Failure (10 highlighted in yellow), 1 Still on treatment, 38 Default, and 2 Unknown.</p>

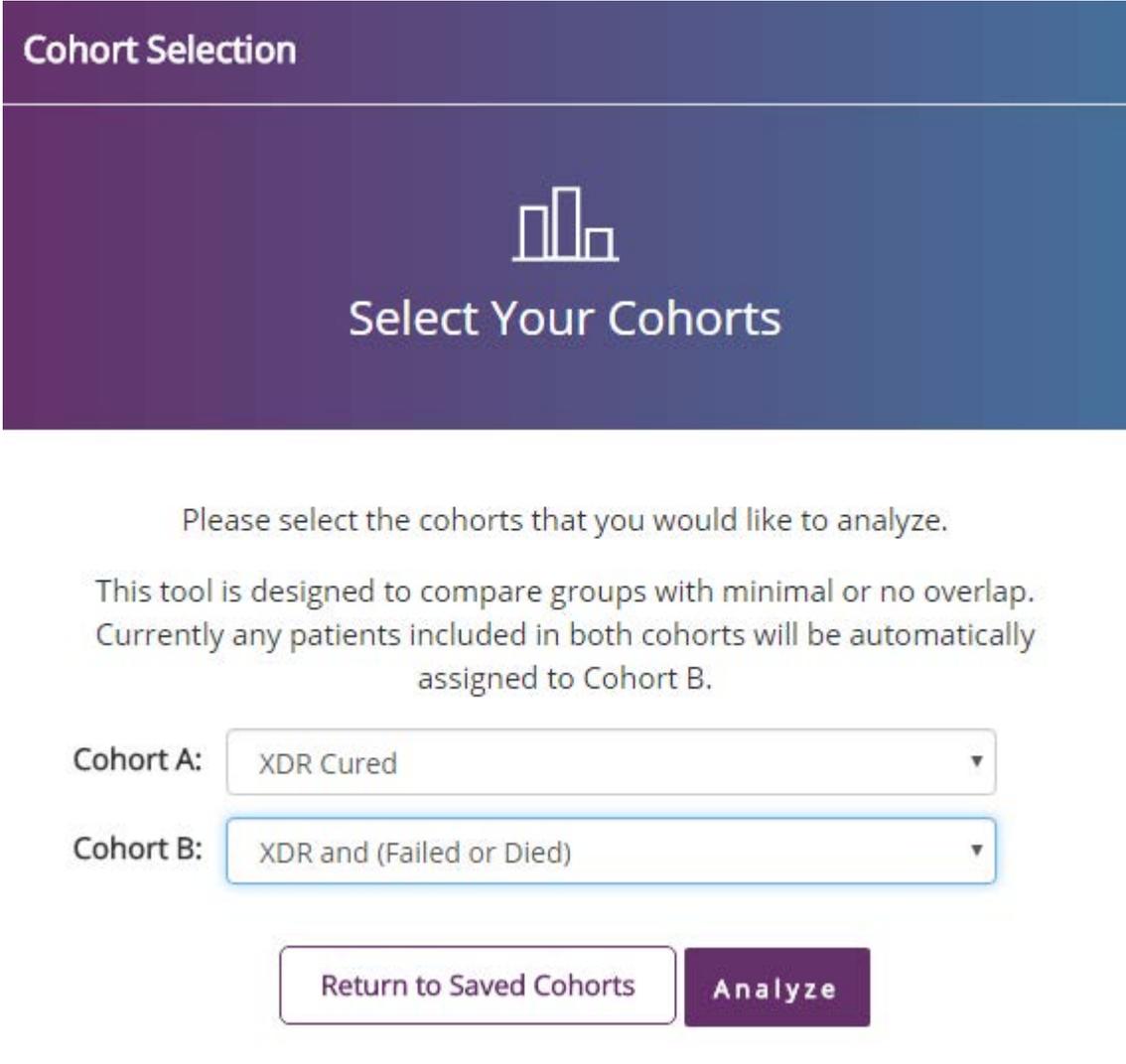
Number	Activity	Visual Result
18	<p>Scroll to the bottom of the page, and select the “SAVE COHORT” button (shown in step 8).</p> <p>Enter the name of the Cohort, “XDR and (Failed or Died)”, and select “Save”. Select “OK” to close the successfully saved information box.</p> <p>This will again return us to the Create Cohort page.</p>	
19	<p>Scroll to the top of the page. Note that the system alerts us that now we have two cohorts saved.</p> <hr/> <p>Create Cohort ▾ Saved <sup>2</sup> Analyze</p> <hr/> <p>Next we will explore the “Analyze” features.</p>	

