



WHONET USER MANUAL

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CAPTURA

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A microscopic view of various bacteria, including rod-shaped and spherical forms, set against a blue background. The bacteria are rendered in a semi-transparent, glowing blue color, creating a sense of depth and movement. The overall image has a clean, scientific aesthetic.

CHAPTER-1

GETTING STARTED

Getting Started

1. What is WHONET?

WHONET is a free desktop Windows application for the management and analysis of microbiology laboratory data with a particular focus on antimicrobial resistance surveillance developed and supported by the WHO Collaborating Centre for Surveillance of Antimicrobial Resistance at the Brigham and Women's Hospital in Boston, Massachusetts. WHONET, available in 28 languages, supports local, national, regional, and global surveillance efforts in over 2,300 hospital, public health, animal health, and food laboratories in over 130 countries worldwide.

WHONET analytical tools facilitate:

- The understanding of the local epidemiology of microbial population
- The selection of antimicrobial agents
- The identification of hospital and community outbreaks
- The recognition of quality assurance problems in laboratory testing

2. What can WHONET do?

WHONET has three main components:

1. Laboratory configuration - WHONET permits the customization of software. This allows for correct antimicrobial testing in the laboratory, patient care areas served, choosing data fields relevant to the surveillance program, and microbiological alerts of unusual or important organisms and resistance phenotypes.
2. Data entry and clinical reporting-WHONET enables routine entry of susceptibility test results as well as the retrieval, correction and printing of clinical records. During data entry, WHONET can provide immediate feedback to technicians on important phenotypes.
3. Data analysis - WHONET has a user-friendly interface permitting many types of analysis. Options include isolate line-listings and summaries, such as organism frequencies over time, antimicrobial susceptibility test statistics, zone diameter MIC histograms, antibiotic scatterplots and regression curves; WHONET also has several alert features which permit the detection of unlikely or important results as well as possible hospital or community outbreaks of bacterial or non-bacterial species.

3. What is BaLink?

The purpose of the BaLink software is to facilitate the conversion of data from your computer system into WHONET. You can do this interactively on a weekly, monthly, or ad hoc basis. By using BaLink, you can avoid the time-consuming process of manually entering results into WHONET.

4. Installing WHONET and BaLink

You must install WHONET onto your computer to use it. WHONET is compatible with all versions of Microsoft Windows, from Windows 95 to the most recent. You can obtain the software by downloading it from the web and the installation process is automatic. For installation, go to the site: <https://whonet.org/>

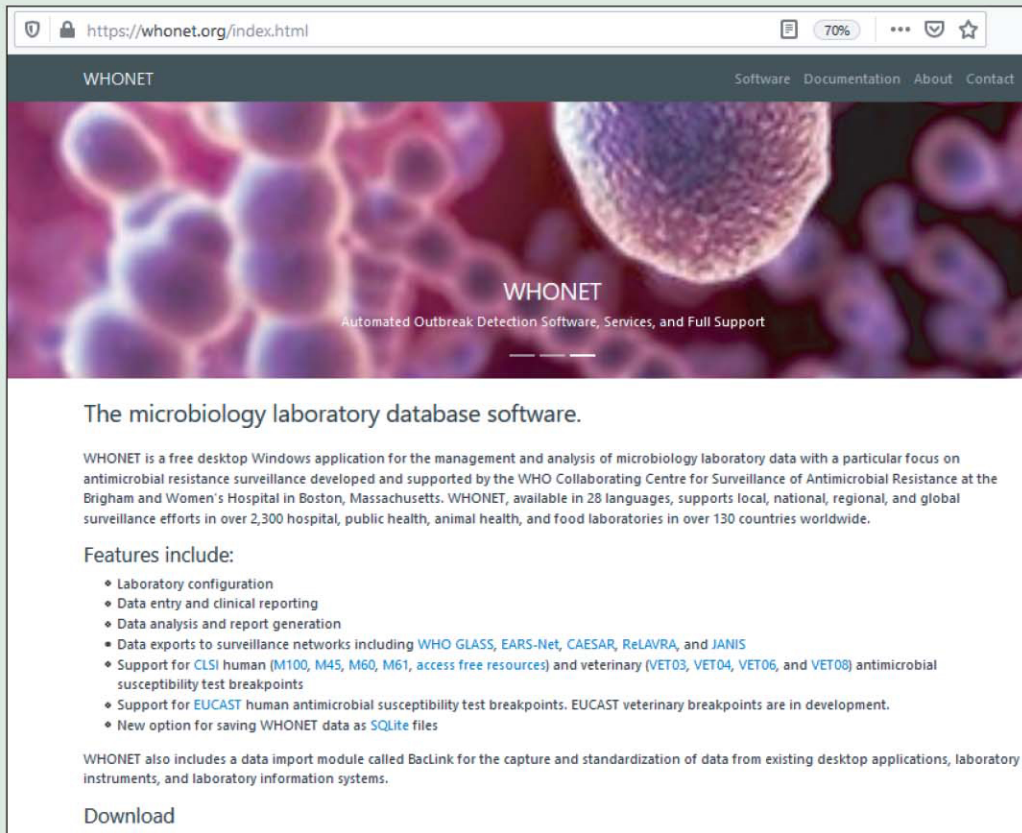


Figure 1. WHONET website interface

Depending on the version of Microsoft Office installed on your computer, i.e. 32-bit or 64-bit, choose the installation package. Click on 32-bit installation (142 MB). The program file is large, thus takes longer to download.

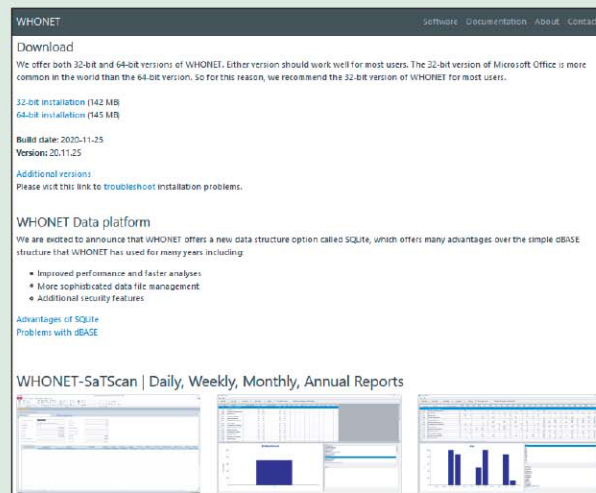


Figure 2. WHO 2020 installation options

Once downloaded, navigate to your 'Downloads' folder. Double-click on the file WHONET2020--Setup-x86. You should get a screen asking if you want to "Run" the file, click "Run".

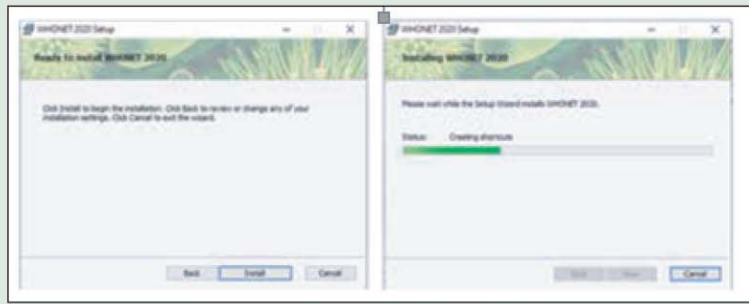


Figure 3. "Run" WHONET 2020

After that, another screen will pop-up, and you need to agree to terms and conditions and click "Install". The installation will begin

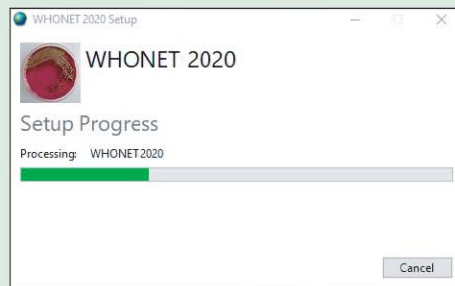


Figure 4. WHONET 2020 License Agreement window

Once you see the below screen, click "Next".



Figure 5. WHONET 2020 Setup Wizard

In the next step, you will see a screen requiring you to agree to WHONET end-user agreement. Then, you will see a screen to customize the set-up. For simplicity, accept the default and click "Next".

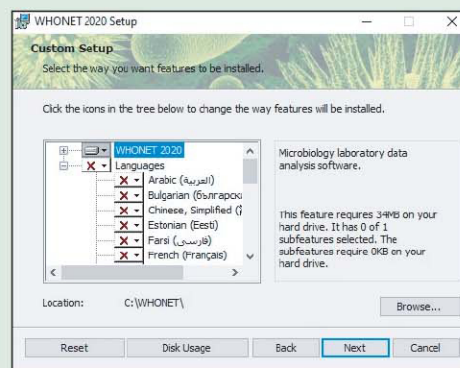


Figure 6. WHONET 2020 Custom Setup window

Once the Setup is ready, click “Install”.

Once the installation is complete, click “Finish”.

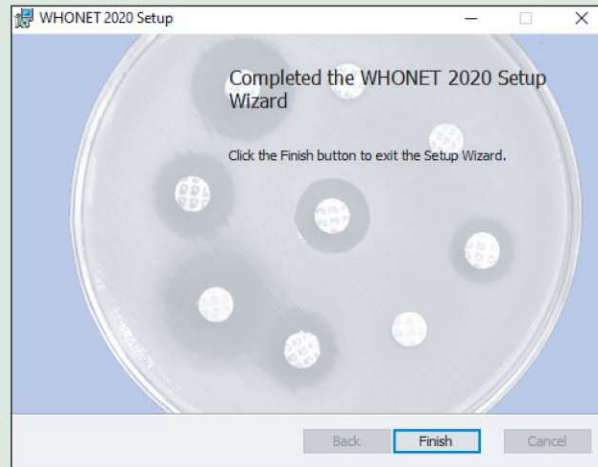


Figure 7. WHONET 2020 completed Setup Wizard

Click “Finish” to conclude the process.

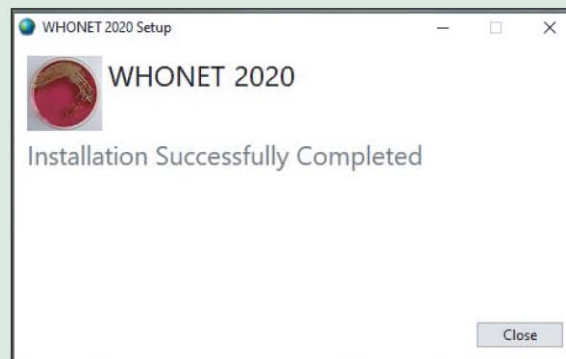


Figure 8. WHONET 2020 Installation Successfully Completed window

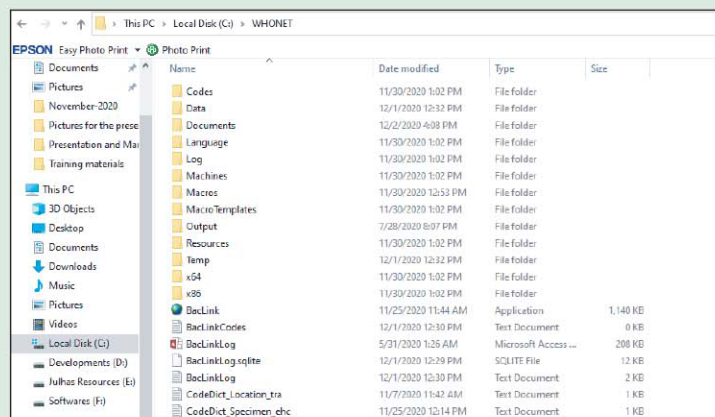


Figure 9. WHONET folder on computer's C drive

If you are having difficulties in installing WHONET on your computer, please contact Julhas Sujana, CAPURA Country Coordinator at julhaspustcse@gmail.com or Dr John Stelling for additional assistance.

5. Running WHONET

Double-click on the WHONET icon to begin the software. On this screen, you will see a list of all laboratory configurations present on your computer. Initially, you will only have three sample laboratories.

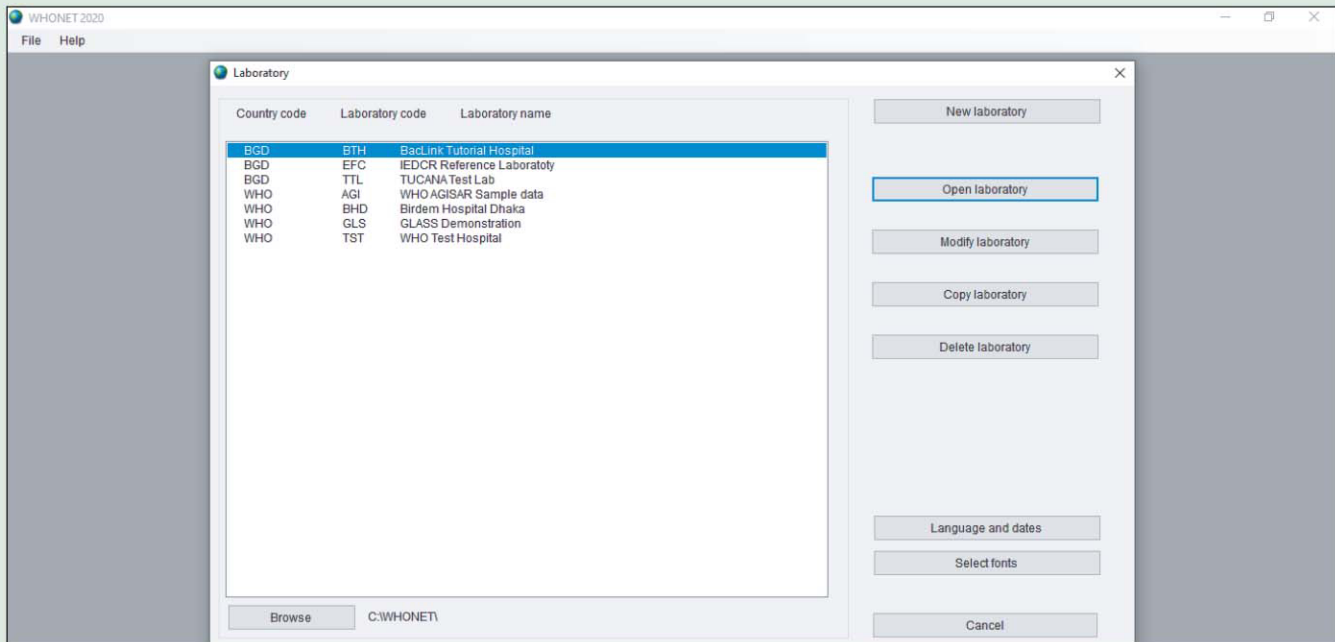


Figure 10. WHONET main screen with the list of laboratories

By default, WHONET begins in English. If you wish to change this, click on “Select Language”, choose the desired language, and click “OK”. The software will then switch to the selected language.

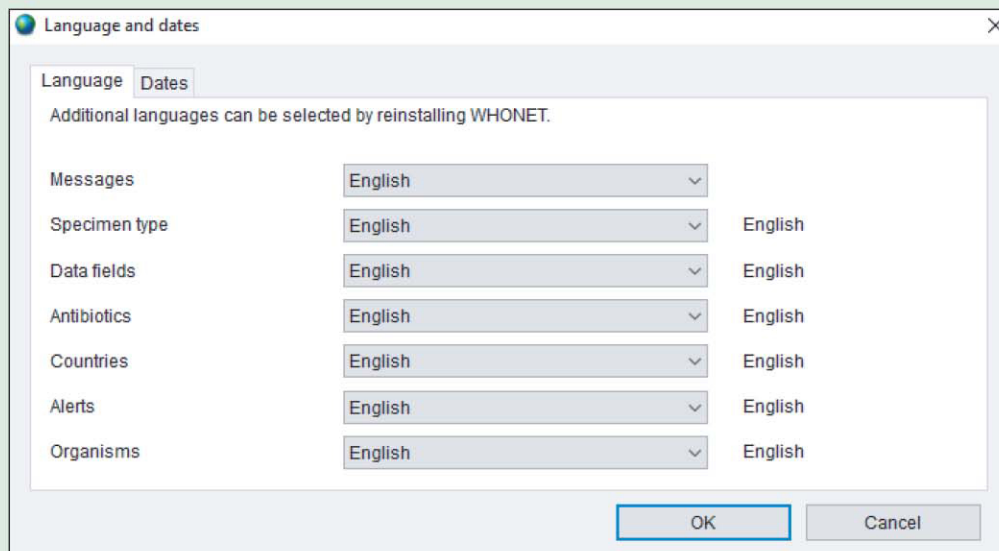


Figure 11. WHONET language customization screen

CHAPTER-2

LABORATORY CONFIGURATION

Laboratory Configuration

The purpose of laboratory configuration is to describe the details about your institution and your laboratory test practices. This module describes how to create a “New laboratory” from the very beginning.

1. Describing your laboratory

Double-click on the WHONET icon on your desktop to begin WHONET. You will see a list of laboratory configurations currently defined on your computer. Click on “New laboratory” to begin.

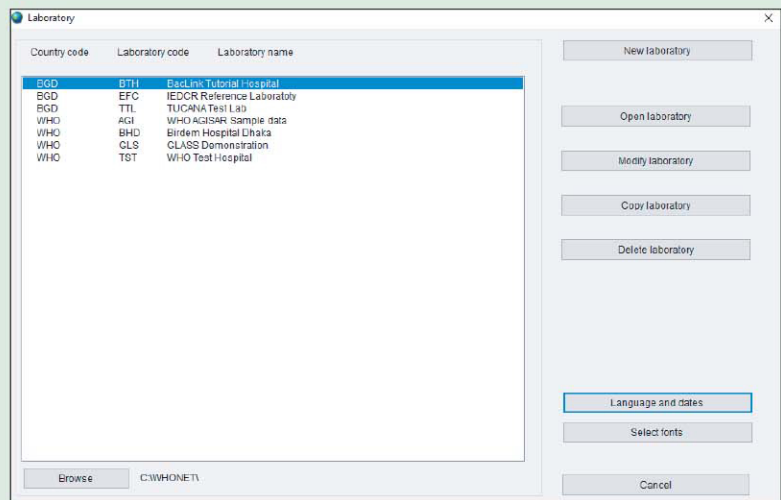


Figure 1. List of WHONET laboratory configurations select “New laboratory”

In this module, you will create an institution in Bangladesh called “National Referral Laboratory” for the human health sector. So, for the country, select “Bangladesh”, and for the laboratory name, type “National Referral Laboratory”. For the laboratory code, put “NRL”. Since we want to use this laboratory for data of the human health sector, please select “Human”. Your screen should look like the figure below.

