WHONET Training Course

Module 5 – Data analysis and interpretation

Exercises

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**WHONET – Getting Started - Exercises**

In Module 4, we covered the mechanics of how to perform an analysis in WHONET, selecting the analysis type, organism, and data filters, as well as additional options, such as for creating isolate filters and saving results in Microsoft Excel. In the below exercises, we will cover more details for each of the WHONET “analysis types”.

1. **%RIS and test measurements**

In the exercises for Module 4, we covered the “detailed report” for the “%RIS and test measurement” analysis. A brief review of that exercise is included below, as well as a description of the “summary report” for this analysis. In the detailed report, you will see one organism for each page of the output with a lot of information, such as breakpoints, %R, %I, %S and graphs for the zone diameter and MIC distributions. This is valuable for detailed review by the microbiologist. In the summary report, you will see many organisms in the same output table with one row for each organism. By default, you will see the “%Susceptible” and the “Number of isolates tested” for each antibiotic. This summary information is valuable for clinicians and pharmacists in the development of treatment guidelines and in revisions to local and national formularies.

* 1. %RIS and test measurements – Detailed report
* Open WHONET, select the “WHONET Test laboratory”, “Open laboratory”, “Data analysis” and “Data analysis again. You should now be in the main screen for data analysis.
* For “Analysis type”, select the option for %RIS and test measurements”, and for report format, select “%RIS and test measurements” to get the detailed report. Click on “OK” when you are finished.
* For “Organism”, select “eco” for *Escherichia coli*. There are three approaches for selecting an organism.
	+ Enter “eco” in the “Code” box, and hit the <Enter> key.
	+ Find “Escherichia coli” on the list on the left, and double-click on it.
	+ Find “Escherichia coli” on the list on the left, click on it, and then click on the “right arrow” key in the middle of the screen.

After you select the organism, it should now appear in the list on the right..

* For “Data file”, select WHO-TST-2000-01.sqlite. After you find the file, you can single-click on it and then click on the “right arrow” key or you can double-click on the file. After you select the file, it should appear on the right side of the screen.
* Click on “One per patient”, and select the option “First isolate with antibiotic results”. Click on “OK” to return to the main data analysis screen.
* Click on “Begin analysis” to see the results.
* You have seen these same results for *Escherichia coli* in the exercises for Module 4. Review the results and click on “OK” when you are finished to return to the main analysis screen.
	1. “%Susceptible summary” – Antibiogram report
* For “Analysis type”, change the “Report format” to “%Susceptible summary”. Leave the other options on the screen unchanged. Click on “OK” to return to the previous screen
* For “Organism”, remove “Escherichia coli” from the list on the right. You can click on “Clear list” or double-click on the organism or single-click on the organism and then click on the “left arrow” key.
* Click on “Organism groups”, and select “All Gram-negative organisms”, which has the code “GM-“. Click on “OK” to return to the previous screen.
* Leave the other options that you selected in the previous exercise unchanged.
* Click on “Begin analysis”, and wait for the results.
* You will now see a table with all of the Gram-negative organisms listed in alphabetical order as well as the total number of isolates, the %Susceptible for each of the antibiotics, and over to the right, you will see columns indicating the “Number tested” for each specific antibiotic.
* This information about “Number tested” for each antibiotic permits you to see which antibiotics were consistently tested as “first-line agents” or selectively tested (*e.g.* in isolates from urine samples only or “second-line agents” if there is resistance to several of the first-line agents.) Understanding the test practices is important in recognizing potential sources of bias, especially for second-line agents that are tested infrequently and primarily for multi-resistant isolates.
	+ In this example, you will see that 94.1% of the isolates were susceptible to cefotaxime with 75 test results, and 100% of the isolates were susceptible to ceftazidime – but it is important to note that only 8 isolates were tested for this drug, and so the statistics may not be representative of all *Escherichia coli* identified by the laboratory.
* Click on the column “Number tested”, and the table will now be sorted in ascending order with the least commonly identified organisms at the top of the list. Click on this column again, and you will see the most commonly identified organisms at the top of the list.
* When you are finished, click on “Continue” to return to the previous screen.