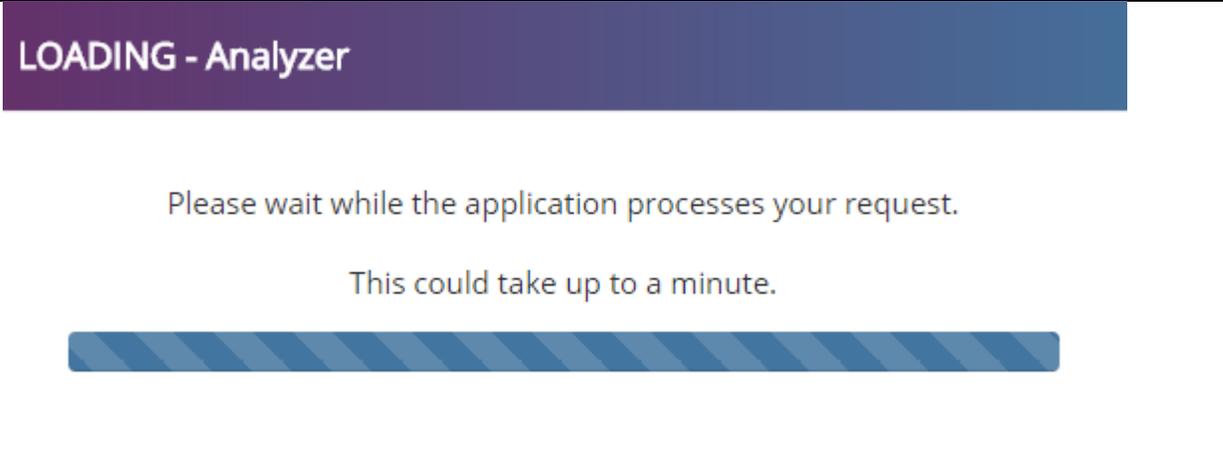
## Analyze

The Analyze feature set enables the user to conduct statistical exploratory analysis of previously defined cohorts. Currently DEPOT offers comparative analysis of two cohorts at a time. Any two cohorts from the previously saved collection can be chosen for comparative analysis.

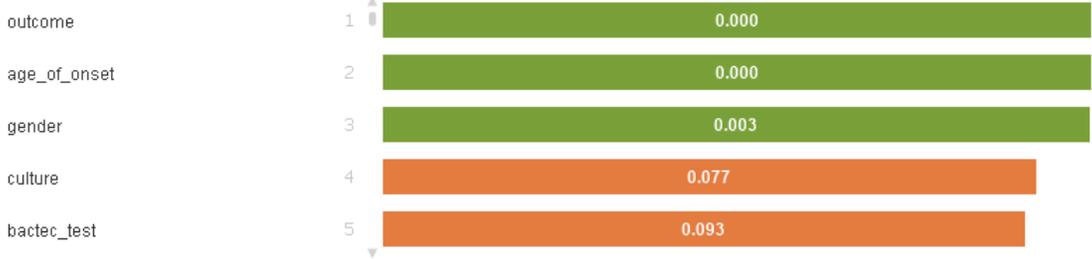
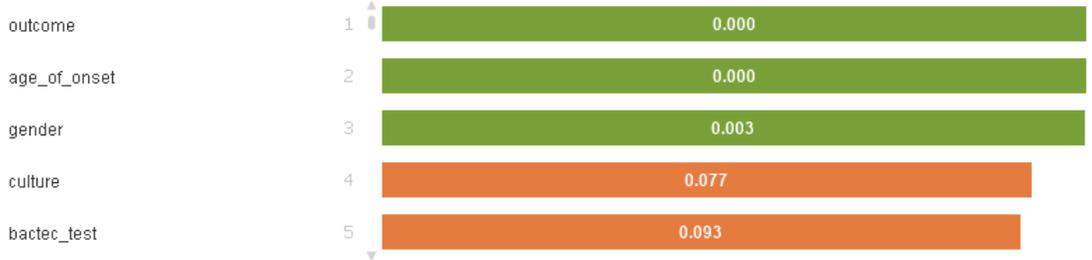
Number	Activity	Visual Result
1	<p>The Analyze feature set is available to the user in the DEPOT header from any page in the system.</p> <hr/> <p>Create Cohort ▾ Saved <sup>2</sup> Analyze</p> <hr/> <p>Select "Analyze".</p>	 <p>The screenshot shows a web browser window with the URL 52.21.110.21:8080/Home.aspx. The page header includes the U.S. Department of Health &amp; Human Services, National Institutes of Health, and National Institute of Allergy and Infectious Disease. The MXDR-TB Portals DEPOT logo is displayed. In the top right corner, there are links for 'Central Portal' and 'Request Data'. Below the logo, there are three buttons: 'Create Cohort ▾', 'Saved <sup>2</sup>', and 'Analyze'. The 'Analyze' button is highlighted in yellow.</p>