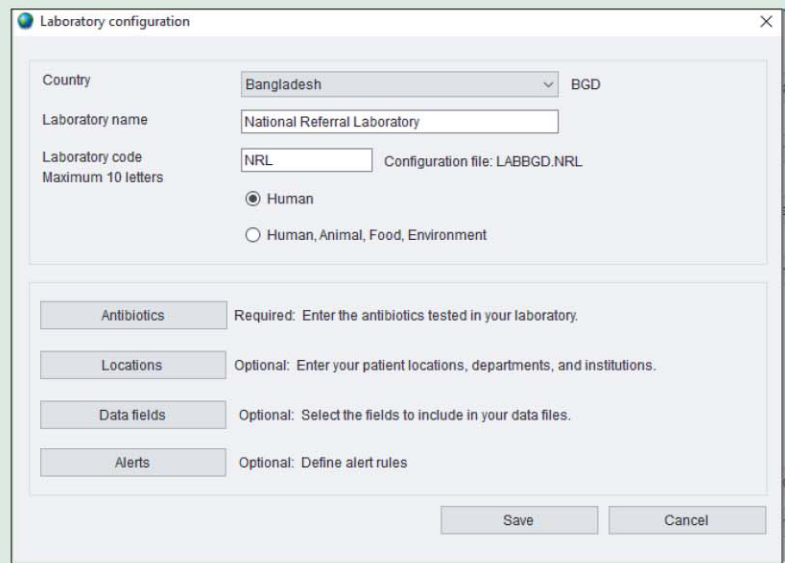


Figure 2. WHONET laboratory configuration screen

2. Selecting your antibiotics

The only part of the laboratory configuration which is required, indicates the antimicrobials tested in the laboratory. To do this, click on “Antibiotics” to get the following screen. You will see a long list of antibiotics to your left – this is the WHONET list. On the right is the list of antibiotic tests used in your laboratory. In the beginning, this list is empty.

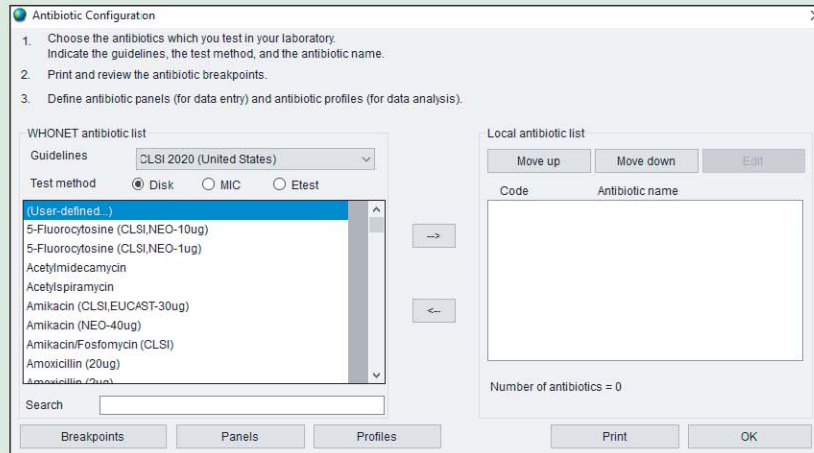


Figure 3. Antibiotics selection screen

To indicate the tests that you are using, you should indicate three things: 1. the reference guidelines (for example CLSI, EUCAST, SFM, DIN, etc.); 2. the test method (Disk diffusion, MIC, or Etest); and 3. the name of the antibiotic and for the disk diffusion testing, the disk potency.

In this module, indicate that the method is CLSI, and you will choose a few drugs tested by disk diffusion and a few tested by Etest. To select an antibiotic, double-click on the antibiotic to move it to the right side of the screen or single-click on the antibiotic and hit the “>” button.

Find the following antibiotics and move them to the right side of the screen.

- Disk diffusion, ampicillin 10ug
- Disk diffusion, cefoxitin 30ug
- Disk diffusion, ceftriaxone 30ug
- Disk diffusion, ciprofloxacin 5ug
- Disk diffusion, erythromycin 15ug
- Disk diffusion, gentamicin 10ug
- Disk diffusion, imipenem, 10ug
- Disk diffusion, penicillin G 10units
- Disk diffusion, trimethoprim/sulfamethoxazole 1.25ug/23.75ug
- Disk diffusion, vancomycin, 30ug

WHONET assigns a code to each antibiotic test; for example, AMP_ND10 indicates a test of ampicillin (“AMP”) by CLSI (“N”, formerly NCCLS) methods by disk diffusion (“D”) with a 10ug disk (“10”).

Now enter a few drugs tested by Etest. Click on the option labeled “Etest” and select the following drugs. Since the disk potency is not relevant for Etests, it does not matter which “ceftriaxone” you select from the WHONET list.

- Etest, ceftriaxone
- Etest, penicillin G
- Etest, vancomycin

The corresponding test code for the ceftriaxone Etest done by CLSI methods would be CRO_NE. After making these selections, you should have the following screen.

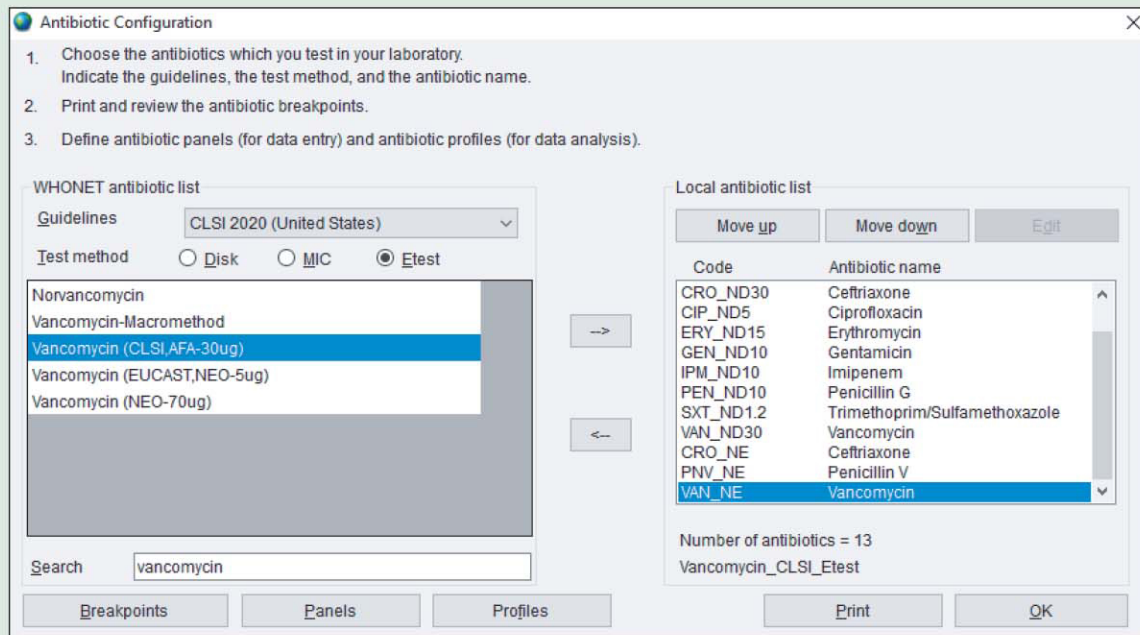


Figure 4. Antibiotic configuration screen with selected antibiotics

You can use the left arrow button “<” to remove a drug from the list. After you complete the above steps, you can proceed directly with data entry if you would like. There are, however, several additional features described in Parts 3 through 6, which may be useful.

3. Configuring your antibiotics

The following steps are not required but may be useful to you.

Antibiotic breakpoints

When you select antibiotic tests, WHONET automatically sets up the correct official breakpoints according to the reference body that you indicate. However, if there are no official breakpoints for the antibiotic that you selected or if you disagree with the breakpoints used by WHONET, then you may wish to make some manual modifications.

In this module, we will not change any of the default breakpoints, but to see the values suggested by WHONET, click on “Breakpoints”. You can then view any of the disk diffusion or MIC/Etest breakpoints. WHONET distinguishes between “General” breakpoints used for most bacterial species and “Species-specific” breakpoints for species in which the recommended breakpoint is different. After reviewing the breakpoints, select “OK” to return to the antibiotic configuration screen.

Figure 5. Species-specific antibiotic breakpoints

Antibiotic panels

When entering results manually into WHONET, it would be useful to the data entry person if you indicate which antibiotics are tested for which organism groups. For example, for *S. aureus*, the software should request results from drugs used in Gram-positive infections.

Antibiotic Panels (Optional)

Indicate which antibiotics you usually test for each organism group.

Antibiotic	Staphylococcus sp.	Streptococcus sp.	Streptococcus pneumoniae	Streptococcus viridans	Enterococcus sp.	Gram positive urine	Gram negative	Gram negative urine
Ampicillin/Subactam_CLSI_Disk_10u...	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Cefoxitin_CLSI_Disk_30ug	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Ceftriaxone_CLSI_Disk_30ug	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Ciprofloxacin_CLSI_Disk_5ug	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Erythromycin_CLSI_Disk_15ug	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Gentamicin_CLSI_Disk_10ug	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Imipenem_CLSI_Disk_10ug	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Penicillin G_CLSI_Disk_10units	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Trimethoprim/Sulfamethoxazole_CLSI...	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Vancomycin_CLSI_Disk_30ug	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Ceftriaxone_CLSI_Etest	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Penicillin V_CLSI_Etest	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Vancomycin_CLSI_Etest	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

Antibiotic sequence Conditional antibiotic reporting OK Cancel

From the Antibiotic configuration screen, click on “Panels”. You will see all the antibiotics selected in the rows and a list of various organism groupings in the columns. Place a checkmark to indicate which drugs are usually tested for each organism. For this module, put checkmarks for the following organisms and antibiotics.

- Staphylococcus: ceftioxin, erythromycin, penicillin, trimethoprim/ sulfamethoxazole, and vancomycin
- S. pneumonia: erythromycin, trimethoprim/sulfamethoxazole, vancomycin, penicillin-Etest, and ceftriaxone-Etest
- Gram-negative: ampicillin, ceftriaxone, ciprofloxacin, gentamicin, imipenem, and trimethoprim/sulfamethoxazole

If there is a drug that you infrequently test, for example, imipenem for *E. coli* isolates, there is no need to include it in the panel. The user will be able to enter results for either “panel” antibiotics or “all antibiotics” at the time of data entry.

Antibiotic Panels (Optional)

Indicate which antibiotics you usually test for each organism group.

Antibiotic	Staphylococcus sp.	Streptococcus sp.	Streptococcus pneumoniae	Streptococcus viridans	Enterococcus sp.	Gram positive urine	Gram negative	Gram negative urine
Ampicillin/Subactam_CLSI_Disk_10u...	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Cefoxitin_CLSI_Disk_30ug	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Ceftriaxone_CLSI_Disk_30ug	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Ciprofloxacin_CLSI_Disk_5ug	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Erythromycin_CLSI_Disk_15ug	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Gentamicin_CLSI_Disk_10ug	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Imipenem_CLSI_Disk_10ug	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Penicillin G_CLSI_Disk_10units	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Trimethoprim/Sulfamethoxazole_CLSI...	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
Vancomycin_CLSI_Disk_30ug	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Ceftriaxone_CLSI_Etest	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Penicillin V_CLSI_Etest	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Vancomycin_CLSI_Etest	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

Figure 5. Species-specific antibiotic breakpoints

Antibiotic resistance profiles

This feature is used in the data analysis option called “Resistance profiles”. In this analysis, bacteria are classified according to their multi-resistance phenotype. This is a very valuable analysis for infection control staff when searching for outbreaks of mul-ti-resistant organisms in the hospital setting.

In this part of the laboratory configuration, you can indicate which drugs should be used to construct a resistant profile.

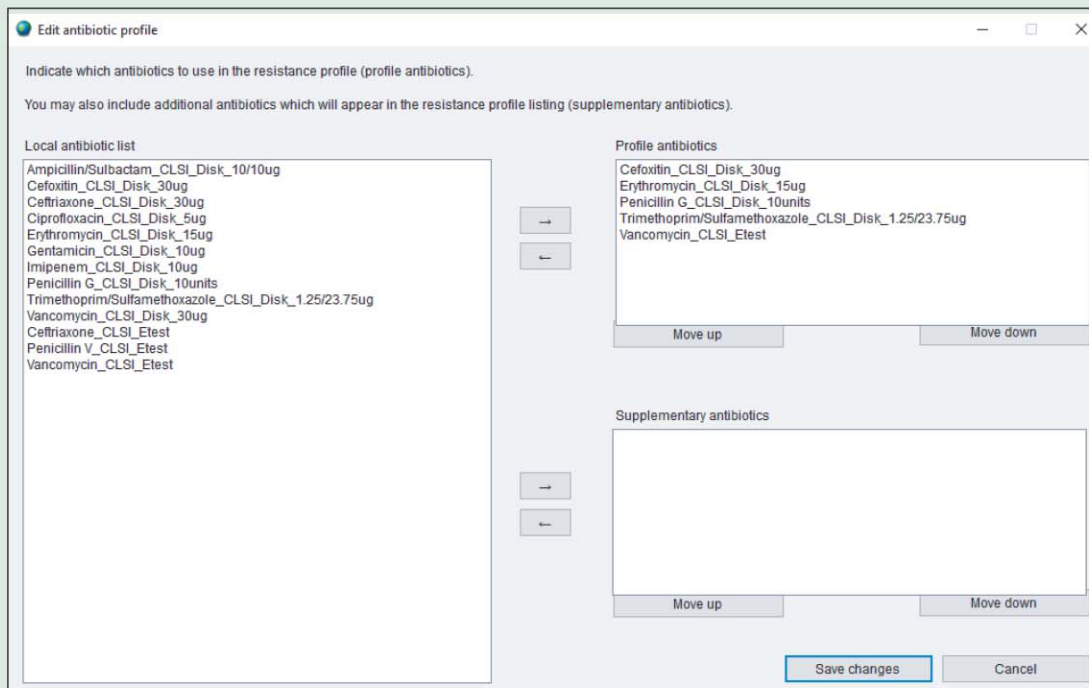
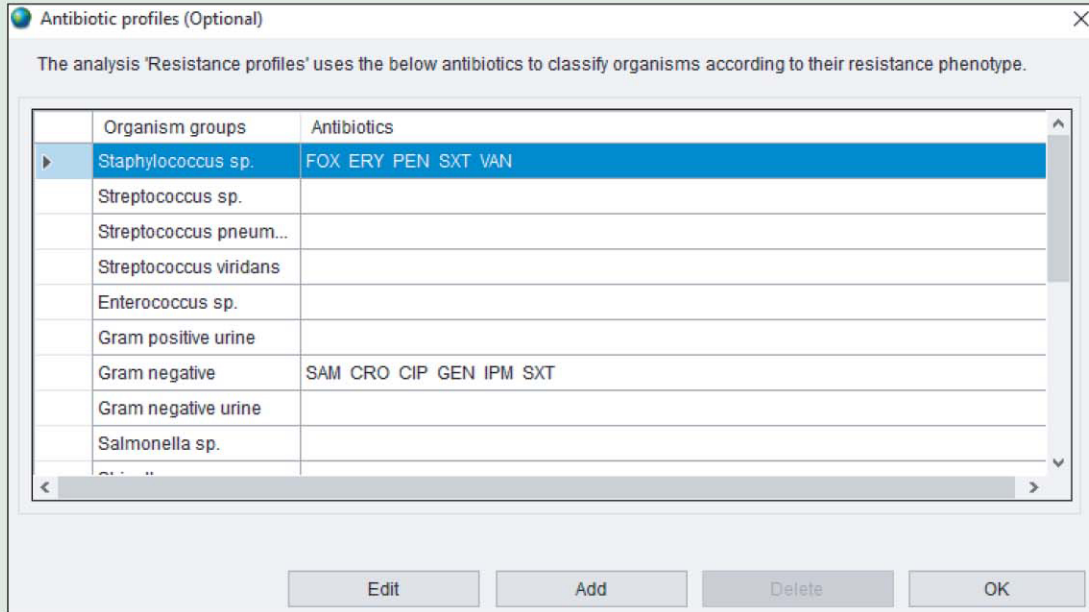


Figure 6. Antibiotic resistance profile configuration

4. Locations

If you enter data manually into WHONET, it would be useful to enter a list of the most common locations from which you get isolates.

Enter the following locations and values for the columns “Location”, “Code”, “Department”, “Institution”, and “Location type”.

Location	Code	Institution	Department	Type
Dhaka	DHK	NRL	lab	in
Chattagram	CHT	NRL	lab	out
Rajshahi	RAJ	NRL	lab	out
Khulna	KHL	NRL	lab	out
Barisal	BAR	NRL	lab	out
Mymensingh	MYM	NRL	lab	in
Rangpur	RNG	NRL	lab	out

You can use the “Edit” buttons to change the list of institutions and departments to match the needs of your laboratory. Once you have added all locations as indicated above, click “OK”.

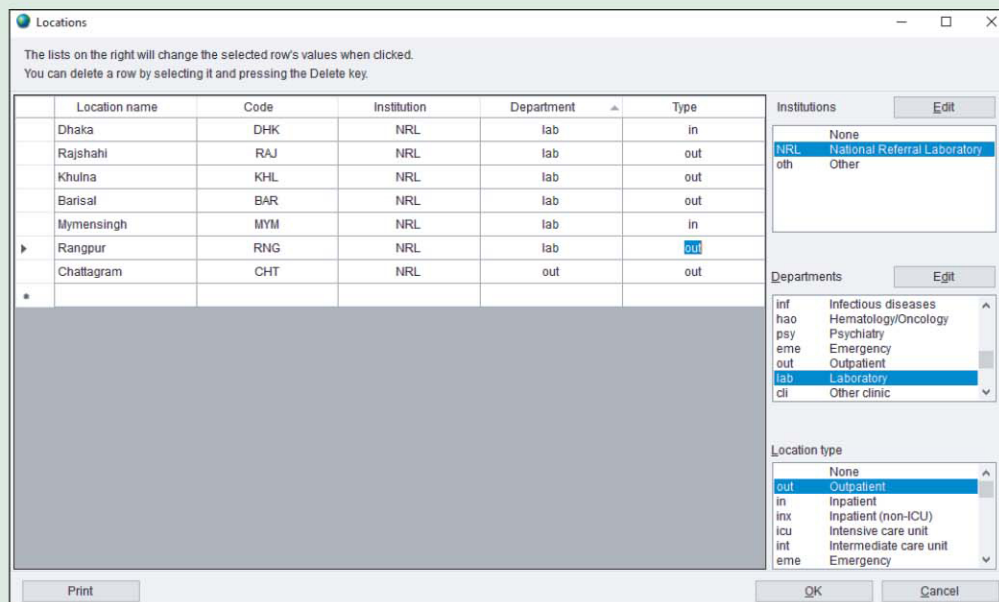


Figure 7. WHONET location configuration screen

5. Data fields

From the main configuration screen, click on “Data fields”. You will see the default list of WHONET data fields. This list includes questions about the subject (identification number, age, sex), location (location, department, institution, location type), speci-men (number, date, type), and microbiological results (organism, serotype, beta-lac-tamase, ESBL).