* 1. Other options
* Click on “Analysis type”, and you will see several additional options on this screen that might be useful for you. For the purposes of these exercises, there is no need to change any of the below options.
	+ “Select antibiotics” if you only want to include some of the most important antibiotics in the analysis.
	+ “Number of isolates”. By default, WHONET will calculate the %R, %I, and %S, but you can use this option to determine the “Number R”, “Number I”, and “Number S”. This can be particularly useful when resistance is rare, and the analyst would like to know exactly how many isolates had a “resistant” result.
	+ “Measurement ranges”. You can adjust the horizontal axis limits for disk diffusion measurements and MIC values.
* One of the most valuable options in WHONET is the use of “Row” and “Column” variables to introduce stratifications into the analyses.
	+ For the %RIS analysis, the first row variable is always “Antibiotic”, and for the %Susceptible summary analysis, the first row variable is always “Organism”. For the second row variable, you can select “Sex” if you would like to see the results separated for “Male” and “Female” isolates. Or you can select “Age” (and WHONET will present the determine the “WHO Age groups”), “Location type”, “Analysis species”, or “Laboratory” depending on the variable that you select.
	+ For this exercise, choose the “%Susceptible summary” analysis, and for the “Row 2” variable, select “Sex”. You will note that 71.5% of the female isolates (out of 67 tested) were susceptible to ampicillin, but only 55.6% of the male isolates (out of 18 tested) were susceptible. Regarding the lower susceptibility of the male isolates when compared to the female isolates, as a hypothesis, it is conceivable that the majority of the isolates from women were from uncomplicated outpatient urinary tract infections, while many of the male isolates were from healthcare-associated infections. Such hypotheses could be further explored by examining patient-level risk factors for resistance.
1. **Isolate listing and summary**

This analysis offers two report formats: 1) isolate listing, where the patient, location, sample, and microbiological result details are displayed as a table with one isolate on each row; and 2) a summary of this listing, indicating how many isolates there are for different data categories. By default, WHONET will show you the “Number of patients” and the “Number of isolates” for each organism (as the row variable) and for each specimen collection month (as the column variable), but you can change the row and column variables to meet your needs.

* 1. Isolate listing
* Click on “Analysis type” and select “Isolate listing and summary”. For report format, choose “Both”.
* For the summary, by default WHONET will use the variable “Organism” for the rows and “Specimen date” by month for the columns.
* For this tutorial, make one small change to the standard options. For this exercise, you are only analyzing one month of data. So, change the option for “Month” to “Day”, which will provide more interesting graphs. Click on “OK” to return to the main analysis screen and click on “Begin analysis” to start the analysis.
* For “Organism”, click on “Organism groups”, and select “All Organisms / ALL”.
* For “One per patient”, select “By isolate”. This will remove the “First isolate with antibiotic results per patient” that you selected in the previous exercise.
* Click on “Begin analysis” to retrieve the results.
* Examine the results of the analysis. You can click a column heading to sort the database, for example by “Last name”, “Animal species” or “Specimen date” so you can determine the range of dates in the file (and this can also quickly identify dates that were incorrectly entered). You can click on “Show hidden columns” to see additional information such as “Date of birth”, “Sex”, and “Comment”.
* When you finish reviewing the results, click on “Continue” to proceed to the “Summary” of the isolate listing.
	1. Isolate listing summary
* After you complete the previous exercise, WHONET will proceed to display the summary of the isolate listing. The table presents the day-by-day trend (number of patients per day) in the isolation of each species, while the graph displays the same information in graphic format.
* If you click on the column headings for “Number of isolates” or “Number of patients”, you can determine the organisms that are most frequently and least frequently identified.
* Click on an organism name in the lower right-hand corner to see the distribution of that organism over time, or click on one of the days to see the distribution of organisms for that day.
* When you finish reviewing the results, click on “OK” to return to the main analysis screen.
	1. Microbiology alerts and cluster alerts

Microbiological alerts and cluster alerts: As mentioned in “Laboratory configuration” and “Data entry”, WHONET includes a large number of microbiological alerts, such as “important species”, “important resistance”, and “quality control alert”. You can see these alerts through data analysis as well.

In addition to the microbiological alerts, WHONET can also provide statistical alerts (generated through integration of WHONET with the free SaTScan™ software) that may suggest possible outbreaks based on an increase in the number of observed cases.