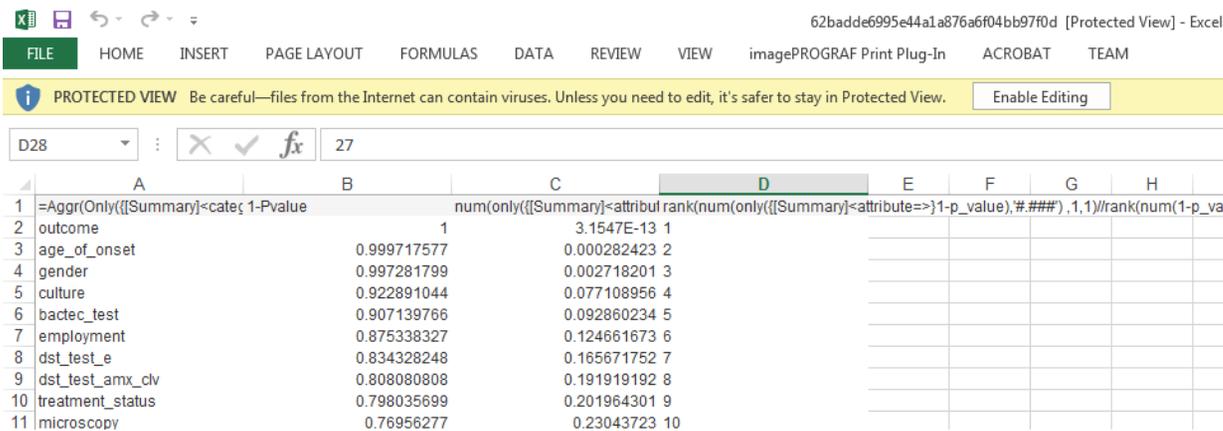
Number	Activity	Visual Result
2	<p>By selecting “Analyze” from the DEPOT header, the user is prompted as shown.</p> <p>Note that there are currently 3 cohorts defined. By default the Population cohort is available representing the entire group of patients from all TB Portals. In the Create Cohort tutorial the other two cohorts were created and will be used here.</p>	

Number	Activity	Visual Result
3	Using the drop-down arrows, the cohort names were selected as defined in the Create Cohorts tutorial – as shown here.	 <p><b>Cohort Selection</b></p> <p>Select Your Cohorts</p> <p>Please select the cohorts that you would like to analyze.</p> <p>This tool is designed to compare groups with minimal or no overlap. Currently any patients included in both cohorts will be automatically assigned to Cohort B.</p> <p>Cohort A: XDR Cured</p> <p>Cohort B: XDR and (Failed or Died)</p> <p>Return to Saved Cohorts Analyze</p>

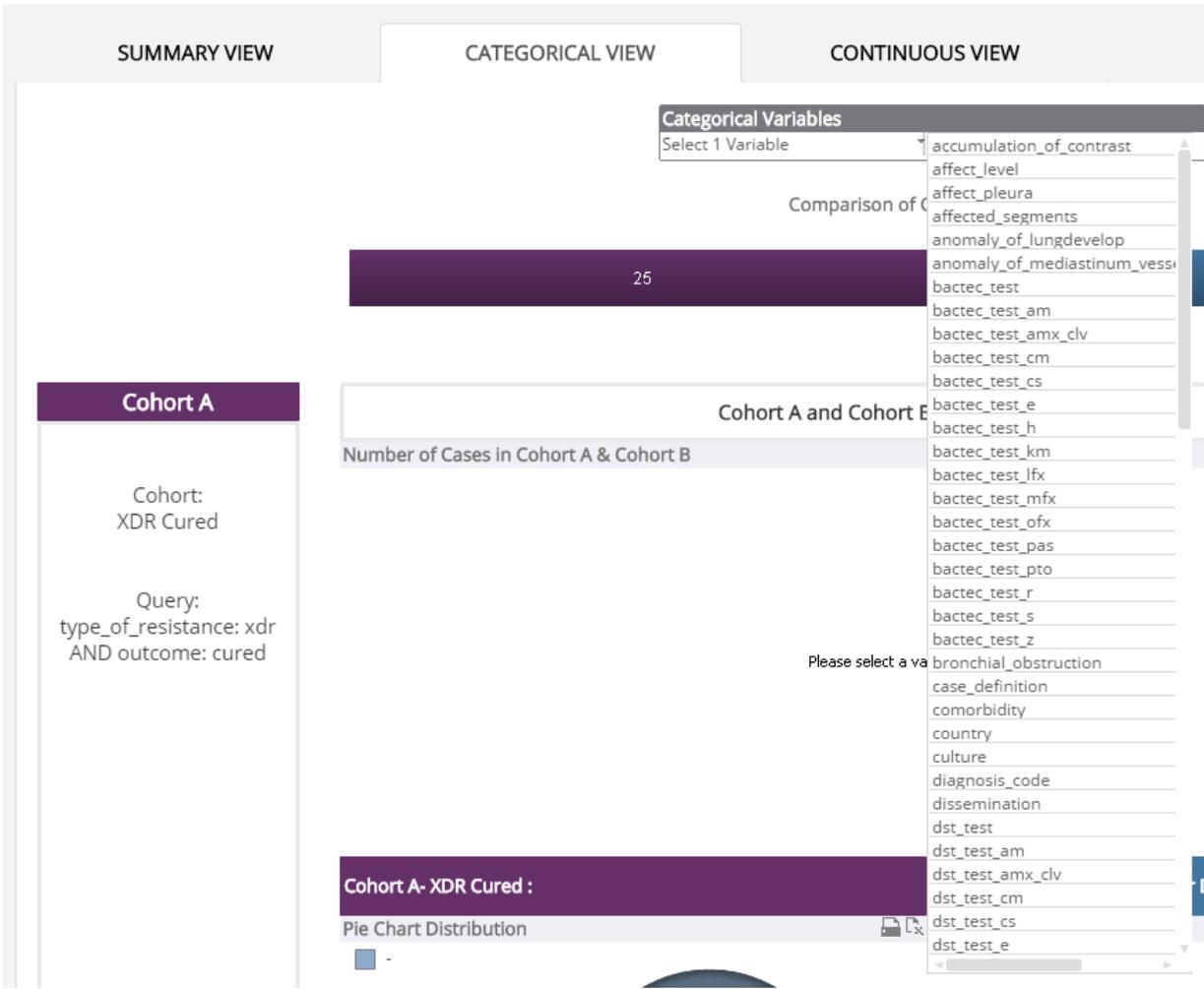
Number	Activity	Visual Result
4	<p>Select "Analyze" button.</p> <p>Note: the DEPOT pre-computes statistical test for the entire collection of clinical, image descriptors, and genomic data to enable the subsequent screen displays where all parameters will be sorted according to the significance between two cohorts.</p>	 <p>LOADING - Analyzer</p> <p>Please wait while the application processes your request.</p> <p>This could take up to a minute.</p>