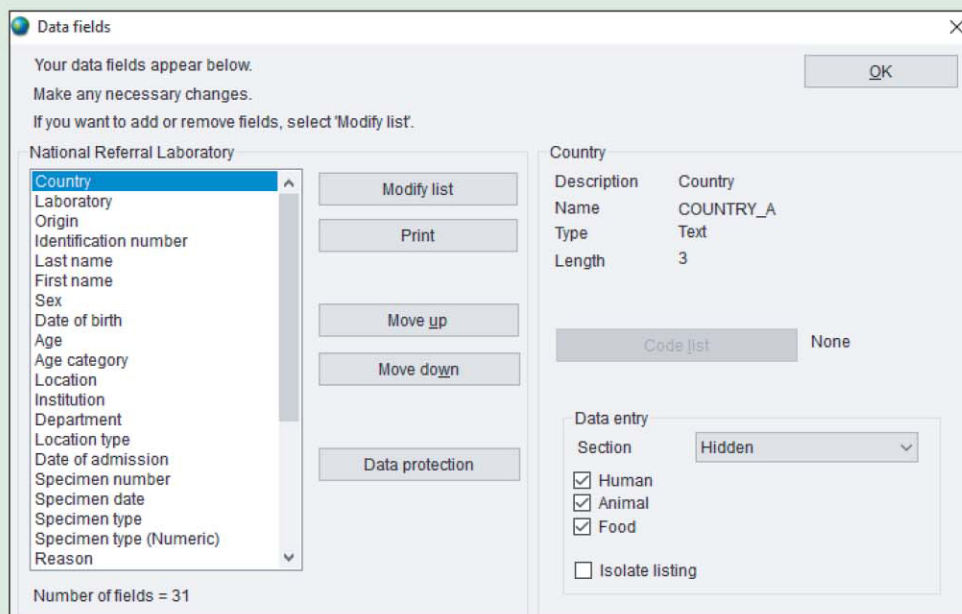


Figure 8. WHONET data field configuration

For most laboratories, this list is adequate for routine surveillance purposes and does not need to be edited. However, for many laboratories, modifications to this list can be very useful.

Adding or removing fields: You can add additional fields to the list or remove fields that you do not need for your work. Click on “Modify list”. On the left, you will see various categories of questions and suggested fields for you to choose from.

For this tutorial, click on “Standard” as the data category. If you want to add any new fields, first select and then move by click on the right arrow.

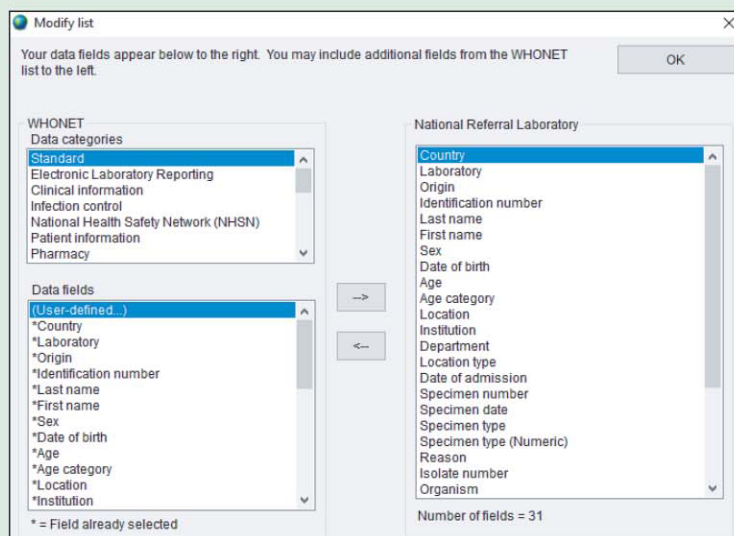


Figure 9. Add additional fields or remove fields from the list of fields for your laboratory

If you cannot find the field that you need, you may define a “User-defined field”, as shown in the figure below.

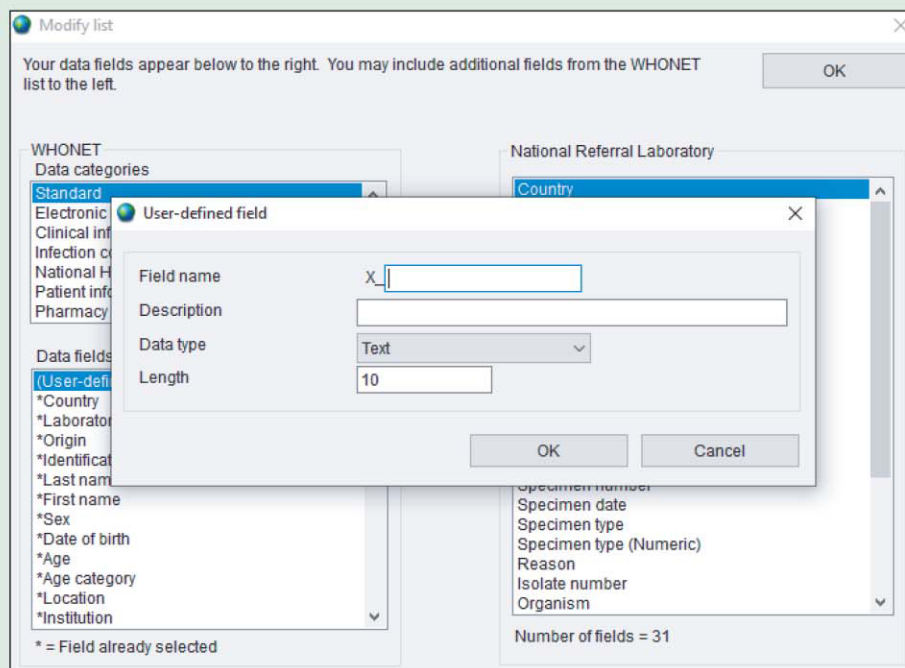


Figure 10. Add the “User-defined” data field

Changing field lengths: WHONET assigns a default length for each data field, but the user can change the length of most fields. For example, the location code, by default, is at most six characters in length. However, for many laboratories, six letters may not be sufficient. To change the length, click on “Location”, and change the length on the right side of the screen from 6 to a larger value, for example, 20. For this module, you can leave these settings unchanged.

The appearance of the data entry screen and isolate listings: You can use “Move up” and “Move down” to change the order of the questions appearing on the data entry screen. You can indicate whether a question applies to humans, animals, or food. You can also indicate which “box” the question appears in during data entry. For this tutorial, you can leave these settings unchanged.

6. Isolate alerts

From the main configuration screen, click on “Alerts”. You will see a long list of microbiological alerts suggested by WHONET – alerts about possible laboratory errors, important results that should be confirmed at the local or national level, and findings that should be communicated to other groups, such as the infection control team. You can easily activate or deactivate the rules suggested by WHONET.

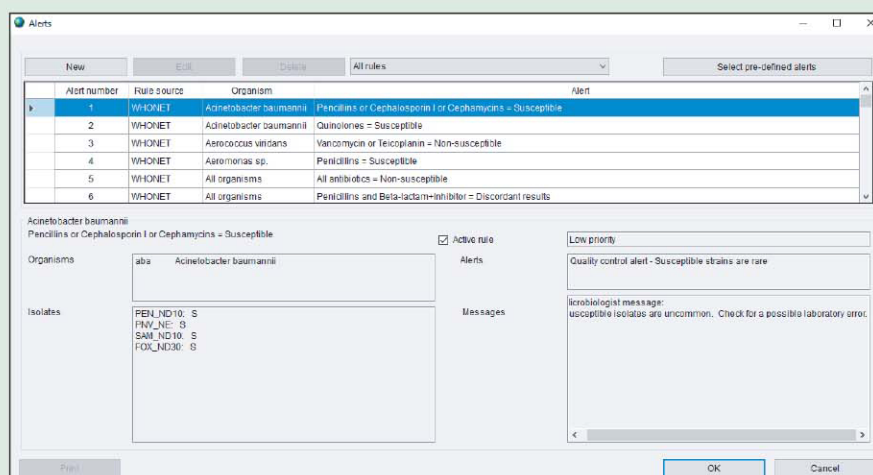


Figure 12. List of microbiological alerts for your laboratory

CHAPTER-3

DATA ENTRY



Data Entry

In this module, you will learn how to enter results into WHONET data files, how to edit isolate results, and how to print clinical reports.

1. Creating a new data file

Begin WHONET and select the laboratory “National Referral Laboratory” that you created in the module on laboratory configuration. Click on “Open laboratory”.

At the top of the screen, you will see the main “Data Entry” menu. If you select this menu, you will see several options. To begin a new data file, select “New data file”.

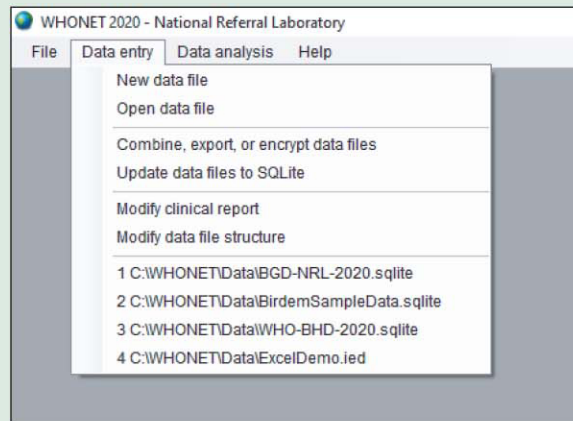


Figure 1. Main WHONET menu with the Data entry options selected

Every file on a computer needs: 1) a name and 2) a location. By default, the location of WHONET files is C:\WHONET\Data on your computer’s hard drive; however, it can be moved to where most convenient for you.

For the file name, WHONET suggests a name indicating the year, the country code, and the laboratory code, for example, Country-LAB-Year. For this module, change the file name to BGD-NRL-2020 to indicate that you will enter data from 2020 from the country “BGD” from the “NRL” laboratory. Then click “OK”.

2. Data Entry

In this step, you will enter results from two isolates and one quality control strain.

Data entry example:

	Data Entry Fields	Sample data
Origin	Identification number	12345
	Date of birth	1990-10-10
	Last name	Sujan
	First name	Julhas
	Age	Y-M-d
	Age Category	adu = Adult
	Sex	m = Male

Location	Location	DHK = Dhaka
	Location type	Out = Outpatient
	Institution	NRL = National Referral Laboratory
	Date of Admission	12-Feb-2020
	Department	lab = Laboratory
Specimen	Specimen Number	443321
	Specimen type	Bl = Blood
	Specimen date	12-Feb-2020
	Reason	d = diagnostics
Microbiology	Organism	eco = Escherichia coli
	Serotype	Escherichia coli
	Beta-lactamase	+
	ESBL	-
	Carbapenemase	+
	MRSA Screening Test	-
	Antibiotic Panel	Gram Negative
Disk	SAM	12
	CRO	20
	CIP	23
	GEN	13
	IPM	20
	SXT	12
Other	Comments	None

You can also add the R.I.S directly instead of zone diameters.

Origin	Data Entry Fields	Sample data
	Identification number	12346
	Date of birth	1990-05-08
	Last name	Hasnat
	First name	Abul
	Age	Y-M-d
	Age Category	adu = Adult
	Sex	m = Male
Location	Location	DHK = Dhaka
	Location type	In = Inpatient
	Institution	NRL = National Referral Laboratory
	Date of Admission	13-December-2020
	Department	lab = Laboratory
Specimen	Specimen Number	443322
	Specimen type	Ur = Urine
	Specimen date	13-December-2020
	Reason	d = diagnostics
Microbiology	Organism	eco = Escherichia coli
	Serotype	Escherichia coli
	Beta-lactamase	
	ESBL	
	Carbapenemase	
	MRSA Screening Test	
	Antibiotic Panel	
Disk	CEP	R
	CRO	I
	CIP	R
	GEN	S
	IPM	R
	AMP	R
Other	Comments	None

When you finish, your screen should look like the following. As you put in the antibiotic measurements, WHONET will automatically determine and display the interpretation.

Data entry

Origin: Human

Origin

Identification number: 12345 Date of birth: 10-Oct-1990

Last name: Sujan Age: 29

First name: Julhas Age category: adu

Sex: m

Location

Location: DHK Location type: in

Institution: NRL Date of admission: 12-Feb-2020

Department: lab

Specimen

Specimen number: 443321 Specimen type: bl

Specimen date: 12-Feb-2020 Reason: d

Microbiology

Organism: eco Escherichia coli

Serotype: Escherichia coli

Beta-lactamase: + Positive

ESBL: - Negative

Carbapenemase: + Positive

MRSA screening test: + Positive

Inducible clindamycin:

Antibiotic panel: Salmonella sp.

Disk MIC Etest

SAM 12 CRO 20 CIP 23 GEN 13

IPM 20 SXT 12

Save isolate

View database

BacTrack summary

Print

Exit

Callper Clear

Clinical reports

<F8> Include or exclude an antibiotic

<F9> Include all tested antibiotics

Trimethoprim/Sulfamethoxazole

CLSI

1.25/23.75ug

11 - 15 Human, Human

Alerts

WHONET-18 High priority

Enterobacteriaceae

Carbapenems = Non-susceptible

Important resistance

Save the isolate

Send to a reference laboratory

Infection control alert

Microbiologist message:

Non-susceptible isolates are rare.

Figure 2. Data entry screen after the entry of the first isolate.

After you enter all the results, click on “Save Isolate”.

Save isolate

View database

BacTrack summary

Print

Exit

Callper Clear

Figure 3. Save the isolate

Save the isolate

Do you want to save this isolate?

Save the isolate
 Save the isolate and continue with the same specimen
 Save the isolate and continue with the same patient

Alerts

Quality control alert
 Important species
 Important resistance
 Save the isolate

Send to a reference laboratory
 Infection control alert
 Therapy comment
 Other alert

Carbapenems = Non-susceptible
Non-susceptible isolates are rare.

OK Cancel

Figure 4. High-priority alert for Enterobacteriaceae non-susceptible to carbapenems

Save the isolate as before by clicking on “Save Isolate”.

3. Viewing the database

You have now entered the results for three strains into WHONET. To see these results, click on “View the database” to get the following screen listing all of the isolates.

Identification number	Specimen number	Organism	Country	Laboratory	Origin	Last name	First name	Sex	Date of birth	Age	Age category	Location	Institution	Department	Location type	Date adm
12345	443321	eco	BGD	NRL	h	Sujan	Juihas	m	10/10/1990	29	adu	DHK	NRL	lab	in	12/2/20

Figure 5. Viewing the database in table format

Print results

Select the print format

Clinical report
 Conditional antibiotic reporting
 Isolate listing

Isolates

Current isolate only
 Select isolates

Date of data entry: 2-Dec-2020 – 2-Dec-2020

Print Printer setup Modify clinical report Cancel

Figure 6. Print clinical reports and isolate listings

4. Clinical reports

Some laboratories use WHONET to report laboratory results back to senders/clinicians. To print out clinical reports or logbook isolate listings, click on “Print” from either the main “Data entry” screen or from the “View database” screen.

For this module, you will print clinical reports above. Click on “Clinical reports”. Choose “Select isolates”. The default is to print out all isolates entered today (“Date of data entry” = today’s date). Click on “Print” and then “Print” on the following screen. WHONET will now print the individual clinical reports.

National Referral Laboratory

Identification number = 12345	Location = Dhaka
Last name = Sujan	Specimen number = 443321
First name = Julhas	Specimen date = 12-Feb-2020
Date of birth = 10-Oct-1990	Specimen type = Blood

Date of admission 12-Feb-2020
Organism = Escherichia coli

Ampicillin/Sulbactam	I 12 mm	Ceftriaxone	I 20 mm
Ciprofloxacin	I 23 mm	Gentamicin	I 13 mm
Imipenem	I 20 mm	Trimethoprim/Sulfamethoxazole	I 12 mm

Beta-lactamase Positive
ESBL Negative
Carbapenemase Positive
MRSA screening test Positive

2-Dec-2020 17:35 R = Resistant I = Intermediate S = Susceptible NS = Non-susceptible

Figure 7. Printing clinical report of an isolate

5. Finishing up

After you finish exploring the Data entry program, click on “x” to return to the main WHONET menu. Now you will learn how to return to open a data file that already exists. Click on “Data entry”, and you will see the following choices.

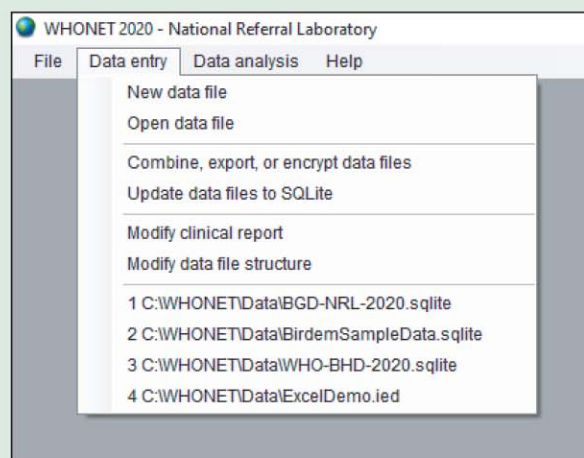


Figure 8. The main WHONET screen with the most recently opened data file

You will notice that the data file BGD-NRL-2020.sqlite appears at the bottom of the list. WHONET shows you the list of the most recently opened files. Click on “BGD -NRL-2020.sqlite” to open the file. Alternatively, you could use “Open data file” to open any data file.

You are now back in the data entry program where you can enter results for additional isolates or edit or print results from existing isolates. When you finish reviewing data entry, select “x” from the top left of the data entry screen to return to the main WHONET menu.

6. Other options for managing data files

Additional features are not essential but are useful to many users.

Combining data files: In the above example, you created a data file for December 2020. If you continue in this way, you will have twelve monthly files at the end of the year. Many users find it convenient at the end of the year to combine the twelve files into a single larger file.

Encryption: If you want to share your data files with other institutions, you may wish to protect the confidentiality of individuals with this feature. When you use this option, WHONET will create a copy of your data file but with patient and specimen information either removed or encrypted. WHONET uses unidirectional encryption, so subsequent “decryption” of the results is not possible.

Data file locations: When you install WHONET, by default, all data files will be saved into the C:\WHONET\Data folder. For people using WHONET on a single computer not connected to a network, this is a practical location. However, for computers connected into a network, it is often more convenient to put the data files onto a common central computer where multiple users can have access to the same data files. In this way, data entry and data analysis can be done with the same data files by several individuals using different computers.

Backing up files: Backing up WHONET data files is crucial in case of computer damage, theft, or virus. You can back files up by copying your WHONET files onto another computer, cloud, CD-ROM, USB-memory stick, or diskettes. To make copies of your WHONET data files, go to C:\WHONET\Data (or other location that you have selected), and find the files that you want to backup. You can use Ctrl-C or right-click on the file and select “Copy”. Then go to the location where you want to back up the files and select “Edit”, “Paste” (or Ctrl-V or right-click on the location and select “Paste”).