* Continuing from the previous exercise, click on “Analysis Type”. Using the checkbox, select the option: “Include isolate alerts”.
* Using the checkbox, select the option: “Include cluster alerts”. This analysis offers many “Options”, but we will not review these in this exercise.
* Click on “OK” to return to the previous screen.
* Click on “One per patient” and select “By patient”, “First isolate only”. This allows us to remove “repeat isolates” from the cluster detection algorithms.
* Click on “Begin analysis”.
* First you will see the “Isolate listing”. Scroll to the right to see the antibiotic results, and screen down. You will begin to see that some of the cells appear in red. These are the alerts for important and/or unlikely results.
* Continue to scroll to the right, and you will see that the alerts are categorized as “High”, “Medium”, or “Low priority” with a brief description of the alert. Alerts re also categorized as “Important species”, “Important resistance”, and “Quality control alert”.
* After you have reviewed the listing and the alerts, click on “Continue” to advance to the summary.
* You will now see the table and graphs that you saw earlier in this exercise, but this time you will see additional columns in the table with details about two possible clusters: 1) *Corynebacterium* sp. (diphtheroids); and 2) *Klebsiella pneumoniae*. We will discuss the interpretation of the results in the exercises for the “Cluster alerts” analysis later in this document.
* Click on the graphs for “Corynebacteriumsp / cdp” and “Klebsiella pneumoniae / kpn”. You will see certain bars highlighted in red suggestive of possible outbreaks or contaminations or changes in test practices leading to an increase in the number of cases.
* After you finish reviewing the table and the graphs, click on “Continue” to refer to the main analysis screen.
* After you have completed the above steps, return to “One per patient” and select “By isolate”. Then for the subsequent analyses, you will see the results for all results, not only “first isolate” results. Click on “OK” to return to the main analysis screen.
	1. Other options

WHONET includes additional useful options for the analysis. There are no exercises associated with these features, but they may be useful for your work.

* “Test results” versus “Test interpretations” in the listing. By default, WHONET will show you the disk diffusion zone diameters or MIC values if they are available, but using this feature, you can instead request the listing includes the “R”, “I”, and “S” interpretations, which can be more convenient when sharing data with colleagues or exporting to other data management systems.
* “Number of patients” versus “Number of isolates” in the summary. By default, WHONET will calculate the “number of patients” for the column variable, for example, there might be “5 patients with *Escherichia coli* in January”. This is valuable for epidemiologic tracking of disease. Instead, you can request the “number of patients”, which can be useful if you are tracking the data volume of work performed by the laboratory, for example, there might be 8 isolates of *Escherichia coli* identified in January.
1. **Scatterplots**

In a scatterplot, you can compare the results from two antibiotic tests. This could be between two similar drugs such as cefotaxime and ceftazidime, between two dissimilar drugs such as cefotaxime and amikacin, or between two different test methods such as imipenem-disk and imipenem-MIC. Such comparisons can provide valuable information on mechanisms of resistance, linkages of resistance genes, quality evaluation, and support for the development of first- and second-line treatment alternatives for therapy guidelines.

WHONET supports both quantitative scatterplots utilizing disk diffusion zone diameters and/or MIC values (especially useful for infection control staff and researchers of resistance mechanisms) and qualitative scatterplots based on R, I, and S category interpretations (especially useful for pharmacists and clinicians in the development of treatment guidelines).