Number	Activity	Visual Result																																							
5	<p>The Summary view is shown. On the left is Cohort A “XDR Cured”, and on the right side is Cohort B “XDR and (Failed or Died)”.</p> <p>Note: Two most significant results are highlighted for the end user. “age_of_onset” is statistically significant with P value less than 0.001, and “lung_capacity_decrease” is statistically significant with P value less than .05.</p>	<p><b>Result of Cohort Analysis - Summary View</b></p> <p>Analysis results are divided into clinical, imaging, and genomic asymmetries. Ranking is based on uneven distribution characterized by p-values. Categorical variables were assessed using a Fishers Test and continuous variables were assessed using a t-test. Scroll through the bar charts in appropriate categories to see all attributes.</p> <p><b>SUMMARY VIEW</b>   CATEGORICAL VIEW   CONTINUOUS VIEW   SCATTERPLOT   KAPLAN-MEIER CURVE</p> <p><b>Cohort A</b> Cohort: XDR Cured Query: type_of_resistance: xdr AND outcome: cured</p> <p><b>Cohort B</b> Cohort: XDR and (Failed or Died) Query: type_of_resistance: xdr AND ( outcome: failure OR outcome: died)</p> <p><b>Top Clinical Asymmetries - P Value</b></p> <table border="1"> <tr><td>outcome</td><td>1</td><td>0.000</td></tr> <tr><td>age_of_onset</td><td>2</td><td>0.000</td></tr> <tr><td>gender</td><td>3</td><td>0.003</td></tr> <tr><td>culture</td><td>4</td><td>0.077</td></tr> <tr><td>bacter_test</td><td>5</td><td>0.093</td></tr> </table> <p><b>Top Imaging Asymmetries - P Value</b></p> <table border="1"> <tr><td>lung_capacity_decrease</td><td>1</td><td>0.044</td></tr> <tr><td>x_ray_count</td><td>2</td><td>0.139</td></tr> <tr><td>bronchial_obstruction</td><td>3</td><td>0.149</td></tr> <tr><td>process_prevalence</td><td>4</td><td>0.267</td></tr> <tr><td>shadow_pattern</td><td>5</td><td>0.389</td></tr> </table> <p><b>Top Genomics Asymmetries - P Value</b></p> <table border="1"> <tr><td>strain</td><td>1</td><td>0.080</td></tr> <tr><td>high_confidence</td><td>1</td><td>0.080</td></tr> <tr><td>gene_name</td><td>3</td><td>0.080</td></tr> </table>	outcome	1	0.000	age_of_onset	2	0.000	gender	3	0.003	culture	4	0.077	bacter_test	5	0.093	lung_capacity_decrease	1	0.044	x_ray_count	2	0.139	bronchial_obstruction	3	0.149	process_prevalence	4	0.267	shadow_pattern	5	0.389	strain	1	0.080	high_confidence	1	0.080	gene_name	3	0.080
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9	<p>Select the Send to Excel icon “”.</p> <p>The browser will download an Excel table of results for the current analysis window. The Excel data file example is shown here.</p>	 <p>62badde6995e44a1a876a6f04bb97f0d [Protected View] - Excel</p> <p>FILE HOME INSERT PAGE LAYOUT FORMULAS DATA REVIEW VIEW imagePROGRAF Print Plug-In ACROBAT TEAM</p> <p>PROTECTED VIEW Be careful—files from the Internet can contain viruses. Unless you need to edit, it's safer to stay in Protected View. <input type="button" value="Enable Editing"/></p> <p>D28 : X ✓ fx 27</p> <table border="1"> <thead> <tr> <th></th> <th>A</th> <th>B</th> <th>C</th> <th>D</th> <th>E</th> <th>F</th> <th>G</th> <th>H</th> </tr> </thead> <tbody> <tr> <td>1</td> <td>=Aggr(Only({{Summary}&lt;cateç 1-Pvalue</td> <td></td> <td>num(only({{Summary}&lt;attribul rank(num(only({{Summary}&lt;attribute=&gt;}1-p_value),# ###),1,1)/rank(num(1-p_val</td> <td></td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>2</td> <td>outcome</td> <td>1</td> <td>3.1547E-13</td> <td>1</td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>3</td> <td>age_of_onset</td> <td>0.999717577</td> <td>0.000282423</td> <td>2</td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>4</td> <td>gender</td> <td>0.997281799</td> <td>0.002718201</td> <td>3</td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>5</td> <td>culture</td> <td>0.922891044</td> <td>0.077108956</td> <td>4</td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>6</td> <td>bactec_test</td> <td>0.907139766</td> <td>0.092860234</td> <td>5</td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>7</td> <td>employment</td> <td>0.875338327</td> <td>0.124661673</td> <td>6</td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>8</td> <td>dst_test_e</td> <td>0.834328248</td> <td>0.165671752</td> <td>7</td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>9</td> <td>dst_test_amx_clv</td> <td>0.808080808</td> <td>0.191919192</td> <td>8</td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>10</td> <td>treatment_status</td> <td>0.798035699</td> <td>0.201964301</td> <td>9</td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>11</td> <td>microscopy</td> <td>0.76956277</td> <td>0.23043723</td> <td>10</td> <td></td> <td></td> <td></td> <td></td> </tr> </tbody> </table>		A	B	C	D	E	F	G	H	1	=Aggr(Only({{Summary}<cateç 1-Pvalue		num(only({{Summary}<attribul rank(num(only({{Summary}<attribute=>}1-p_value),# ###),1,1)/rank(num(1-p_val						2	outcome	1	3.1547E-13	1					3	age_of_onset	0.999717577	0.000282423	2					4	gender	0.997281799	0.002718201	3					5	culture	0.922891044	0.077108956	4					6	bactec_test	0.907139766	0.092860234	5					7	employment	0.875338327	0.124661673	6					8	dst_test_e	0.834328248	0.165671752	7					9	dst_test_amx_clv	0.808080808	0.191919192	8					10	treatment_status	0.798035699	0.201964301	9					11	microscopy	0.76956277	0.23043723	10				
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11	microscopy	0.76956277	0.23043723	10																																																																																																										