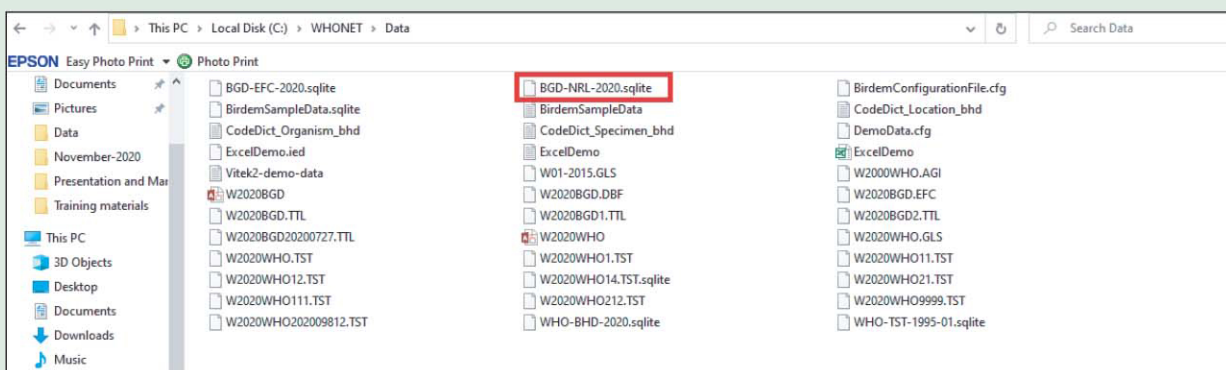


Figure 9. Contents of folder C:\WHONET\Data

In addition to backing up your WHONET data files, you should also backup your WHONET laboratory configuration file. In this module, the name of this file is LAB-BGD.NRL. The file is in your C:\WHONET folder. Go to this file and copy and paste the file to the backup location.

When you finish, select “File”, “Exit” to leave WHONET completely.



CHAPTER-4

DATA ANALYSIS

This chapter will illustrate some of the most important features of the WHONET data analysis program. Applications of these analyses include:

- Continuous quality improvement: assessing laboratory test practices and utilization of laboratory services by clinical departments
- Describing trends in the epidemiology of microbial populations and antimicrobial resistance
- Characterizing the molecular epidemiology of antimicrobial resistance trains
- Guiding antimicrobial therapy recommendations and policy
- Supporting infection control interventions, in particular the early identification of hospital and community outbreaks
- Focuses on two of the most commonly used analysis options: 1. %RIS and test measurements; and 2. Isolate listing and summary.

Under the 'Data Analysis' menu of WHONET, you will find two sub menus as Data Analysis and Quick Analysis. Using the data analysis tool, you can start your analysis by selecting the Analysis type, Organisms, Isolates, Data Fields. On the other hand, the quick analysis option will provide you a few more pre-defined reports. We will discuss both options in detail.

PART 1. GETTING STARTED WITH DATA ANALYSIS MENU:

Double-click on the WHONET icon on your desktop to begin the software. You will see a screen similar to the following. For purposes of this tutorial, select the laboratory called "WHO Test Hospital", and click on "Open laboratory". ***Due to the insufficient data in your newly setup laboratory, we are re-opening the "WHO Test Hospital" for showing the below analysis.***

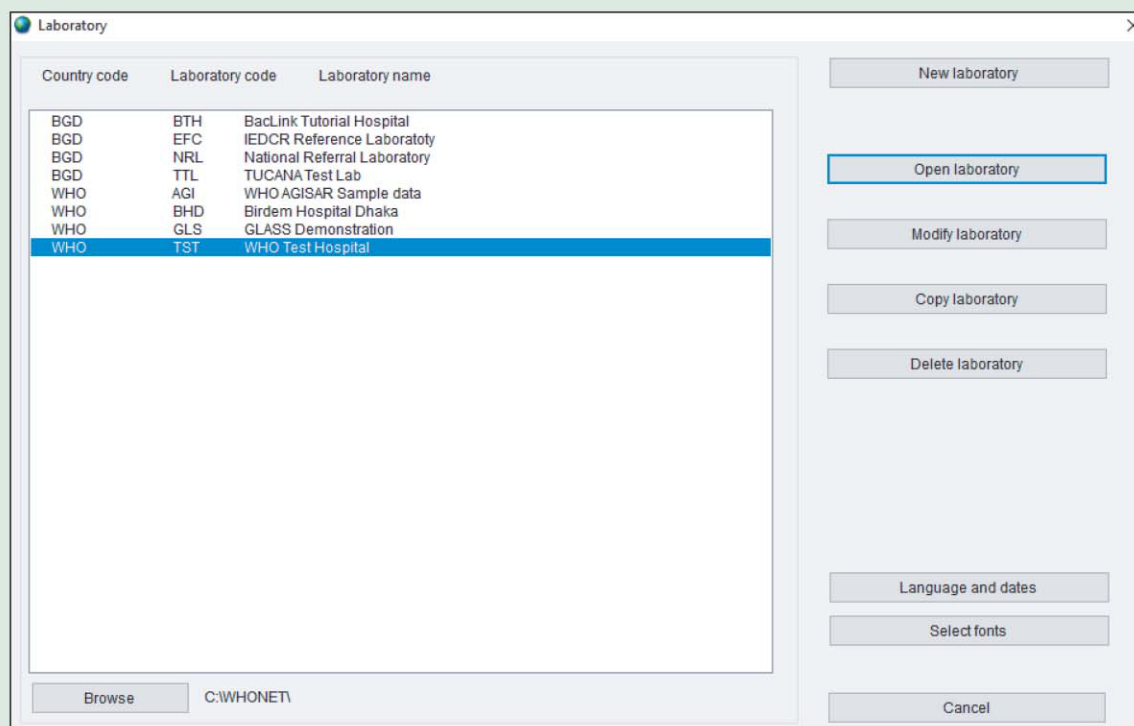


Figure 1. Laboratory selection.

From the main WHONET screen, click on “Data analysis” and “Data analysis” again. You will now see the main WHONET analysis screen. From this screen, you will be able to tell WHONET the type of analysis you want to perform

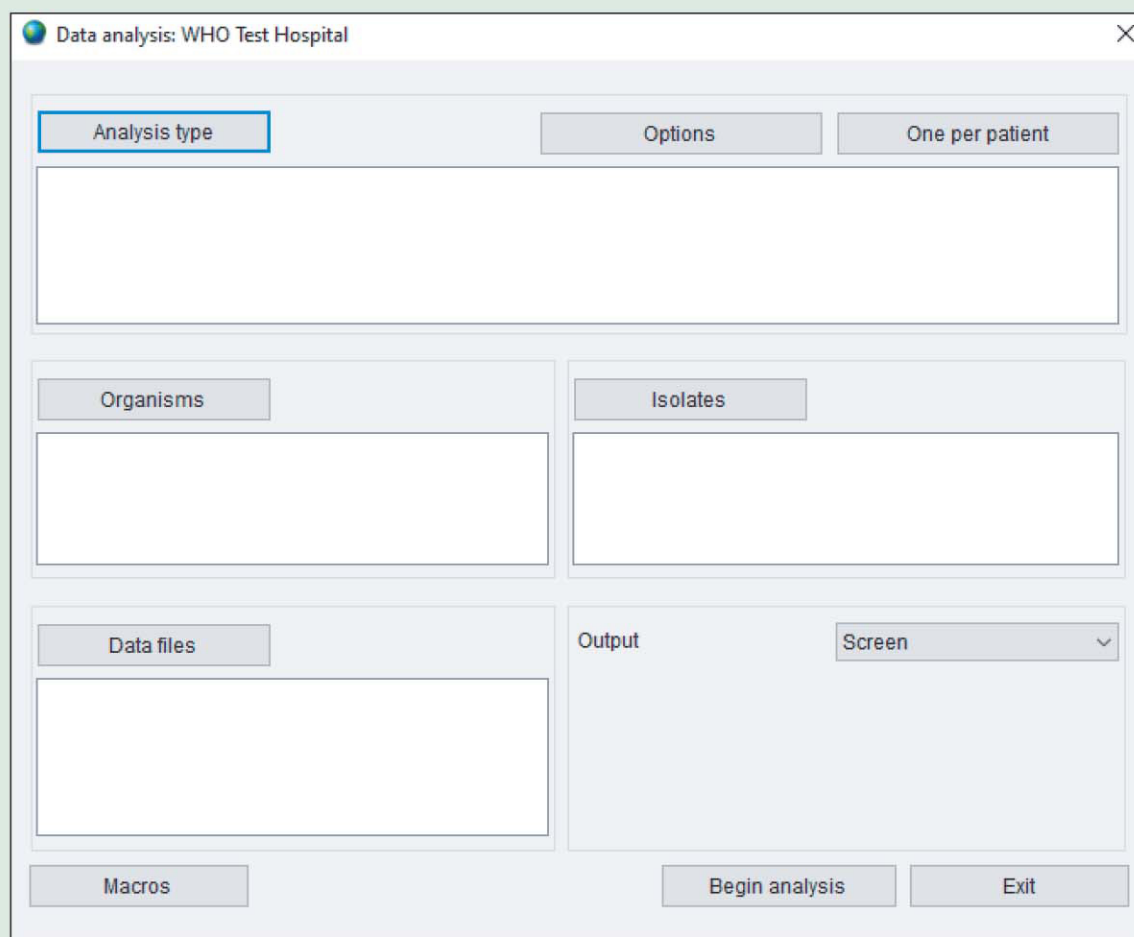


Figure 2. The WHONET data analysis screen.

PART 2. SETTING UP AN ANALYSIS: %RIS AND TEST MEASUREMENTS

In the main analysis screen, there are three sections on the left that you must answer: Analysis type, Organisms, and Data files. On the right, there are some additional options that may be useful to you.

Analysis type: First, you must indicate the kind of analysis that you want WHONET to perform. To do this, click on “Analysis type”. You will see several analysis options. For this first analysis, select the option “%RIS and test measurements”. Click “OK” to return to the main analysis screen.

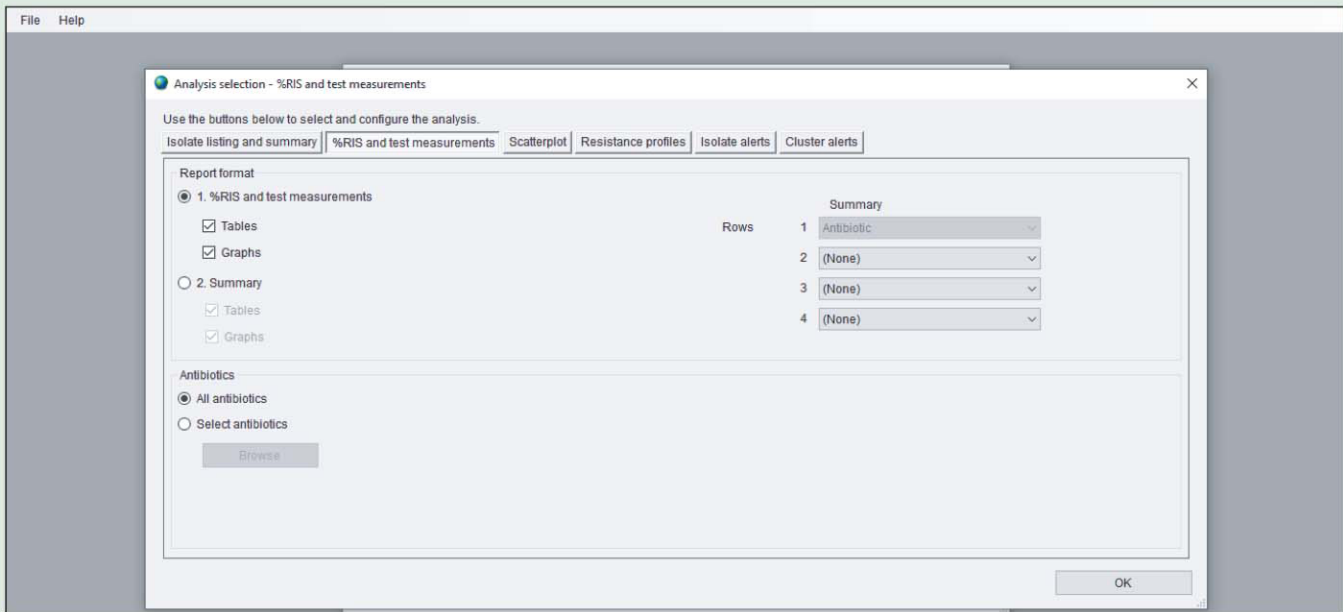


Figure 3. Analysis type: Select the kind of analysis you want to run, as well as the format of the output – graphs, tables, listings, summaries, etc.

Organisms: Click on Organisms. On this screen, as in many of the WHONET screens, you will see the options available to you on the left side of the screen. On the right side of the screen, you will put your selections.

On the left-hand side, you will first of all see a list of relatively common bacteria and fungi. Choose two organisms for this first analysis: *E. coli* (eco) and *S. aureus* (sau). You can select an organism in several possible ways: double-click on the organism or single-click on the organism and hit the right-arrow button “→” or type the three-letter code and hit “```”. Your screen should look like the following.

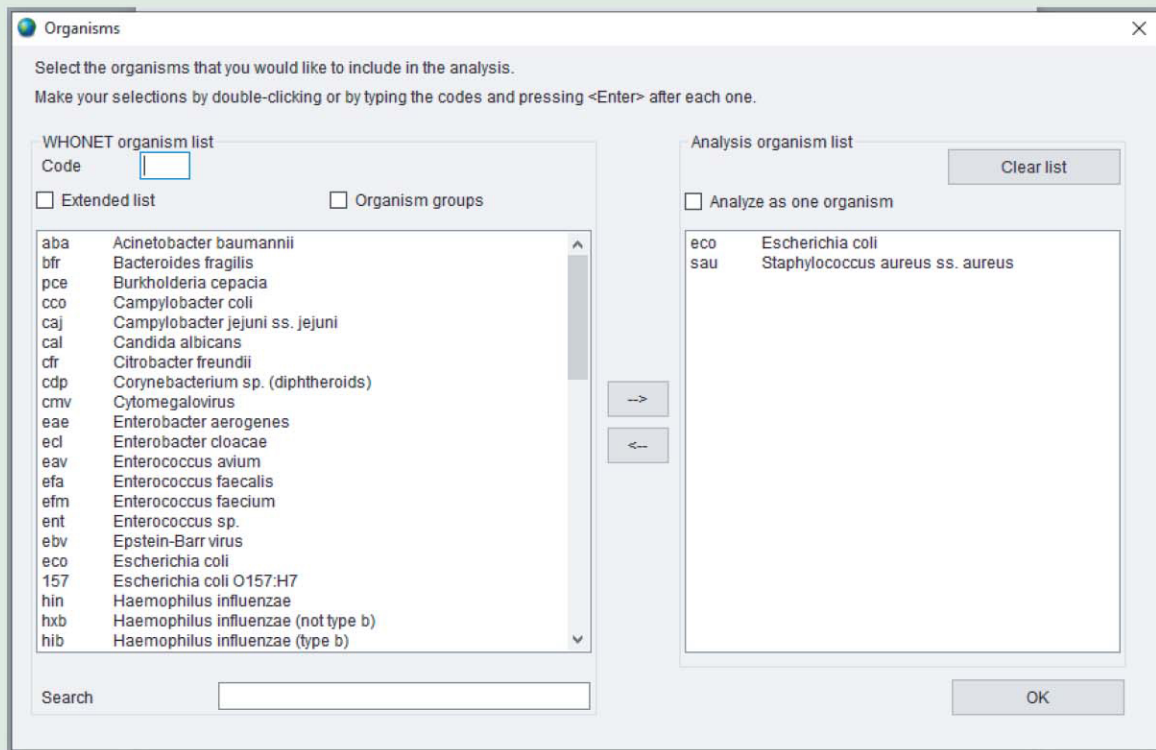


Figure 4. Organism: Select the organisms or organism groups that you want to analyze. There are some other useful options on this screen as well.

Extended list: Initially, WHONET shows you the list of relatively common organisms. To see the complete list, click on “Extended list”. You can use the “Search” box to quickly find an organism.

Organism groups: If you click on “Organism groups”, you will see that WHONET permits you to analyze groups of microorganisms such as “All organisms”, “All Enterobacteriaceae”, and “All Salmonella”.

Analyze as one organism: WHONET generally will analyze each organism selected separately. If you would like WHONET to average results together from multiple organisms (for example “Klebsiella pneumoniae”, “Klebsiella oxytoca” and “Klebsiella sp.”), then click on the option “Analyze as one organism”. When you finish looking at the available options, click “OK” to return to the main analysis screen.

Data files: Click on “Data files” to select the data files to include in the analysis. For this tutorial, select the file WHO-TST-1995-01.sqlite”. You can do this by double-clicking on the file or by single-clicking and using the right-arrow button “->”. After selecting the file, click on “OK” to return to the main analysis screen.

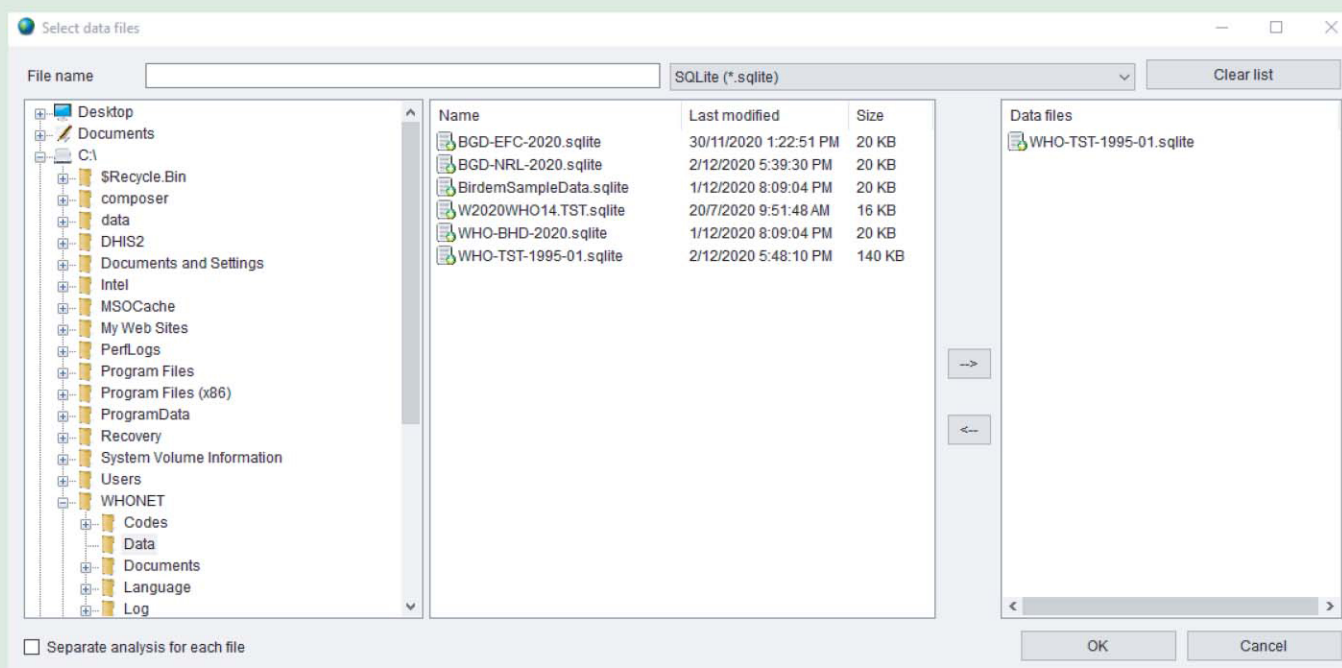


Figure 5. Data files: Select the data files to include in the analysis. Files to be analyzed should appear on the right side of the screen.