* 1. Scatterplot with test measurements
* Continuing from the previous exercise, click on “Analysis type” and select “Scatterplot”.
* For the first exercise, put the Penicillin-Disk test on the X axis and the Cefoxitin-Disk test on the Y axis.
* For “Organism”, select “Staphylococcus aureus / sau”.
* Then click “OK” and “Begin analysis”.
* You will see a graph with the zone diameter distribution of isolates tested against both penicillin and cefoxitin. Numbers in the figure represent percentage of isolates, and the red lines indicate the interpretative breakpoints.
* For example, in the upper right-hand corner of the graph, there are many isolates with large zone diameters for penicillin and large zone diameters for cefoxitin. These isolates are susceptible to both agents – this is the traditional wild-type phenotype for *Staphylococcus aureus*. The lower left-hand quadrant represents isolates resistant to both drugs; these would be the MRSA isolates.
* The greatest number of isolates is in the upper left-hand section of the graph. Such isolates are resistant to penicillin (to the left of the red line), but susceptible to cefoxitin (above the red line). This is the classical phenotype for penicillinase- producing *Staphylococcus aureus*. Fortunately, there are no isolates in the lower right-hand quadrant. Such isolates would have the phenotype penicillin-susceptible and cefoxitin-resistant. Microbiologically, such results could often be attributed to a testing or data entry error.
* Click on “Continue” to return to the main data analysis screen.
	1. Scatterplot with test interpretations
* Click on “Analysis type”, and select “Test interpretations”.
* Click on “OK” and “Begin analysis”.
* In this output, you see the same kind of results seen in the quantitative scatterplot, but using the R, I, S categories. You will again observe the three major subtypes of *Staphylococcus aureus* in this chart. 21.2% of the isolates have the wild-type phenotype (PEN-S, FOX-S), 68.2% have the penicillinase-producer phenotype (PEN-R, FOX-S), and 10.6% have the MRSA phenotype (PEN-R, OXA-R).
* When you have finished reviewing the results, click on “Continue” to return to the data analysis screen.
	1. Options

WHONET offers a few options that might be of value to you, but there are no exercises associated with these features.

* “Percentage of isolates” versus “Number of isolates”. By default, WHONET will indicate the percentage of isolates for each data point, for example “2.5% of isolates were resistant to imipenem and to ciprofloxacin”. However, sometimes the data analyst would like to know the precise number of patients in each data category, especially when the number of resistant isolates is small, for example “8 isolates were resistant to imipenem and to ciprofloxacin.
* “Regression line”. Linear regression lines are used for under special and limited circumstances, for example, correlating the results of two very similar antibiotics, such as cefotaxime and ceftriaxone (or ceftriaxone with ceftriaxone using reagents from different vendors) or for two distinct test methods, for example cefotaxime-disk with cefotaxime-MIC. Presentations of the second type are useful to CLSI and EUCAST as they evaluate the comparability of results generated by the two methods.
1. **Antimicrobial resistance profiles**

The “Resistance profile” analysis in WHONET is valuable for the study of multidrug resistance for a range of antibiotics in the same class and/or across different classes. Such information is valuable in the development of recommendations for first-line and second-line treatment options. The use of multidrug resistance profiles is also valuable for the tracking of “phenotypic microbial subpopulations”, facilitating the recognition of hospital and community outbreaks and can guide sampling strategies for whole-genome sequencing studies.

This analysis supports two output formats: 1) isolate listing; and 2) summary of the isolate listing. We will review both in this exercise.

* 1. Resistance profile listing
* Continuing from the previous exercise, click on “Analysis type”, and select “Resistant profiles”.
* Because you are analyzing only one month of data, change the option for “Month” to “Day”. We will leave the organism unchanged, *Staphylococcus aureus*.
* Click “OK” and “Begin analysis”.
* WHONET will display a list of all isolates of *Staphylococcus aureus* with details such as identification number, location, specimen date, and specimen type.
* WHONET will also show several antibiotic results, but not all of them. Specifically WHONET will display the antibiotics defined for the “Resistance profile” analysis in “Laboratory configuration”, which you can access through “Modify laboratory” when you open WHONET. We would generally recommend including 5 to 10 antibiotics for this analysis, focusing on those antibiotics that are routinely tested against all isolates (omitting “second-line antibiotics” or “urine-only antibiotics” where only a subset of isolates are tested.
* This listing is very similar to the one you did earlier in the “Isolate listing” analysis, but with some additional columns, such as “Profile”, which utilizes one-letter antibiotic codes such as “P” and “E”, and “Resistance profiles, which utilizes three-letter codes, such as “PEN” and “ERY”.
* The “resistance profile” column indicates those antibiotics to which the organism is “resistant”, “intermediate”, or “non-susceptible”. For example a resistance profile of “PEN ERY” would indicate that the isolate is not susceptible to penicillin or erythromycin, but is susceptible to the other antibiotics included in the resistance profile definition.
* Completely susceptible isolates appear at the top of the listing, followed by isolates non-susceptible to one drug, then to two drugs, *etc*. Multi-resistant isolates appear at the bottom of the listing.
* Review the listing. You will see examples of distinct resistance profiles, as well as the associated locations and specimen types. Such as review can facilitate the identification of possible outbreaks.
* When you finish reviewing the listing, click on “Continue” to advance to a summary of this listing.