Number	Activity	Visual Result
10	<p>Click on the “CATEGORICAL VIEW” tab.</p> <p>Note that there is no variable selected in the “Select 1 Variable” drop-down.</p> <p>Also, note the “Please select a variable for analysis” note in the display results area.</p>	<p>The screenshot displays the MXDR-TB Portals DEPOD interface. At the top, there are three tabs: SUMMARY VIEW, CATEGORICAL VIEW (which is active), and CONTINUOUS VIEW. Below the tabs is a 'Categorical Variables' dropdown menu with the text 'Select 1 Variable'. A yellow callout box highlights this dropdown. Below the dropdown is a header for 'Results of Cohort Analysis - Categorical View' with a sub-header 'Comparison of Cases In Cohorts'. A horizontal bar chart shows two bars: a purple bar for 'Distinct A' with a value of 25, and a blue bar for 'Distinct B' with a value of 20. Below the chart are two cohort panels. The left panel is for 'Cohort A' with the query 'type_of_resistance: xdr AND outcome: cured'. The right panel is for 'Cohort B' with the query 'type_of_resistance: xdr AND ( outcome: failure OR outcome: died)'. At the bottom center, a yellow callout box highlights the text 'Please select a variable for analysis'.</p>

Number	Activity	Visual Result
11	<p>Select the drop-down icon “” in the “Select 1 Variable” drop-down field.</p>	 <p>The screenshot displays a software interface with three tabs: SUMMARY VIEW, CATEGORICAL VIEW, and CONTINUOUS VIEW. The CATEGORICAL VIEW is active, showing a 'Categorical Variables' dropdown menu with 'Select 1 Variable' selected. The dropdown list includes variables like 'accumulation_of_contrast', 'affect_level', 'affect_pleura', 'affected_segments', 'anomaly_of_lungdevelop', 'anomaly_of_mediastinum_vess', 'bactec_test', 'bactec_test_am', 'bactec_test_amx_clv', 'bactec_test_cm', 'bactec_test_cs', 'bactec_test_e', 'bactec_test_h', 'bactec_test_km', 'bactec_test_lfx', 'bactec_test_mfx', 'bactec_test_ofx', 'bactec_test_pas', 'bactec_test_pto', 'bactec_test_r', 'bactec_test_s', 'bactec_test_z', 'bronchial_obstruction', 'case_definition', 'comorbidity', 'country', 'culture', 'diagnosis_code', 'dissemination', 'dst_test', 'dst_test_am', 'dst_test_amx_clv', 'dst_test_cm', 'dst_test_cs', and 'dst_test_e'. The interface also shows 'Cohort A' with 'XDR Cured' and a query 'type_of_resistance: xdr AND outcome: cured'. A bar chart shows a value of 25 for 'Cohort A and Cohort B'. A 'Pie Chart Distribution' section is visible at the bottom.</p>

12

Use the vertical scroll bar to find the "lung\_capacity\_decrease" variable and select it.

SUMMARY VIEW      CATEGORICAL VIEW      CONTINUOUS VIEW

**Cohort A**

Cohort:  
XDR Cured

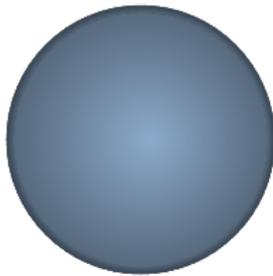
Query:  
type\_of\_resistance: xdr  
AND outcome: cured

Comparison of Cohort A and Cohort B

Number of Cases in Cohort A & Cohort B

Cohort A- XDR Cured :