After making all of the above selections, your screen should look like the following:

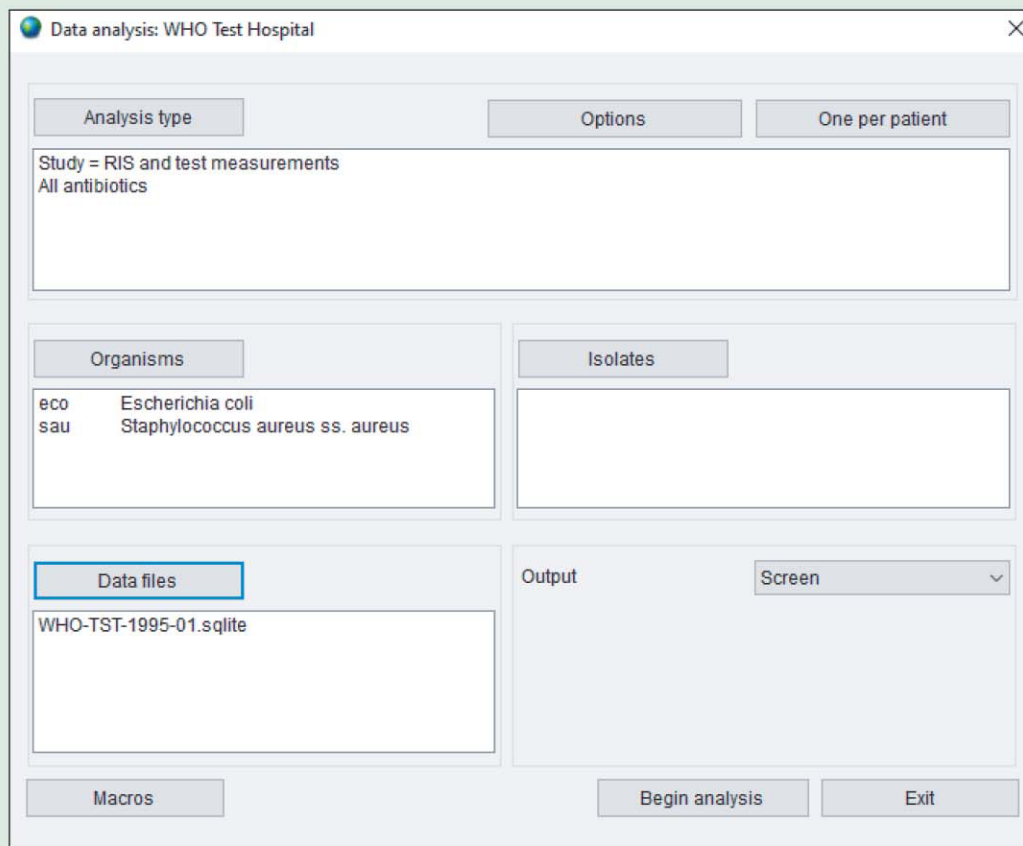


Figure 6. WHONET analysis screen. WHONET will run a “%RIS and test measurement” analysis on E. coli and S. aureus from the file WHO-TST-1995-01.sqlite.

PART 3. RUNNING THE ANALYSIS AND INTERPRETING THE RESULTS

Now that you have given WHONET the details of the analysis to perform, click on “Begin analysis”. If you have answered the questions correctly, WHONET will then read and analyze the data file, and should soon show the following screen.

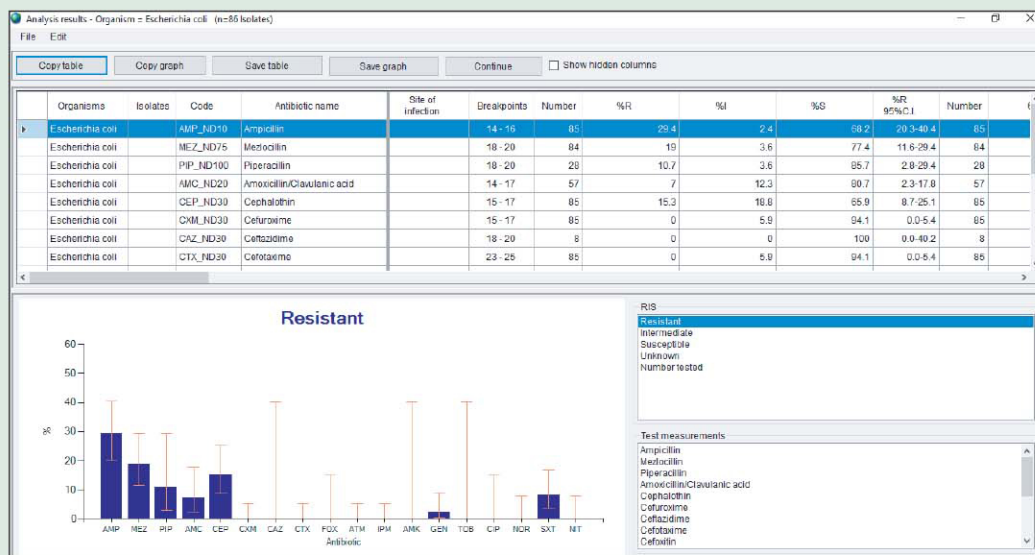


Figure 7. WHONET output screen for the %RIS and test measurement analysis with E. coli.

On the top of this screen, you see a table with the antimicrobial susceptibility test statistics for each of the antimicrobials tested. If you want to sort the table alphabetically or numerically, click on the heading for the column on which you want to sort.

For the E. coli, the output tells you how many isolates in total were found (86 isolates) and which antimicrobials were tested. When you review results such as these, you should evaluate whether the antimicrobials tested are appropriate and whether the laboratory can optimize their test practices by adding, removing, or changing the antimicrobials tested. The results may also have suggested typing errors in data entry (for example if there are vancomycin results tabulated for E. coli).

You should also look at the column “Number” to see how often each antimicrobial was tested. This will give you an idea of the laboratory’s testing practices – which antimicrobials are tested in all isolates and which are tested only in urine or highly resistant isolates. If the number of tests per antibiotic is very irregular, this may suggest a problem with antimicrobial disk availability in the laboratory.

For example, in the data presented in this example, one could conclude that the laboratory staff is most

likely testing antimicrobials in the following way:

Tested for all isolates: AMP, ATM, CTX, CXM, CEP, GEN, IPM, SXT (9 drugs)
 Tested for urine isolates: AMC, NIT, NOR (3 drugs)
 Tested for non-urine isolates: FOX, CIP, PIP (3 drugs)
 Tested for organism’s resistant to first-line agents: AMK, CAZ, TOB (3 drugs)

In the other words, there is a urine panel which includes 12 antimicrobials (as one 15cm plate or two 9cm plates), a non-urine panel with 12 antimicrobials, and three additional drugs used in second-testing.

Additional columns indicate the antimicrobial breakpoints used, the percent of isolates resistant (including a 95% confidence interval), intermediate, and susceptible, as well as the distribution of zone diameters of MIC values.

diameters of MIC values.

The lower part of the screen shows some of the same data presented in the table, but in graphical format. For example, click on the options for “Number tested” and “%Resistant”.

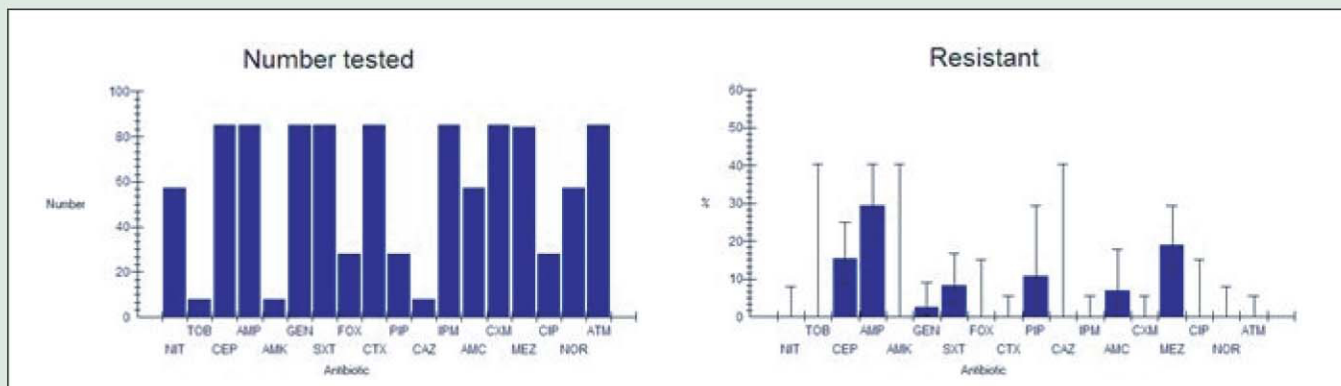


Figure 8. Results from the %RIS analysis. The number of isolates tested for each antimicrobial is indicated to the left, while the percent of isolates resistant to each antimicrobial is depicted to the right.

Now click on some of the antimicrobials listed in the lower panel, for example ampicillin and trimethoprim/sulfamethoxazole. WHONET will display the zone diameter or MIC distribution of the selected drug. The red lines in the graph represent the interpretative breakpoints. For disk diffusion results, susceptible bacteria will appear to the right of the red lines; resistant isolates are to the left; and intermediate results are between the two lines. For MIC data, the susceptible bacteria will appear to the left and resistant bacteria to the right.

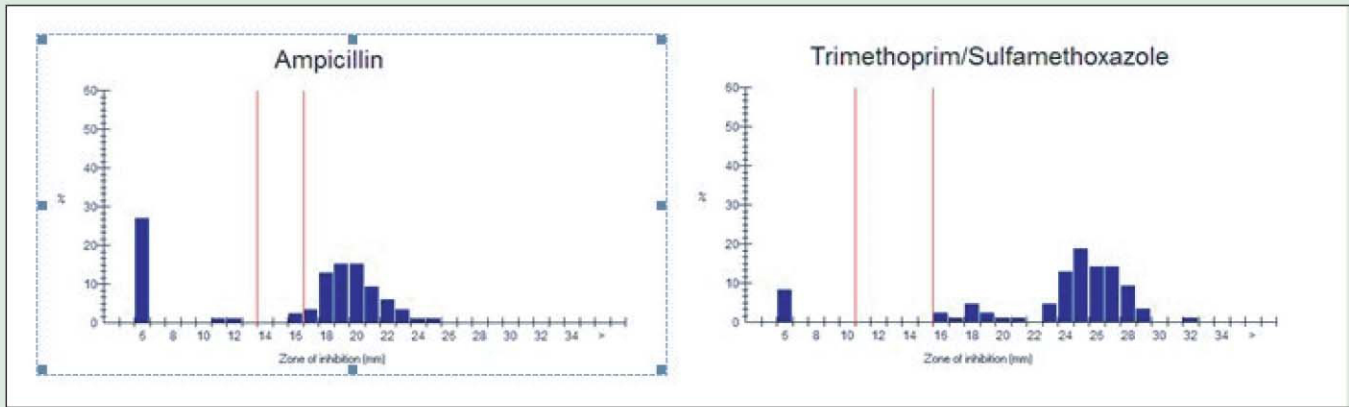


Figure 9. Zone diameter histograms for ampicillin and trimethoprim/sulfamethoxazole for *E. coli* isolates.

For most antimicrobials and organisms, the susceptible bacteria should form a fairly “normal” Gaussian distribution. You can see this for the *E. coli* histograms, even for those antibiotics with very few test results. Deviations from this pattern are common for some organisms and antimicrobials, but can also suggest test problems in laboratory practices – for example poor reagent quality (disks or test medium), inoculum preparation, or result measurement (for example number preference).

The ampicillin histogram suggests three principal bacterial subpopulations: 1. the wild-type susceptible population with large zone diameters; 2. a group with high-level resistance to ampicillin (zone diameter = 6mm = no inhibition); and 3. a group with low-level resistance (zone diameters 11 and 12mm). The latter two groups presumably possess different resistance genes – an observation not only useful for molecular research, but also in the investigation and characterization of outbreak-associated strains.

The second histogram depicts results for trimethoprim/sulfamethoxazole and illustrates two distinct populations that lie in the susceptible category: one population with the “wild-type” phenotype with relatively large zone diameters and a second population with “decreased susceptibility” with diminished zone diameters.

PART 5. %SUSCEPTIBLE SUMMARY

In the previous analysis, WHONET analyzed first the *E. coli* and then the *S. aureus*. For clinicians and policy makers, it would be useful to prepare a summary report with many species on the same page. With WHONET, this is easy to do.

Click on “Analysis type”. In the middle of the screen, you will see two options: 1. %RIS and test measurements, and 2. Summary. The first of these is the detailed report presented earlier. For this example, select “Summary”.

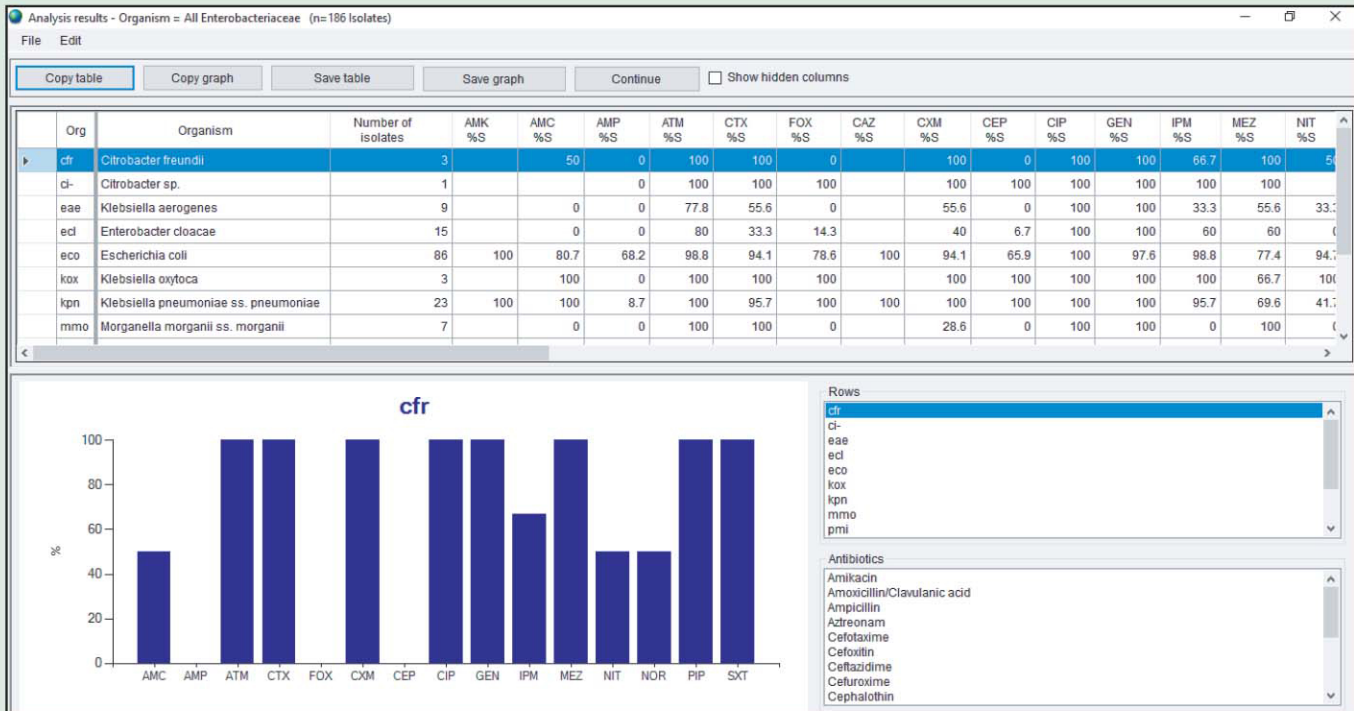


Figure 14. %S Summary for Enterobacteriaceae. The graph for E. coli results is displayed below.

PART 6. ISOLATE LISTING AND SUMMARY

Another useful feature of WHONET is the creation of lists of isolates or patients that meet certain criteria – for example a lists of patients with MRSA or positive blood cultures from the neonatal intensive care unit. WHONET can create such lists as well as summarize the results in a number of different ways.

Click on “Analysis type”, and select “Isolate listing and summary”. 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 options. Next to specimen date appears the option “Month”. Because there is only one month of data to analyze in this tutorial, it will be more interesting to show the results by day or by week. Select the option “Day”. Leave the other options unchanged, and click “OK”. Click on “Begin analysis”. In this example, WHONET will show you a list of all isolates from the data set with Enterobacteriaceae, as below.