* 1. Summary of the resistance profile listing
* This output summarizes findings for all resistance phenotypes observed in the listing that we just reviewed.
* Click on “Number of isolates” once to sort the table in ascending order and then click again to sort the table in descending order. You will now see the most common organisms listed at the top of the table.
* In this example, you will see that the most common phenotype is susceptible to all of the antibiotics tested (also known as “pan-susceptible”), followed by “PEN” (non-susceptible to penicillin).
* A number of the profiles include “FOX” as one of the nonsusceptible antibiotics. These are MRSA, demonstrating that there is phenotypic diversity among the MRSA. Among MRSA< the most common phenotype is “PEN FOX ERY CLI GEN SXT CIP”, in other words non-susceptible to all drugs requested with the exception of vancomycin.
* You can also click on some of the graphs to see the day-to-day distribution of the different phenotypes in the database, which could reveal suggestions of a possible outbreak based on the phenotype which could then be explored further with molecular typing.
* After you finish reviewing the table and some of the graphs, click on “Continue” to return to the main menu.
	1. Resistance profile summary with cluster alerts
* Continuing from the previous exercise, click again on “Analysis type” and use the checkbox to select “Include cluster alerts. Click “OK” to return to the previous screen.
* Click on “One per patient”, and select the option “First isolate with antibiotic results”. Click on “OK” to return to the main data analysis screen.
* Click on “Begin analysis”.
* You will now see exactly the same listing as in the earlier exercise. Click on “Continue” to advance to the summary.
* In the summary, you will see statistical alerts for a single resistance profile, “ERY”. There were four isolates from four patients who had *Staphylococcus aureus* nonsusceptible only to erythromycin, all on the same day, which is highly statistically unusual (p-value = 0.0004). There were no other isolates like this during the rest of this month. Such a finding would be very unlikely with the normal variation in patient cases and is more likely to be associated with an event such as a true outbreak or to a problem in laboratory testing on that specific day due to poor quality disks or test performance.
* When you have finished reviewing the results, click on “Continue” to return to the main analysis screen.
	1. Other options

There are some additional features that may be useful for your work.

* “Edit profiles”. Continuing from the previous exercise, click on “Edit profiles”. WHONET will show you the sets of antibiotics used to create the “resistance profile” for each group of organisms. To make permanent changes to these lists of antibiotics, you should return to “Modify laboratory”, “Antibiotics”, “Profiles”, and “Edit”. Then make your modifications, and “Save” the results. Or you can make those same changes here on this screen, but they will not be saved when you leave the analysis. This can be useful if you would like to explore the impact of changes in the antibiotics on the resistance profile results before making the changes permanent in “Laboratory configuration”. Click on “OK” when you have finished reviewing the antibiotics.
* “Omit isolate if profile antibiotics are missing”. The resistance profile works best if you select antibiotics that are always tested routinely. But there will still be isolates where one or more of the requested antibiotics was not tested. You can use this feature to omit isolates from analysis that were not completely tested for the full set of resistance profile antibiotics. This will improve the cleanliness of the output, incorporating only results for isolates that were completely tested. This is especially valuable for outbreak detection so that you can avoid the detection of clusters of “incomplete data”, which is not epidemiologically interesting. However, the feature does result in the loss of a certain number of isolates with incomplete results, which could be a problem if the feature leads to exclusion of a high proportion of the isolates (for example more than 10% or 20%).
1. **Microbiology alerts**

As you saw in modules for “Laboratory configuration” and “Data entry”, WHONET includes a large number of pre-defined microbiological rules, such as “Important species”, “Important resistance”, and “Quality control alert”. The alerts are also categorized as “High priority”, “Medium priority”, and “Low priority”.