Pie Chart Distribution



25

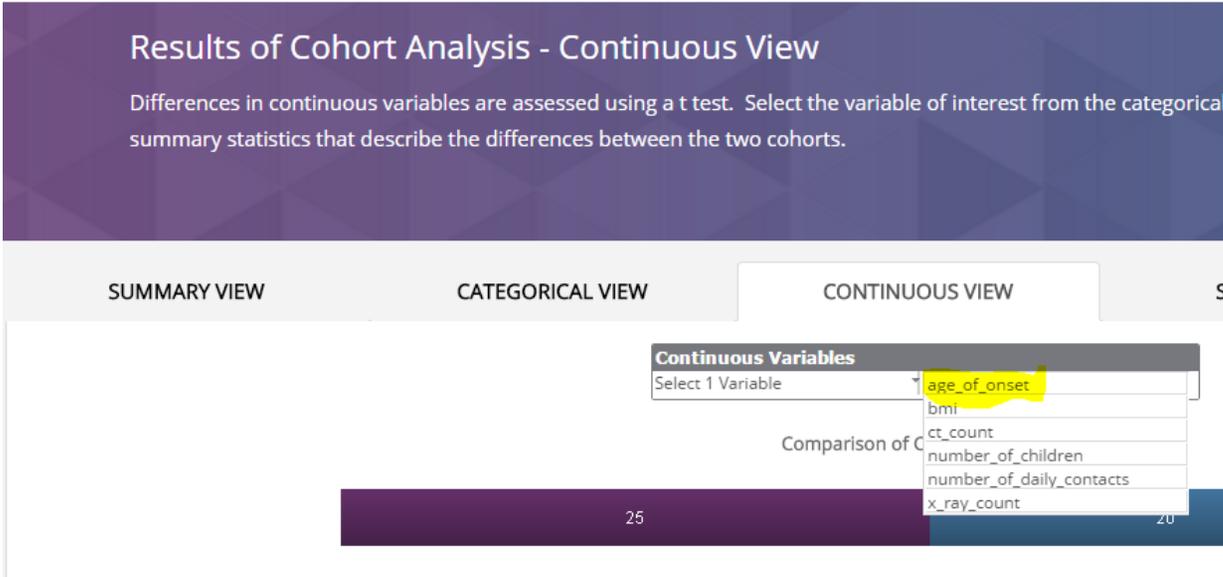
**Categorical Variables**

Select 1 Variable

- gender
- gene\_name
- genexpert\_test
- genexpert\_test\_r
- hain\_test
- hain\_test\_e
- hain\_test\_ft
- hain\_test\_h
- hain\_test\_r
- hain\_test\_s
- high\_confidence
- image\_body\_site
- limfadenopatia
- lowenstein\_jensen\_test
- lowenstein\_jensen\_test\_am
- lowenstein\_jensen\_test\_cm
- lowenstein\_jensen\_test\_cs
- lowenstein\_jensen\_test\_e
- lowenstein\_jensen\_test\_h
- lowenstein\_jensen\_test\_km
- lowenstein\_jensen\_test\_lfx
- lowenstein\_jensen\_test\_mb
- lowenstein\_jensen\_test\_ofx
- lowenstein\_jensen\_test\_pas
- lowenstein\_jensen\_test\_r
- lowenstein\_jensen\_test\_s
- lowenstein\_jensen\_test\_test\_ptc
- lowenstein\_jensen\_test\_z
- lung\_capacity\_decrease
- lung\_localization
- lungcavity\_size
- microscopy
- nodalcalcinatum
- outcome
- plevritis
- pneumothorax
- posttbresiduals
- process\_prevalence
- regimen\_drug
- shadow\_pattern
- social\_risk\_factors
- specimen
- strain
- thromboembolism\_of\_the\_pulm
- totalcavernum
- treatment\_status
- type\_of\_resistance

Number	Activity	Visual Result																																				
13	<p>Note the “lung_capacity_decrease” variable is highlighted in green.</p> <p>Also note the p_value equal to “0.0441” field now appears within the Summary Stats table.</p>	<p><b>Categorical Variables</b> Select 1 Variable: lung_capacity_decrease</p> <p>Comparison of Cases In Cohorts</p> <ul style="list-style-type: none"> <li>Distinct A: 25</li> <li>Common Cases: 20</li> <li>Distinct B: 20</li> </ul> <p><b>Cohort A</b> Cohort: XDR Cured Query: type_of_resistance: xdr AND outcome: cured Number of Cases: 25</p> <p><b>Cohort B</b> Cohort: XDR and (Failed or Died) Query: type_of_resistance: xdr AND ( outcome: failure OR outcome: died) Number of Cases: 20</p> <p><b>Cohort A and Cohort B Analysis on Variable : lung_capacity_decrease</b></p> <p>Number of Cases in Cohort A &amp; Cohort B</p> <table border="1"> <thead> <tr> <th>lung_capacity_decrease</th> <th>Cohort A</th> <th>Cohort B</th> </tr> </thead> <tbody> <tr> <td>No</td> <td>16</td> <td>6</td> </tr> <tr> <td>Yes</td> <td>5</td> <td>11</td> </tr> <tr> <td>Not Reported</td> <td>4</td> <td>3</td> </tr> </tbody> </table> <p><b>Cohort A- XDR Cured : lung_capacity_decrease</b></p> <p>Pie Chart Distribution</p> <table