Analysis results - Organism = All Enterobacteriaceae (n=186 Isolates)

File Edit

Copy table Copy graph Save table Save graph Continue Show hidden columns

Identification number	Location	Specimen number	Specimen date	Specimen type	Organism	Organism type	AMK_ND30	AMC_ND20	AMP_ND10	ATM_ND30	CTX_ND30	FOX_ND30	CAZ
8822823545	icu2	_9141950184_	13/1/1995	ur	cf	-		18	14	32	31		
9494551616	op	_5908662293_	11/1/1995	ur	cf	-		17	15	33	30		
9876786254	id	_1266719029_	23/1/1995	wd	cf	-			14	28	27	12	
9876786254	id	_1266719029_	23/1/1995	wd	cl-	-			12	25	31	26	
0180081335	op	_9835142848_	30/1/1995	sp	eae	-			06	30	29	06	
0565716535	icu1	_6343517368_	17/1/1995	sp	eae	-			06	29	28	06	
0591836826	csurg	_3989191575_	7/1/1995	ur	eae	-		08	06	25	27		
1750024603	icu1	_7793316734_	12/1/1995	sp	eae	-			06	28	25	06	
6130695730	id	_5783805452_	3/1/1995	sp	eae	-			06	23	14	06	
6885271928	id	_4842579943_	8/1/1995	sp	eae	-			06	18	14	06	
7103248832	icu1	_1513627174_	20/1/1995	sp	eae	-			06	29	28	06	
7401857119	med2	_3993265680_	1/1/1995	ur	eae	-		08	06	35	30		
9837392987	sicu	_2264870850_	21/1/1995	ur	eae	-		06	06	16	13		
0212379489	sicu	_5455773388_	16/1/1995	wd	ecf	-			10	28	25	09	
0591836826	icu1	_5596078726_	5/1/1995	ti	ecf	-			13	28	30	23	
0684226152	card	_3427363378_	7/1/1995	sp	ecf	-			06	25	25	06	
1006370926	id	_2303593844_	3/1/1995	wd	ecf	-			06	16	06	06	
1108707769	med1	_8977801081_	21/1/1995	sp	ecf	-			06	13	06	06	
1238843072	oncol	_4268300617_	26/1/1995	ur	ecf	-		06	06	24	24		
2083490590	oncol	_2363590948_	29/1/1995	ur	ecf	-			06	22	15	06	
3072695177	icu1	_5452866009_	8/1/1995	sp	ecf	-			06	28	25	06	

Figure 15. Isolate listing of Enterobacteriaceae. The most important fields are displayed. To view additional columns, click on “Show hidden columns”.

This listing shows some of the most important data fields: identification number, location, specimen date, specimen type, organism, and antibiotic results (in this example, with disk diffusion zone diameters).

Note: You can configure the fields which appear in this isolate listing. To do so, you would have to go back to laboratory configuration “Modify laboratory”, “Data fields”. For the data fields that you want to appear in the list, make sure that the box for “Isolate listing” is checked.

If you click on the box “Show hidden columns”, WHONET will show you all of the available fields. As in other parts of WHONET, you can click on a column heading to sort the database by that column. This could be useful, for example, to find errors in the entry of specimen dates.

When you finish looking at the isolate listing, select “Continue”. WHONET will proceed to display the summary of the isolate listing. As mentioned earlier, this summary is comparing “Organism” and “Specimen date” (by day). But by changing the analysis parameters, you can summarize any WHONET variable by any other variable.

The tables present 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.

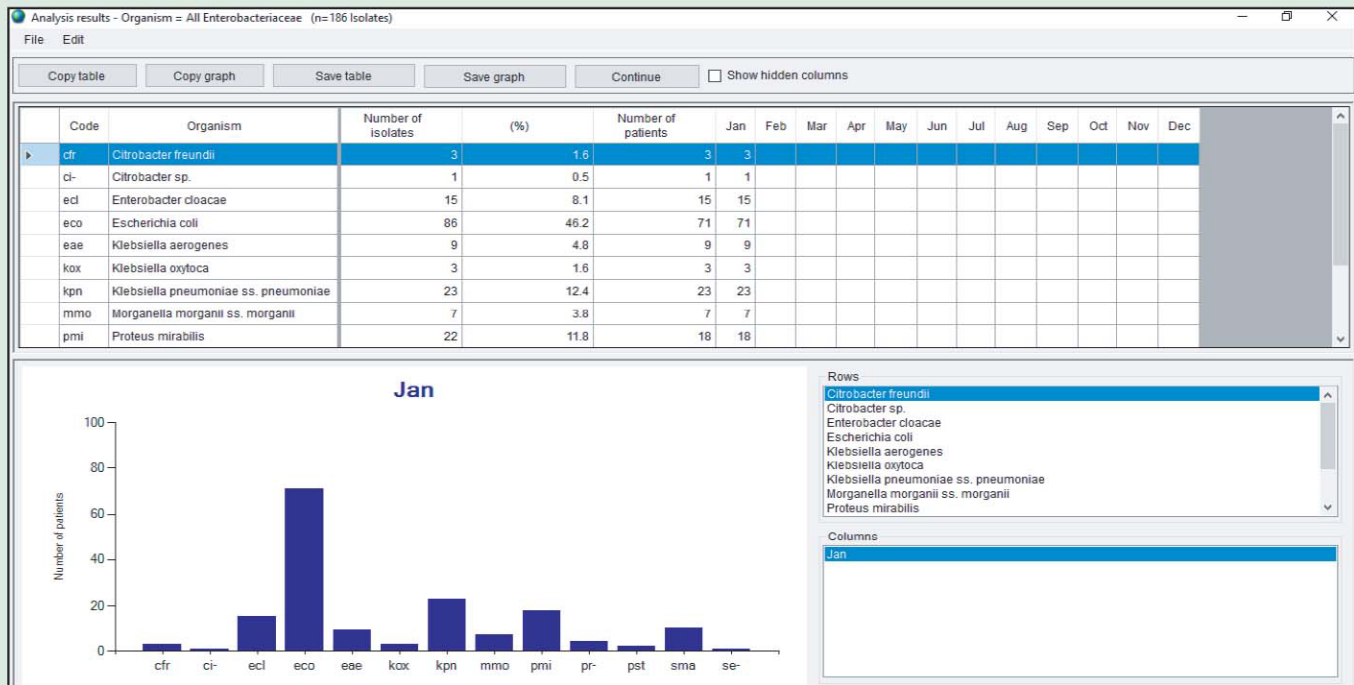


Figure 16. Summary of the Enterobacteriaceae isolate listing. The daily distribution of E. coli isolates is displayed in the graph.

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.

Now that you have completed this tutorial, you can exit WHONET completely or continue with Data analysis 2. If you want to leave the software completely, click on “Exit” to leave the data analysis program, and then “File”, “Exit” to leave WHONET.

PART 7. TRANSFERRING WHONET RESULTS TO EXCEL AND OTHER SOFTWARES

After you finish reviewing results from the E. coli, click on “Continue” to proceed to the S. aureus results. Review the results shown in the table and histograms.

The WHONET results that you see on the screen can easily be transferred to other softwares such as Microsoft Excel, Word, or PowerPoint. You can do this either by using “Copy” and “Paste” or by saving the results as a file.

Copy and Paste: Click on “Copy table”. Now open Microsoft Excel, for example by clicking on your Windows “Start”, “All Programs” menus and looking for Microsoft Excel. (Alternatively, if you want to immediately go to your Windows Desktop, click on the “Windows” key on your keyboard and hit the letter D, in other words “Windows”-D.)

After you have Excel open, go to “Edit”, “Paste”. The WHONET results are now in Excel. You can now use Excel to edit, correct, format, or graph your results.

Now return to WHONET (for example, by clicking on the WHONET icon on the bottom of your screen). Click on “Copy graph”. Go back to Excel, find an empty part of the spreadsheet, and again choose “Edit”, “Paste”.

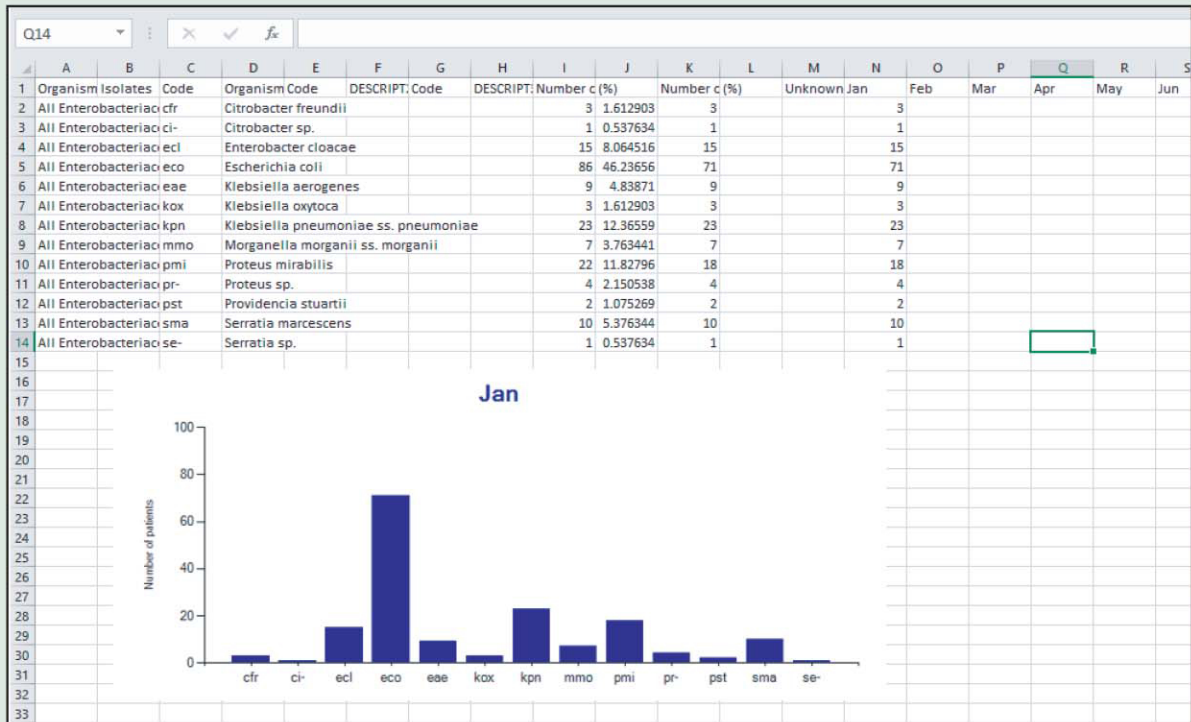


Figure 10. Copying and pasting results to Excel using “Copy table” and “Copy graph” from WHONET.

Save the file: WHONET also has an option for saving the results directly to a file. Because “Copy” and “Paste” works well and is usually very fast, there is often no need to do this, but there are a few situations where saving the results as a table can be useful. 1. For “isolate listings” or “resistance profile listings” with thousands of rows, the “Copy” and “Paste” approach can be very slow. In this case, saving the results as an Excel or as a text file would be much faster. 2. When you save the table as an Excel file, WHONET does some automatic formatting of the results and automatically makes a number of Excel graphs. So by using the “Save table” option, this may save you some time formatting the data in Excel.

To save the tables and graphs as an Excel file, click on “File”. Give a name to the file, for example “S. aureus RIS results.xls”. For type of file, select “Excel”. Notice that the default location for this file is c:\WHONET\Output. Then click ‘OK’

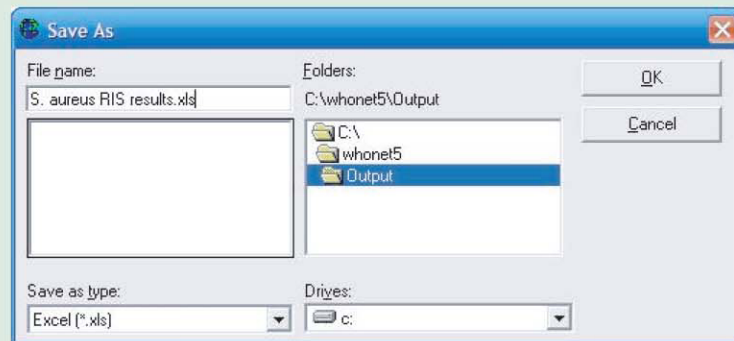


Figure 11. Saving results from WHONET to an Excel file.

Now go back to Excel and select “File”, “Open”. Look in the folder c:\WHONET\Output for the file that you just created, and open it up. You will see something the following.

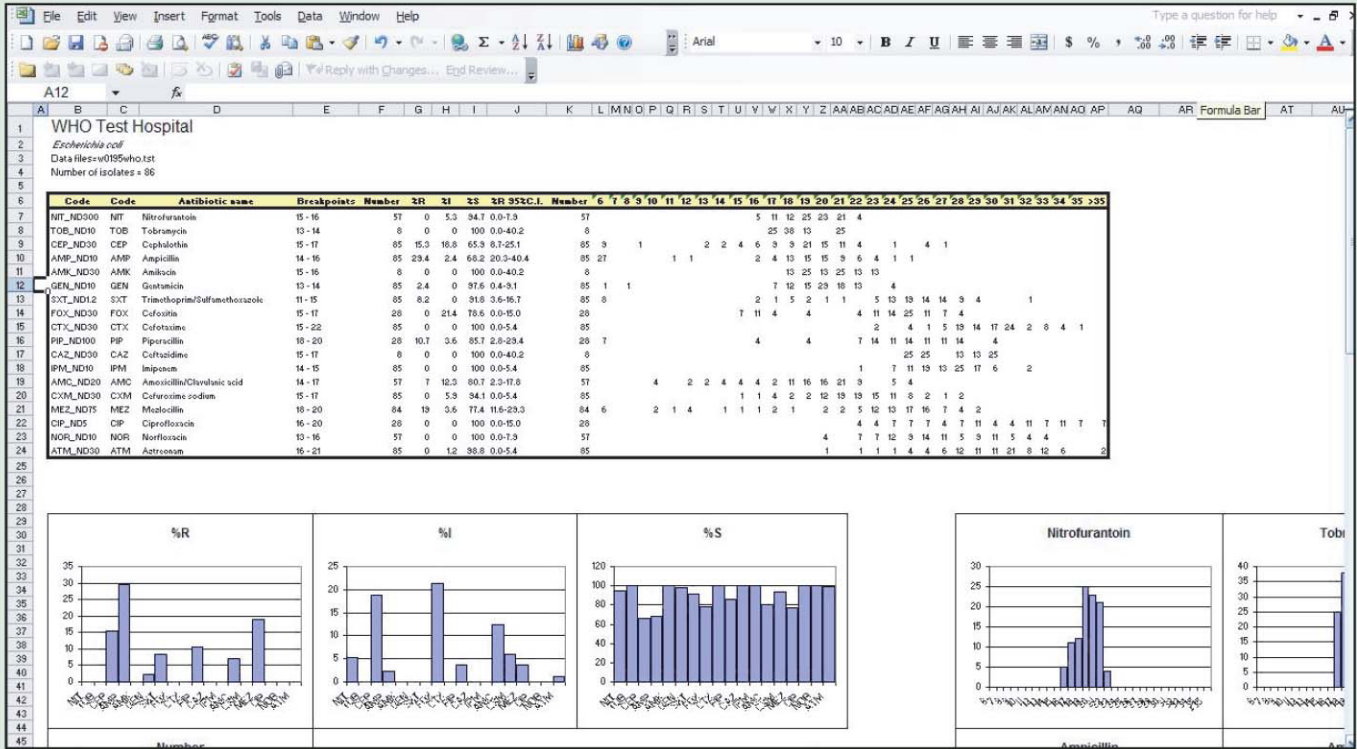
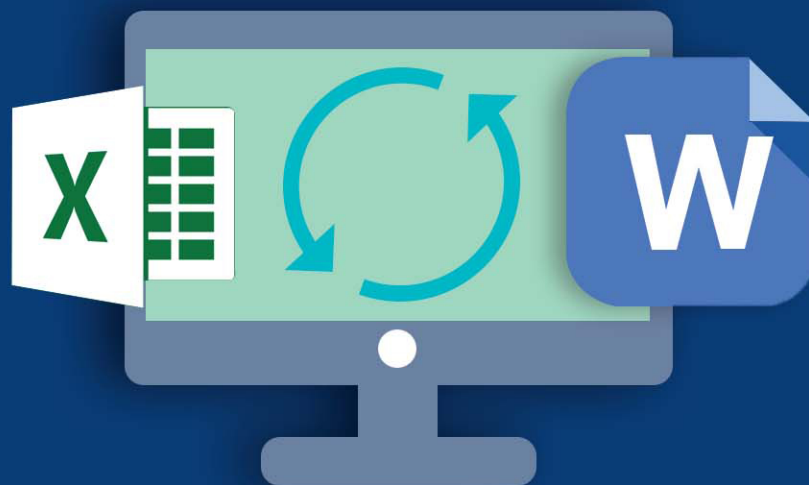


Figure 12. A formatted Excel file created from WHONET.

Then return to WHONET and click "Continue" to return to the main analysis screen.

CHAPTER-5

BACLINK CONVERSION



This chapter will focus on the following areas:

- Baclink
- What systems are Baclink compatible with Baclink?
- How does Baclink work?
- Example of the conversion of LIS file (Excel/ CSV) to WHONET

What is Baclink?

Many laboratories around the world already have well-established computer databases that meet the day-to-day needs of clinical reporting, specimen processing, and long-term data storage. Unfortunately, most of these systems have limited capacity for sophisticated data analysis. It is in these areas that WHONET is a valuable supplement to existing systems.

This purpose of the Baclink software is the conversion and standardization of microbiology data from existing systems into WHONET. You can convert data on a weekly, monthly, or ad hoc basis, or in a number of institutions, it has also been possible to automate and schedule the entire process. Both WHONET and Baclink are available free-of-charge from the World Health Organization website: www.who.int/drugresistance/whonetsoftware.

By converting data to WHONET, laboratories have the benefits of:

1. flexible data analysis capabilities; and
2. the ability to share data with other laboratories, for example in a national surveillance network.

What systems are compatible with Baclink?

Baclink is compatible both with “User-defined” data formats as well as “Proprietary” or “Fixed” data formats. More specifically, Baclink can convert data from the following systems:

Standard desktop software’s and text files: Baclink can directly import data files with the following formats: Microsoft Access, dBASE, and EpiInfo. In addition, Baclink has a flexible, configurable interface for the import of simple text files. So most systems capable of creating text files (such as Excel and most laboratory information systems) should be able to create files that can be converted with Baclink.

Laboratory organism identification and susceptibility test instruments: Baclink is compatible with the following commercial systems.

- MIC systems: ATB, MiniAPI, Microscan, Pasco, Sceptor, Sensititre, Vitek, Wider
- Disk diffusion readers: Aura, Biomic, Osiris, SirScan, Videobac, Wider

In most cases, Baclink cannot access data from the internal, proprietary databases of these instruments since these are protected by the vendor. Fortunately, most systems have an “export”, “report”, or “interface” capability which can be used for the transfer of data to text files which Baclink can use to create WHONET files.

Laboratory information systems: We have developed specific guidelines for the export and conversion of data from the following commercial information systems.

- Meditech Magic
- Cerner Classic

It is also possible to convert data from the following systems, but we have not developed formal documentation describing the process. For further details, please contact us directly.

- ADBakt (Sweden, Denmark)
- MADS (Denmark)
- Oman Health Information System (Oman)
- WinPath (Malaysia)

Other standard formats: BacLink can understand the following standard data formats.

- EARSS (European Antimicrobial Resistance Surveillance System)
- JIAQA (Japan-International Association for Quality Assurance)
- NORM (Norwegian Resistance Monitoring)

If your system does not appear on these lists, you can still use BacLink if your system can create simple text files. Guidance on how to do this is provided in the document “BacLink and Laboratory information systems”.

How does BacLink work?

BacLink allows you to take data from a number of different sources and create new data files with the standard WHONET file structure. Detailed instructions for specific systems are provided in other tutorials or in the BacLink manual, but for each the overall process is the same:

Step 1. Create a file compatible with BacLink If your data file is already compatible with BacLink, for example with simple text files, Access, and a few other formats, there is nothing that you need to do in this step – the data file that you have is already compatible with BacLink.