In the earlier exercise on “Isolate listing and summary”, you saw that it was possible to include these isolate alerts in that analysis, appearing as red cells on the WHONET screen for important findings or with a “!” symbol for data exports. That analysis showed the results for all requested isolates, both with and without alerts. The isolate listing in the “Microbiology alerts” analysis will be nearly identical to what you saw earlier, but it will only include results for isolates that include an alert.

This analysis includes two output formats: 1. Create dictionary (WHONET’s BacTrack feature); and 2. Microbiological alerts. We will only cover the second of these formats in this exercise. You can refer to the full manual for information on use the “BacTrack dictionary”.

* 1. Listing of microbiology alerts
* Continuing from the previous exercise, click on “Analysis type”, and select “Microbiological alerts”.
* Select the second report format, “Microbiological alerts”. Click on “OK” to return to the main analysis screen.
* For “Organisms”, select “ALL” organisms
* Click on “Begin analysis”.
* You will then see an listing of isolates very similar to the one you saw earlier in the exercise on “Isolate listing and summary”. The distinction is that in this analysis, you will only see results for isolates which include at least one isolate alert. On the screen, you will see these appearing in red.
* Scroll to the right of the screen, and you will see columns indicating whether the isolate has received “High”, “Medium”, or “Low” priority alerts, a brief description of the alert, and checkboxes indicating whether the isolate has “important resistance”, “important species”, and/or “quality control” alerts.
* When you have finished reviewing the results, click on “Continue” to return to the main analysis screen.
	1. Options
* Continuing from the previous exercise, click on “Analysis type” and “Options”. You will see that you can control which types of alerts you would like to see, such as “High priority” or “Important resistance”. There is no exercise for this feature.
* When finished reviewing the options, click “OK” to return to the previous screen, and then “OK” againto return to the main analysis screen.
1. **Cluster alerts**

WHONET has been integrated with the free SaTScan software for the automated statistical detection of possible outbreaks. In two earlier analysis (“Isolate listing and summary” and “Resistance profile listing and summary”), you were introduced to the concept of statistical “cluster alerts” suggesting that the number of isolates in a given time period is more than one would normally expect.

One important explanation for elevated numbers of cases could include a possible community or hospital outbreak of disease. Other possible explanations contamination of samples or laboratory reagents, changes in sampling practices or laboratory diagnostic techniques, or increases in the numbers of patients seeking medical care.

The “cluster alert analysis” in WHONET offers three output formats: 1. Daily signals; 2. Signal summary; and 3. Isolate listing. In this exercise, we will not cover all of the cluster detection features and parameters available within WHONET, but you may can find additional information in two sessions of the WHONET webinar series available at [whonet.org/webinars.html](https://whonet.org/webinars.html). For these exercises, we will rely on WHONET’s default parameter settings.