border="1"> <thead> <tr> <th>lung_capacity_decrease</th> <th>Count</th> </tr> </thead> <tbody> <tr> <td>No</td> <td>16</td> </tr> <tr> <td>Yes</td> <td>5</td> </tr> <tr> <td>Not Reported</td> <td>4</td> </tr> </tbody> </table> <p><b>Cohort B- XDR and (Failed or Died) : lung_capacity_decrease</b></p> <p>Pie Chart Distribution</p> <table border="1"> <thead> <tr> <th>lung_capacity_decrease</th> <th>Count</th> </tr> </thead> <tbody> <tr> <td>No</td> <td>6</td> </tr> <tr> <td>Yes</td> <td>11</td> </tr> <tr> <td>Not Reported</td> <td>3</td> </tr> </tbody> </table> <p><b>Summary Stats: lung_capacity_decrease</b></p> <table border="1"> <thead> <tr> <th>Cohort</th> <th>Count</th> <th>p_value</th> </tr> </thead> <tbody> <tr> <td>Cohort A (XDR Cured)</td> <td>25</td> <td rowspan="2">0.0441</td> </tr> <tr> <td>Cohort B (XDR and (Failed or Died))</td> <td>20</td> </tr> </tbody> </table>	lung_capacity_decrease	Cohort A	Cohort B	No	16	6	Yes	5	11	Not Reported	4	3	lung_capacity_decrease	Count	No	16	Yes	5	Not Reported	4	lung_capacity_decrease	Count	No	6	Yes	11	Not Reported	3	Cohort	Count	p_value	Cohort A (XDR Cured)	25	0.0441	Cohort B (XDR and (Failed or Died))	20
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Number	Activity	Visual Result
14	Select the "CONTINUOUS VIEW" tab as shown.	<p>The screenshot displays a software interface with the following elements:</p> <ul style="list-style-type: none"> <li><b>Navigation Tabs:</b> SUMMARY VIEW, CATEGORICAL VIEW, CONTINUOUS VIEW (selected), SCATTERPLOT, KAPLAN-MEIER CURVE.</li> <li><b>Continuous Variables:</b> A dropdown menu labeled "Continuous Variables" with the text "Select 1 Variable" and a green bar.</li> <li><b>Comparison of Cases In Cohorts:</b> A horizontal bar chart showing two segments: a purple segment with the value 25 and a blue segment with the value 20. A legend on the right identifies the colors: Distinct A (purple), Common Cases (grey), and Distinct B (blue).</li> <li><b>Cohort A Panel:</b> <ul style="list-style-type: none"> <li>Cohort: XDR Cured</li> <li>Query: type_of_resistance: xdr AND outcome: cured</li> </ul> </li> <li><b>Cohort B Panel:</b> <ul style="list-style-type: none"> <li>Cohort: XDR and (Failed or Died)</li> <li>Query: type_of_resistance: xdr AND ( outcome: failure</li> </ul> </li> <li><b>Analysis Window:</b> A central window titled "Cohort A and Cohort B Analysis on Variable : lung_capacity_decrease" containing a yellow highlighted message: "Please select a variable for analysis".</li> </ul>