For most laboratory instruments and information systems, you will first need to export data from your system into a format compatible with BacLink, most frequently a delimited text file. The accompany tutorials and BacLink manual provide instructions on how you can accomplish this.

Step 2. Configure the conversion You will need to tell BacLink what kind of file you want to import and details about the file: what is the file format (text, Access, Vitek, Cerner, etc.), what susceptibility test methods are included, how the data fields are organized, date formats, etc.

For propriety data structures, configuration is very easy since BacLink is already programmed with all of the necessary details about the file structure. For generic structures, there are a few additional screens where you provide details about the data file contents and organization. If you have multiple files with the same data format, configuration only needs to be done once.

Step 3. Running the conversion After configuring the conversion, you are ready to convert your files. BacLink will show you the first three isolates on the screen so that you can check the accuracy of the conversion, and BacLink will also notify you of any problems or unrecognized codes that it encounters. The file created by the BacLink conversion is a valid WHONET data file that you can subsequently analyze with WHONET.

At the present time, most laboratories run BacLink interactively, for example once a week, month or quarter. For a number of systems, it is also possible to schedule BacLink, for example to convert data automatically on a daily basis.

In Summary:

Standard desktop softwares: If you have data in Microsoft Access, Excel, EpiInfo or dBASE, or other system that can create simple text files, proceed with the tutorial “BacLink and Excel, text files, and other desktop applications”.

Laboratory instruments: If you want to transfer data from your laboratory instrument, consult the instructions provided in the main BacLink manual or specific guideline developed for that instrument.

Laboratory information systems: If you have a Meditech Magic or Cerner Classic system, continue with the detailed instructions provided with the accompanying documentation. For ADBakt, MADS, the Oman Hospital Information System, and WinPath, contact us for further details. For any other system, then you should proceed with the tutorial “BacLink and Laboratory information systems”.

Example: Excel, text files, and other desktop applications to WHONET conversion process:

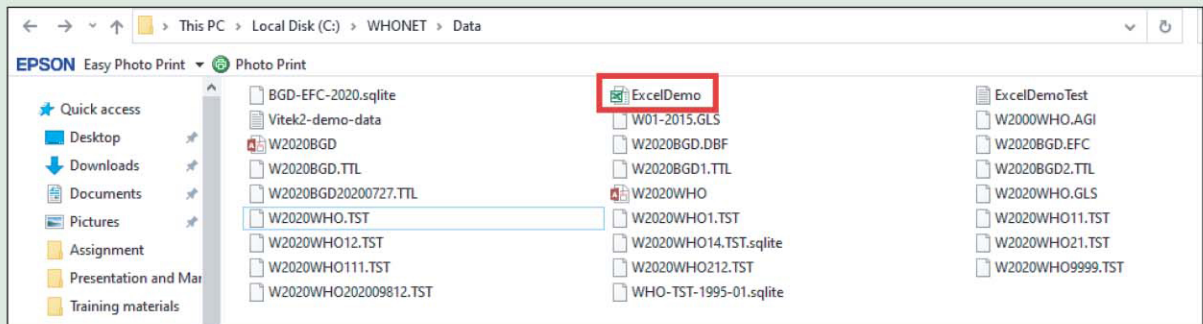
The chapter covers the following areas:

- Part 1. Inspecting your data file
- Part 2. Preparing your file for BaLink
- Part 3. Starting BaLink
- Part 4. Configuring a new file format
- Part 5. Running the conversion
- Part 6. Getting started with WHONET

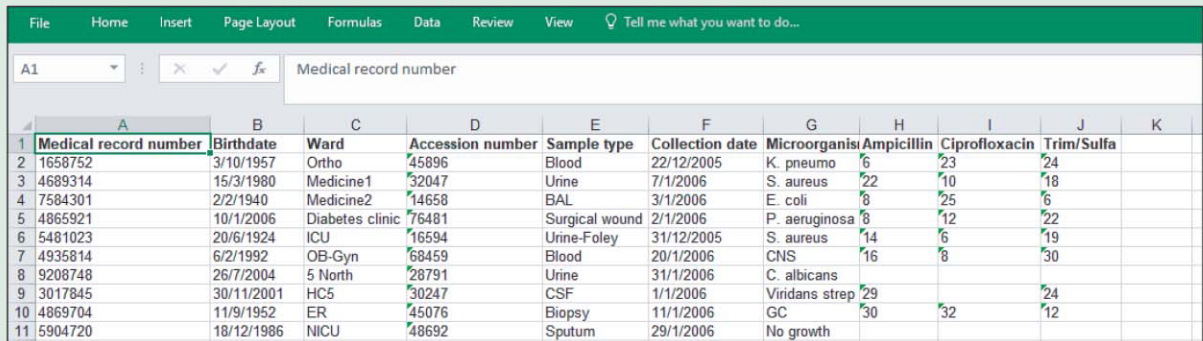
The tutorial assumes that you have already installed WHONET and BaLink on your computer. If you have not, refer to the WHONET Tutorial: Getting Started.

PART-1. INSPECTING YOUR DATA FILE

In this tutorial, you will be working with the file “ExcelDemo.xls” in the folder C:\WHONET\Data. Use “My Computer” or “Excel” to open this file.



When you open this file, you will see the following data.



	A	B	C	D	E	F	G	H	I	J	K
	Medical record number	Birthdate	Ward	Accession number	Sample type	Collection date	Microorganism	Ampicillin	Ciprofloxacin	Trim/Sulfa	
2	1658752	3/10/1957	Ortho	45896	Blood	22/12/2005	K. pneumo	6	23	24	
3	4689314	15/3/1980	Medicine1	32047	Urine	7/1/2006	S. aureus	22	10	18	
4	7584301	2/2/1940	Medicine2	14658	BAL	3/1/2006	E. coli	8	25	6	
5	4865921	10/1/2006	Diabetes clinic	76481	Surgical wound	2/1/2006	P. aeruginosa	8	12	22	
6	5481023	20/6/1924	ICU	16594	Urine-Foley	31/12/2005	S. aureus	14	6	19	
7	4935814	6/2/1992	OB-Gyn	68459	Blood	20/1/2006	CNS	16	8	30	
8	9208748	26/7/2004	5 North	28791	Urine	31/1/2006	C. albicans				
9	3017845	30/11/2001	HC5	30247	CSF	1/1/2006	Viridans strep	29		24	
10	4869704	11/9/1952	ER	45076	Biopsy	11/1/2006	GC	30	32	12	
11	5904720	18/12/1986	NICU	48692	Sputum	29/1/2006	No growth				

Before you begin converting your data, you should familiarize yourself with the organization of the information in the file. The type of data presented here is fairly typical of files created by manual data entry into Excel.

There are a few useful observations from this file that we will come back to later:

- Each row of this file corresponds to the results of one isolate.

- The file has results from three antibiotics: ampicillin, ciprofloxacin, and trimethoprim/sulfamethoxazole. The measurements (6, 8, 12, 24, 30, 32, etc.) suggest that all results were obtained by the disk diffusion test. If you are uncertain what method was used, ask one of the laboratory staff responsible for doing the tests.
- Each column is appropriately labeled with a column “header” indicating the meaning of each field.

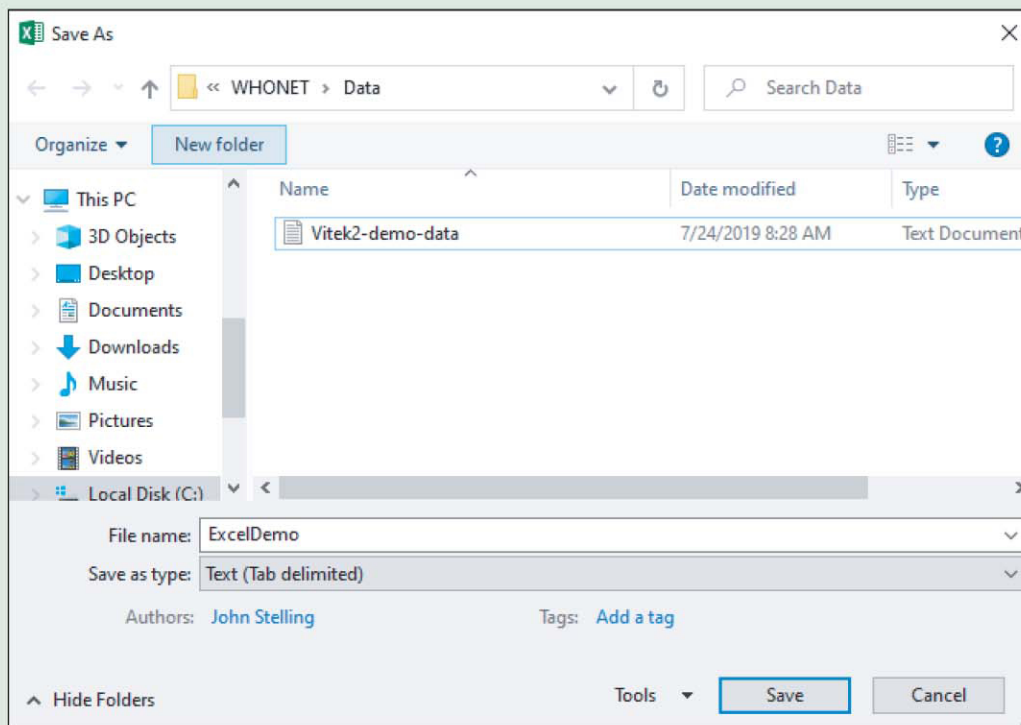
PART 2. PREPARING YOUR FILE FOR BACLINK

Unfortunately, BaLink does not have a direct import option for Excel files, so we need to make some modifications to create a file that can be converted with BaLink.

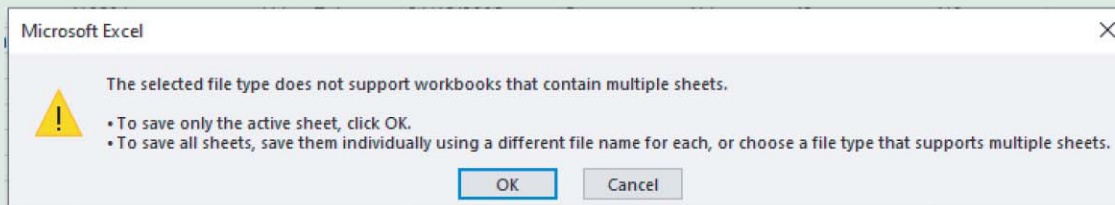
First of all, you should delete any extraneous information in the Excel file which is not part of the data to be converted – for example graphs or unneeded descriptive information. The data to be converted should begin in the cell A1, as in the example. So for the sample file used in this tutorial, no data “cleaning” is needed.

You then need to save the Excel file in a format compatible with BaLink. The most convenient format is a delimited text file format. To do this, click on “File”, “Save as”. Instead of using the default “Excel Workbook” format, click on “Save as type” and select the option “Text (Tab delimited) (*.txt)”.

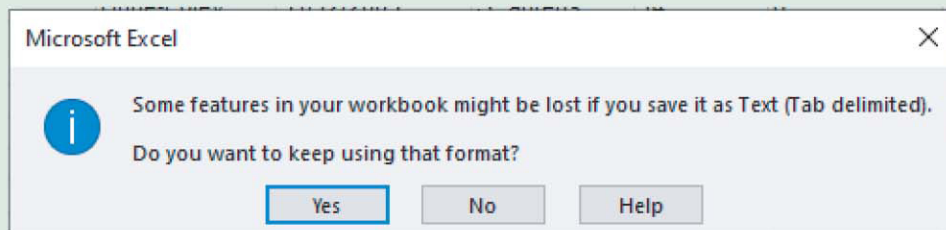
Note: For a step that we will come to later, remember that Excel, by default, is using “Tab” as the field delimiter.



When you select “Text (Tab delimited)” as your file format, Excel will change the name of the file from “ExcelDemo.xls” to “ExcelDemo.txt”. Now click on “Save”. When you click on “Save”, you will get two warning messages.



The first message warns you that Excel cannot save all three Excel Sheets as a text file as once. Since we only want to save the active sheet, click "OK".



The second message warns you that you will lose special formatting, such as bold letters, fonts, and lines when you save an Excel file as a text file. Since we are only interested in the data, and not the Excel formatting of the data, this is not a problem. So in answer to the question "Do you want to keep the workbook in this format?", click "Yes".

We will now leave Excel completely. Click on "File", "Exit".

If you look at your c:\whonet\data folder, you will now see that there is a file called "ExcelDemo.xls" (the original file) and a file called "ExcelDemo.txt" that you just created with Excel. We will use BaLink to convert the latter file to WHONET format.

PART 3. STARTING BAHLINK

Start the BaLink program by double-clicking on the BaLink shortcut icon installed on your desktop. The main BaLink screen should appear. In the top half of this screen, you will describe the file that you want BaLink to convert, and in the lower part of the screen, you will give a name to the new WHONET file that BaLink will create.



Note: BacLink is currently available in 17 languages. To change the language, click on “Select language”, and look for the desired language.

BacLink has two parts:

1. configuring a data conversion and
2. running a data conversion.

In configuration, you describe to BacLink the file structure, codes, and date formats used in your data file. This only needs to be done once. Then after configuration is complete, you can run a conversion for any file that has the same structure. For example, if you configure BacLink for importing your January data, you can then use this same configuration for data from all subsequent months which have the same data file structure.

Part 4 of this tutorial discusses the configuration of a file format. Part 5 covers the steps in running the conversion.

PART 4. CONFIGURING A NEW FILE FORMAT

To convert the sample file, you need to give BacLink enough details for it to perform the conversion. To do this, click on “New Format”.

Configuration – Laboratory name

Click on the New Format button. The File Format screen opens. From the drop down box, select the Country: World Health Organization. Enter the Laboratory Name – enter the name of the laboratory. For this tutorial, enter BacLink Tutorial Hospital.

Enter up to three characters for the Laboratory Code, for example BTH. The laboratory code that you indicate will be used by BacLink and WHONET as the default file extension for your WHONET data files.

Baclink Configuration Baclink Tutorial Hospital

Configuration file bth.cfg

Country Bangladesh BGD

Laboratory name Baclink Tutorial Hospital

Laboratory code IED
Maximum 10 letters

File structure Describe the structure of your data files.

Codes and dates Enter the codes and date formats used in your data files.

New data file Indicate the name and format of the new data file.

Data filter Indicate the isolates to be included in the new data file.

Save as Save Exit

Configuration – File format

Click on the File Structure button, and the below screen will appear. Select the options indicated below.

File structure – when you saved the file in Excel, you selected the format “Text (Tab delimited)”. So in this screen, under the option for “File format”, select “Text, delimited”.

Delimiter – Select the option “Tab”.

File location – For this tutorial, the location of the file is c:\whonet\data, so no change is required for this question. In many institutions, data files are placed in a folder on a central server, so you can use this option to indicate the default location for data files.

File name – You can either give the precise name of the data file here at this step or later, just prior to converting the data. For this tutorial, leave this response unchanged as “*.txt”.

File origin – Since Excel is a Windows program, select “Windows (ANSI)”. The difference between “DOS (ASCII)” and “Windows (ANSI)” is only important if your data file includes accents (for example é, ñ, ö, ø, etc.) or non-Latin characters (such as in Greek, Russian, Chinese, Thai, etc.). For English and data files without accents or non-Latin characters, there is no significant difference between the two.

File structure

File structure: Text (Delimited)

Field delimiter: Tab

File location: C:\WHONET\Data [Browse]

File name: *.txt [Browse]

Table name: []

File origin: Windows (ANSI)

Antibiotics Enter information about the antibiotics in your data file

Guidelines	No answer
Number of rows of data for each isolate	No answer
Antibiotic sequence	No answer
Test methods	No answer
Number of test methods in one row of data	No answer

Does the first row of the data file have the names of the data fields?
 Yes No

Data fields Define the relationship between your data fields and WHONET data fields.

OK

Configuring – Antibiotics

You now need to give BaLink information about the antibiotic results in your file. Click on “Antibiotics”, and give the indicated responses.

Does your file include antibiotic results? Answer Yes.

Guidelines: The sample data file in this tutorial represents results tested by the United States CLSI guidelines (Clinical and Laboratory Standards Institute) for performance of antimicrobial susceptibility tests. So for this question, choose CLSI. In your institution, if you do not know the answer to this question, ask your laboratory staff.

Data rows. When someone makes a simple data file with antibiotic test results, there are two common variations in how the results are saved: one data row = one isolate or one data row = one antibiotic result. As you observed earlier in this tutorial, all of the results from one isolate are saved in the same data row of the Excel file. For data entered manually into Excel, this is the most common and logical way of organizing data. So in answer to the question: “The antibiotics of one isolate require how many rows of data?”, give the answer “One row”.

Antibiotic sequence. For the sample data file in this tutorial, all of the isolates have antibiotic results saved in the sequence: “Ampicillin”, “Ciprofloxacin”, “Trimethoprim/Sulfamethoxazole”. This is an example of a “Fixed antibiotic sequence”. For data entered manually into Excel, this is the most common way of organizing data. So for this answer, select “Fixed antibiotic sequence”.

For data exported from relational databases, laboratory information systems or laboratory instruments, a variable sequence is more common. The first isolate may have results for ampicillin, ciprofloxacin, and trimethoprim/sulfamethoxazole, but the second isolate may have different antibiotics and presented in a different sequence, one antibiotic result in each data row.

Test methods. The most important routine susceptibility test methods are disk diffusion, MIC, and Etest. The data presented in this tutorial are disk diffusion results, so click on “Disk diffusion” If your data file includes more than one test method, then BaLink will ask you a few more questions so that it can reliably distinguish results tested by the different methods.

If you have answered all of the questions correctly, your screen should look like the following. When finished, click “OK”.

Configure antibiotics

File format: TEXT (DELIMITED)

Does your file include antibiotics results? Yes No

Guidelines: CLSI

The antibiotics of one isolate require how many rows of data? One row More than one row

In what sequence do the antibiotics appear? Fixed antibiotic sequence Variable antibiotic sequence

The data file includes what test methods?

Disk diffusion	<input checked="" type="checkbox"/>
MIC	<input type="checkbox"/>
Etest	<input type="checkbox"/>

OK Cancel

Configuration – Data fields

You will now continue with the most important part of configuration – defining the relationship between the data fields in your file and the corresponding data field in WHONET.

You should see the question: “Does the first row of the data file include the names of the data fields?” In other words, does the file have a field “header”. When you inspected the data file earlier in Excel, you saw that indeed each column is labeled appropriately, so the answer to this question is “Yes”.

File structure

File structure: Text (Delimited)

Field delimiter: Tab

File location: C:\WHONET\Data\ [Browse]

File name: *.bt [Browse]

Table name: []

File origin: Windows (ANSI)

Antibiotics Enter information about the antibiotics in your data file

Guidelines: CLSI

Number of rows of data for each isolate: One row

Antibiotic sequence: Fixed antibiotic sequence

Test methods: Disk

Number of test methods in one row of data: One method

Does the first row of the data file have the names of the data fields?