* 1. *Daily signals*
* Continuing from the previous analysis, click on “Analysis type”, and select “Cluster alerts”.
* Because we will only analyze a single month of data, change “Month” to “Day” for the column variable. Leave the other settings unchanged and click “OK” to return to the main analysis screen.
* For “Organism”, select “Staphylococcus aureus / sau”. Click “OK” to return to the main analysis screen.
* For “One per patient”, choose “By patient” and “First isolate only”. Click “OK” to return to the main analysis screen.
* Click on “Begin analysis”.
* First you will see a listing of cluster alerts in the “Daily signals”. This feature is especially useful when performing a “simulated prospective analysis”, but by default, WHONET is doing a “retrospective analysis”. For a retrospective analysis, the “Daily signals” and the “Signal summary” details will be identical, so click on “Continue” to proceed directly to the “Signal summary” output.
	1. *Signal summary*
* You can now review the summary of the cluster alerts, noting two statistical clusters – one for *Corynebacterium* species (diphtheroids) and one for *Klebsiella pneumoniae*.
* The summary that you see here is similar to the summary that you saw in the analysis for “Isolate listing and summary”, but with several additional columns with the details of the statistical cluster, including the cluster dates, the “observed number of cases”, the “expected number of cases”, and a p-value. A small p-value suggests that the observed distribution of cases is not consistent with normal random variation, but more suggestive of an event such as an outbreak or a contamination problem. The traditional p-value threshold is p≤0.05, but this is an arbitrary threshold but is a useful guide for assessing statistical significance.
* Click on the graph for “Klebsiella pneumoniae / kpn” and will see three red bars towards the end of the month representing ten patients in a three-day period. (These details are also available in the table.) If you scroll to the right in the table, you will see that the statistical significance of this finding is a p-value of 0.0222. It would be valuable to gather additional details about these ten patients, such as their locations, specimen types, and antibiotic test results, and we will see those in the next exercise.
* Now click on the graph for “Corynebacterium sp. (diphtheroids) / cdp”, and you will notice that there are seven people with this organism on the same day. Possibly this reflects a true outbreak with so many people on a single day. However, a more likely explanation is that there is some issue here with sample or reagent contamination. This organism is not commonly associated with outbreaks, but is commonly found in contaminated specimens. Also, in most true outbreaks, it would be unexpected to have so many people in a single day with no cases in the days before or after.
* When you finish reviewing the details in the table and in the graph, click on “Continue” to advance to the next screen.
	1. *Isolate listing*
* You will now see a list of all patients associated with the statistical clusters identified in the previous analysis, including the ten patients mentioned above with *Klebsiella pneumoniae* and the seven patients with *Corynebacterium* sp.
* For *Klebsiella pneumoniae*, you will see that over half of the isolates were from patients in “Cardiology / card” or “Cardiac surgery / csurg”, which would be very concerning with regards to a possible outbreak of this organism in patients with cardiac issues. The specimens were from urine, blood, sputum, and wound samples. Review of the resistance results demonstrates that the isolates are all resistant to ampicillin (small zone diameter), which is to be expected for this species, but susceptible to all of the other agents. So this appears to be a possible outbreak due to a phenotypically “wild type” strain of this organism.
* For *Corynebacterium* sp., most of the isolates were from “Outpatients / op” and the “Emergency room / er”, so potentially this could be a community outbreak. However, a review of the zone diameters reveals great diversity in measurements for several antibiotics, suggesting that these isolates are not genetically related with the more likely conclusion that there was a deficiency in sample collection practices on that day or problems in laboratory reagents resulting in a number of contaminated results on one particular day.
* When you finish reviewing the details in the table, click on “Continue” to return to the main analysis screen.
	1. Options

For this exercise, we have used the default settings for cluster selection, but you do have the ability to modify these settings.

* Continuing from the previous exercise, click on “Analysis type” and “Options”.
* You will see the set of features available to you and their options. Further discussion of these parameters are available in the WHONET webinars on “Cluster analysis and outbreak detection” mentioned earlier.
	+ Analysis method: “Retrospective”, “Prospective”, or “Simulated prospective”. You can use the “retrospective” option to explore a question like “Did we have any outbreaks last year?” For the study of historical data, you can also use “simulated prospective” analysis to explore the question “What clusters could we have found last year if we had been running the analyses on a daily basis?” This second question can provide a better understanding of the potential benefits of these algorithms if you decide to implement real-life prospective surveillance.
	+ Analysis method algorithm: WHONET offers a number of statistical and probability models available within SaTScan, such as “Space-Time Permutation”, “Space-Time Uniform”, and “Spatial Multinomial”, as well as other approaches, such as the “CUSUM” algorithms which are part of the Early Aberration Reporting System (EARS) published by the CDC.
	+ Maximum cluster length (in days): This parameter controls the size of the maximum data window that SaTScan utilizes in evaluating the statistical significance of case clusters.
	+ Baseline data. This parameter is utilized for simulated and simulated prospective analyses to determine how much historical data should be used as a comparison for potential clusters. The default is one year of baseline data.
	+ Location options: SaTScan permits the users to enter relevant latitude and longitude data, for example based on clinical location or patient residence if that information is available. You can also define groupings of related locations such as “All intensive care units”, “All locations on the fifth floor”, and “Hospitals in the northeast of the country”.
	+ P-value or recurrence interval threshold. This value determines which case clusters detected by SaTScan are presented to the WHONET user. For retrospective analyses, the default is a p-value of 0.05, while for prospective and simulated prospective analyses, the default threshold is 356 days.
* There is no exercise associated with these features, so click “OK” to return to the previous screen, and then “OK” again to return to the main analysis screen.
* Click on “Exit” to leave the data analysis program.
* Click on “File”, “Exit” to close the WHONET software.