Number	Activity	Visual Result
15	Select the drop-down icon and select the "age_of_onset" variable as shown.	 <p>The screenshot displays the 'Results of Cohort Analysis - Continuous View' interface. At the top, there is a header with the title and a brief explanation: 'Differences in continuous variables are assessed using a t test. Select the variable of interest from the categorical summary statistics that describe the differences between the two cohorts.' Below the header are three tabs: 'SUMMARY VIEW', 'CATEGORICAL VIEW', and 'CONTINUOUS VIEW', with the 'CONTINUOUS VIEW' tab selected. A dropdown menu titled 'Continuous Variables' is open, showing a list of variables: 'age_of_onset' (highlighted in yellow), 'bmi', 'ct_count', 'number_of_children', 'number_of_daily_contacts', and 'x_ray_count'. The background of the interface shows a bar chart with two bars, one purple with the value '25' and one blue with the value '20'.</p>

Number	Activity	Visual Result																									
16	<p>The results for “age_of_onset” are shown here. The Cohorts Summary Statistics table shows a median age for XDR and (Failed or Died) of 45 years, and the median age for the XDR Cured cohort is 30 years. The P Value of the difference in average age of onset between the two cohorts is less than 0.001.</p>	<p><b>Cohort A</b></p> <p>Cohort: XDR Cured</p> <p>Query: type_of_resistance: xdr AND outcome: cured</p> <p><b>Cohort B</b></p> <p>Cohort: XDR and (Failed or Died)</p> <p>Query: type_of_resistance: xdr AND ( outcome: failure OR outcome: died)</p> <p><b>Cohort A - XDR Cured : age_of_onset</b></p> <p>Number of Cases: 25</p> <p><b>Cohort B - XDR and (Failed or Died) : age_of_onset</b></p> <p>Number of Cases: 20</p> <table border="1"> <caption>Cohorts Summary Statistics for age_of_onset</caption> <thead> <tr> <th>Summary Statistics</th> <th>Cohort A: XDR Cured</th> <th>Cohort B: XDR and (Failed or Died)</th> </tr> </thead> <tbody> <tr> <td>Median</td> <td>30.000</td> <td>45.000</td> </tr> <tr> <td>Mean</td> <td>29.880</td> <td>43.550</td> </tr> <tr> <td>Count</td> <td>25</td> <td>20</td> </tr> <tr> <td>Standard Deviation</td> <td>7.502</td> <td>13.173</td> </tr> </tbody> </table> <table border="1"> <caption>Cohorts Summary Statistics for age_of_onset</caption> <thead> <tr> <th>Cohort A</th> <th>Cohort B</th> <th>P Value</th> <th>T Stat.</th> <th>Degrees of Freedom</th> </tr> </thead> <tbody> <tr> <td>XDR Cured</td> <td>XDR and (Failed or Died)</td> <td>0.000</td> <td>-4.135</td> <td>28.613</td> </tr> </tbody> </table>	Summary Statistics	Cohort A: XDR Cured	Cohort B: XDR and (Failed or Died)	Median	30.000	45.000	Mean	29.880	43.550	Count	25	20	Standard Deviation	7.502	13.173	Cohort A	Cohort B	P Value	T Stat.	Degrees of Freedom	XDR Cured	XDR and (Failed or Died)	0.000	-4.135	28.613
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## Training Outcome Questions

1. What would you change in the user interface (query, visualization, wording, etc.)?
2. Did you expect the results that you obtained with the help of the DEPot analyze function for XDR patients? What additional statistical analysis would you suggest?
3. What other cohorts are logical to compare with the XDR cohorts we used in this training? Try to create these new cohorts and execute the analysis. Write down your guess of what is important before the analysis, and then compare your guess with the actual outcome.
4. Based on the results of comparative analysis what data might you suggest to add to the TB Portals and DEPot to augment the analysis of these cohorts?