Yes No

Data fields Define the relationship between your data fields and WHONET data fields.

[OK]

Click on “Data fields” to proceed with the configuration of the data fields. On the left side of this screen, you will see the default list of WHONET fields. If you want to add additional fields to this list or remove fields from it, click on “Modify the list of data fields”. For purposes of this tutorial, we will leave the list as it is.

Data fields

Select a sample data file [OK]

Data fields in the new file

- Identification number = <None>
- Last name = <None>
- First name = <None>
- Full name = <None>
- Sex = <None>
- Date of birth (D/M/Y) = <None>
- Age = <None>
- Location = <None>
- Department = <None>
- Specimen number = <None>
- Specimen date (D/M/Y) = <None>
- Specimen type = <None>
- Isolate number = <None>
- Organism = <None>
- Comment = <None>
- Antibiotic result 1 (Undefined) = <None>

[=]

Data fields in the original file

Select a sample data file

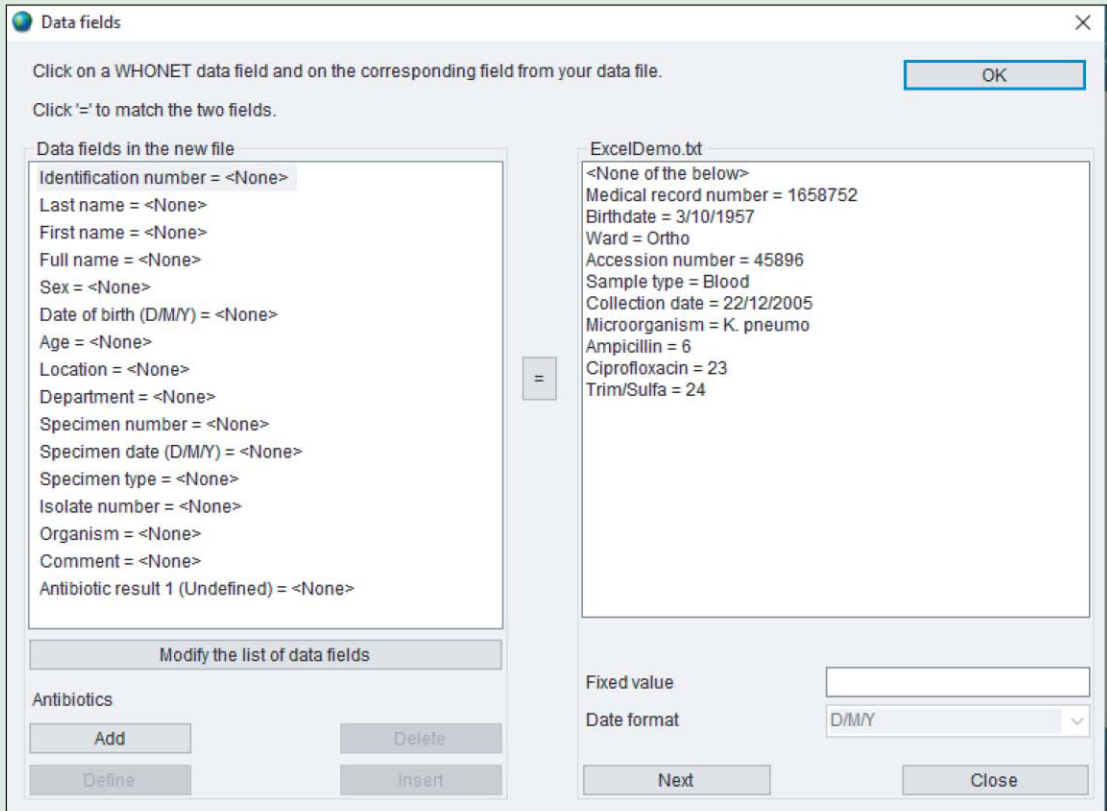
Modify the list of data fields

Antibiotics

Add [Delete]

Define [Insert]

You will now load your data file to the right side of the screen. Click on “Select a sample data file” and open the file “ExcelDemo.txt”. If you have followed all steps correctly up to this point, you should see the following. If you don’t, go back to the previous steps and make sure that you selected “Text, delimited” as the file format and “Tab” as the field delimiter. You should recognize that BacLink is displaying the first record of the data file on the right side of the screen. If you click “Next”, you will be able to see additional records.



You will now need to define the relationship between the WHONET fields and your data fields. To do this, click on a WHONET field on the left, and then click on the corresponding field on the right. After doing this, click the “=” sign in the middle. For example, click on “Identification number” on the left, “Medical record number” on the right, and “=”. Instead of clicking the “=” sign, you could alternatively double-click on “Medical record number” to establish the match.

Continue to do this for the following pairs:

Identification number = Medical record number

Date of birth (D/M/Y) = Date of birth

Location = Ward

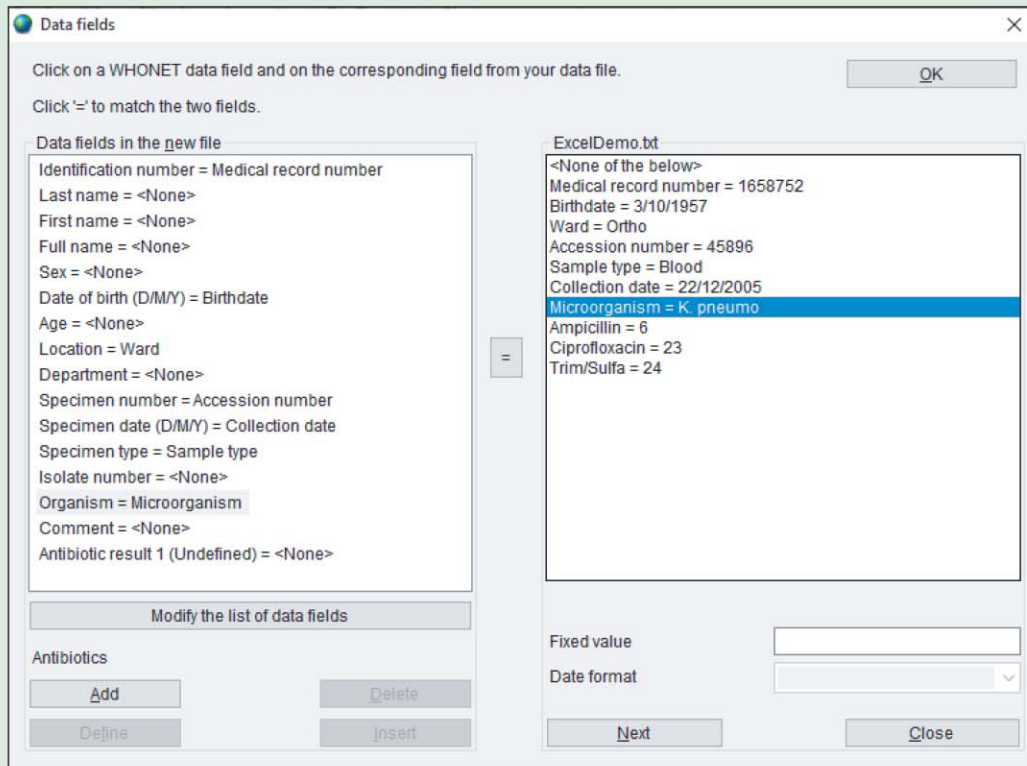
Specimen number = Accession number

Specimen date = Collection date

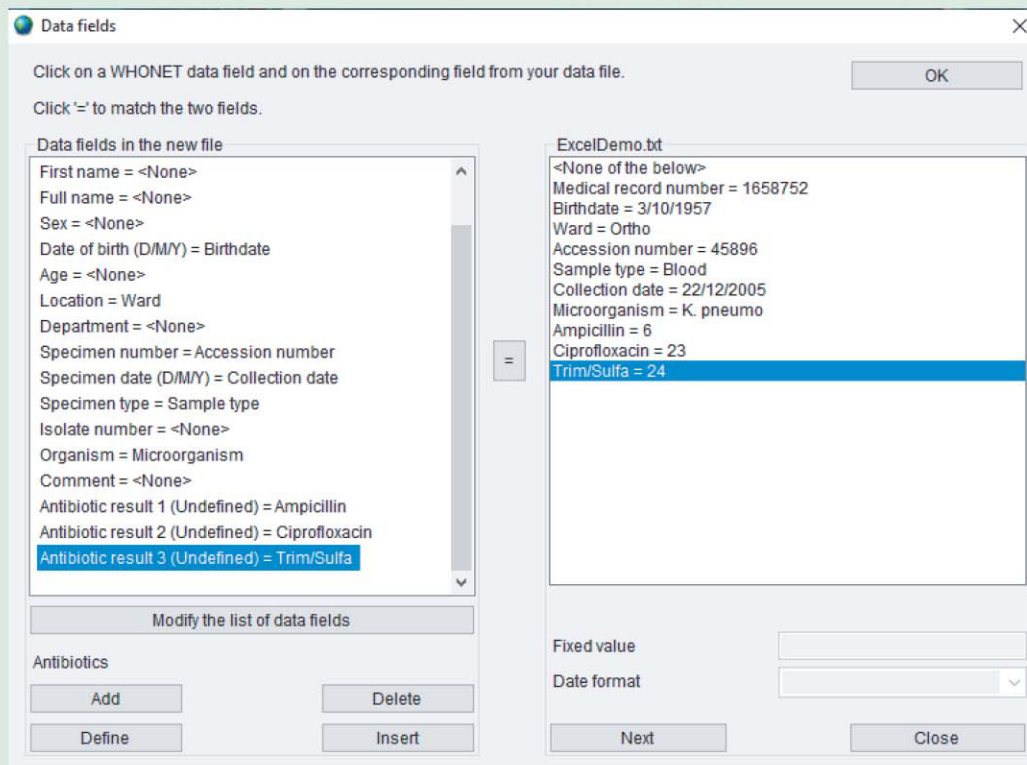
Specimen type = Specimen

Organism = Microorganism

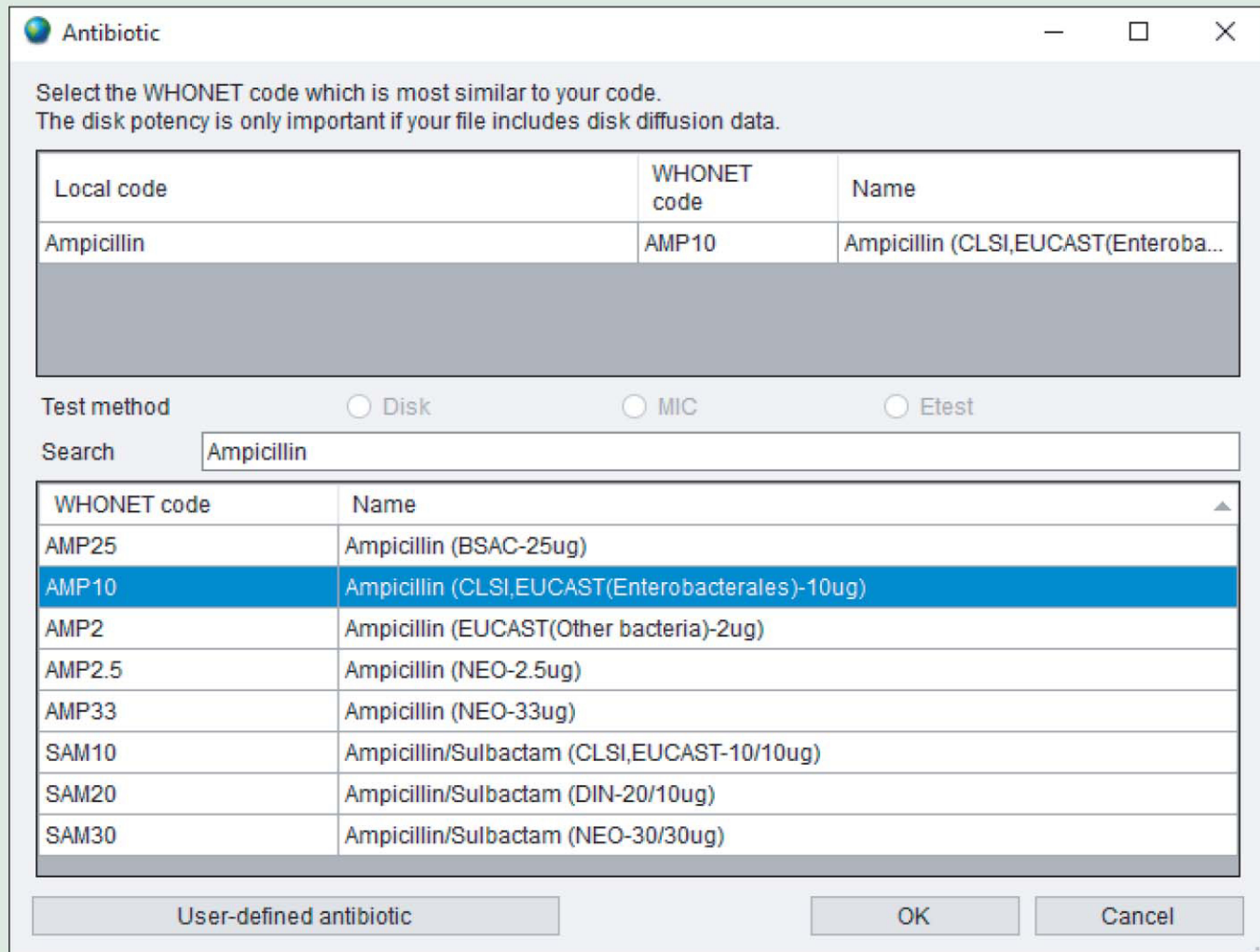
After matching the fields, your screen should look like the following. If you make a mistake, you can use the option “None of the below” to remove an incorrect match.



You will now match up the antibiotic fields. On the bottom of the left list, you will see an option for “Antibiotic result 1”. Since the sample data file has three antibiotics, click on “Add” twice. Then match up these three antibiotics with the three antibiotics on the right.



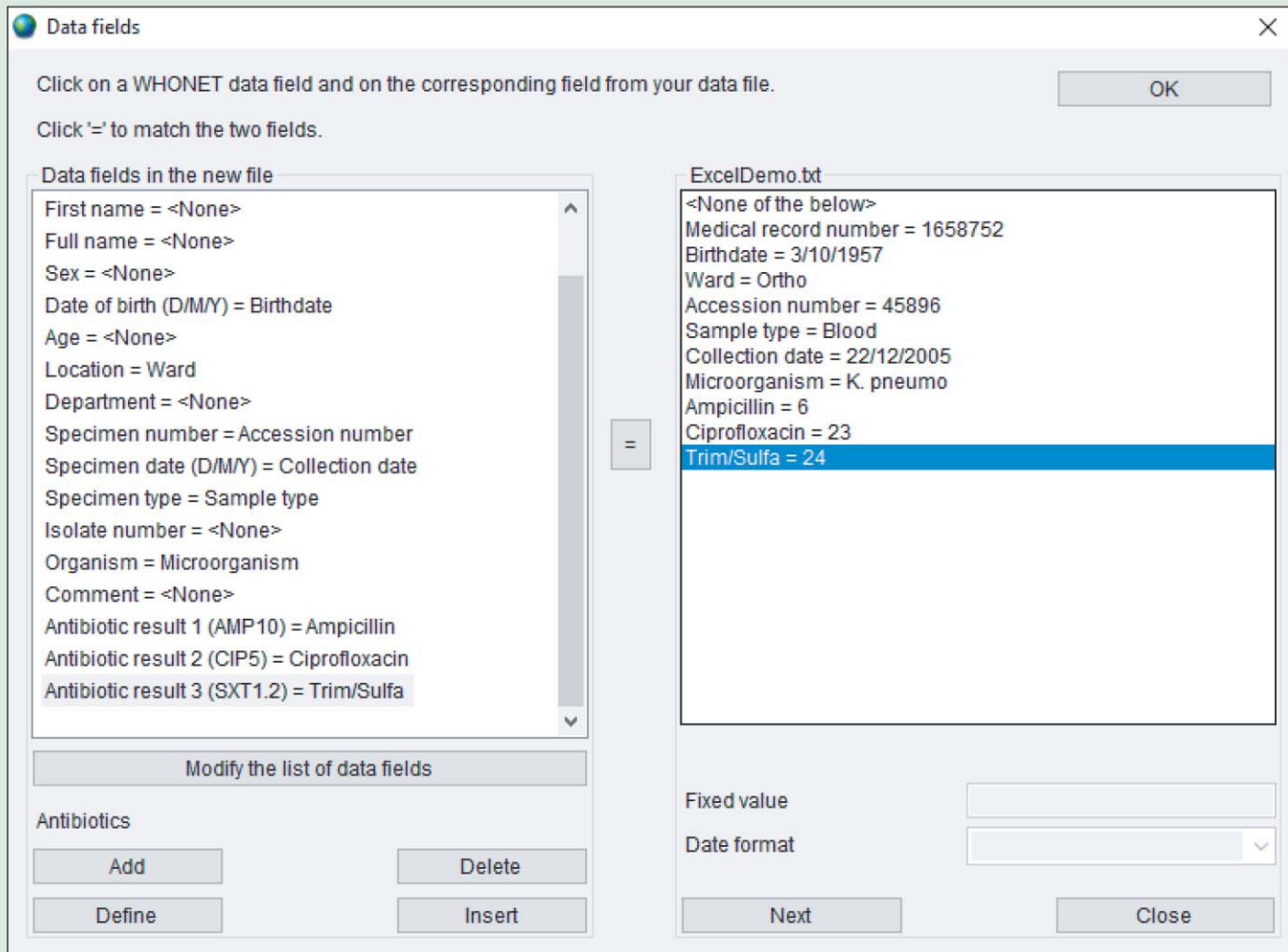
There is one final step. The antibiotics on the left are marked as “Undefined” because BaLink. To define the antibiotics, click on “Define” or double-click on the antibiotic. BaLink will show you a screen where you can define the antibiotics.



In the case of ampicillin, BaLink is suggesting a number of possible matches. Because the laboratory is using CLSI methods, the correct match for ampicillin is the first one given – “Ampicillin (CLSI, BSAC, SFM, DIN, SRGA-10ug)”. If you are doing disk diffusion testing, it is very important to choose the item with the correct disk potency. If you are only doing MIC tests and Etests, then it actually does not matter which of the “ampicillins” you choose.

After you select the correct ampicillin, click on “OK”. Proceed to define the other two antibiotics as well. When you finish, your screen should look like the below.

There is one final step. The antibiotics on the left are marked as “Undefined” because BacLink. To define the antibiotics, click on “Define” or double-click on the antibiotic. BacLink will show you a screen where you can define the antibiotics.

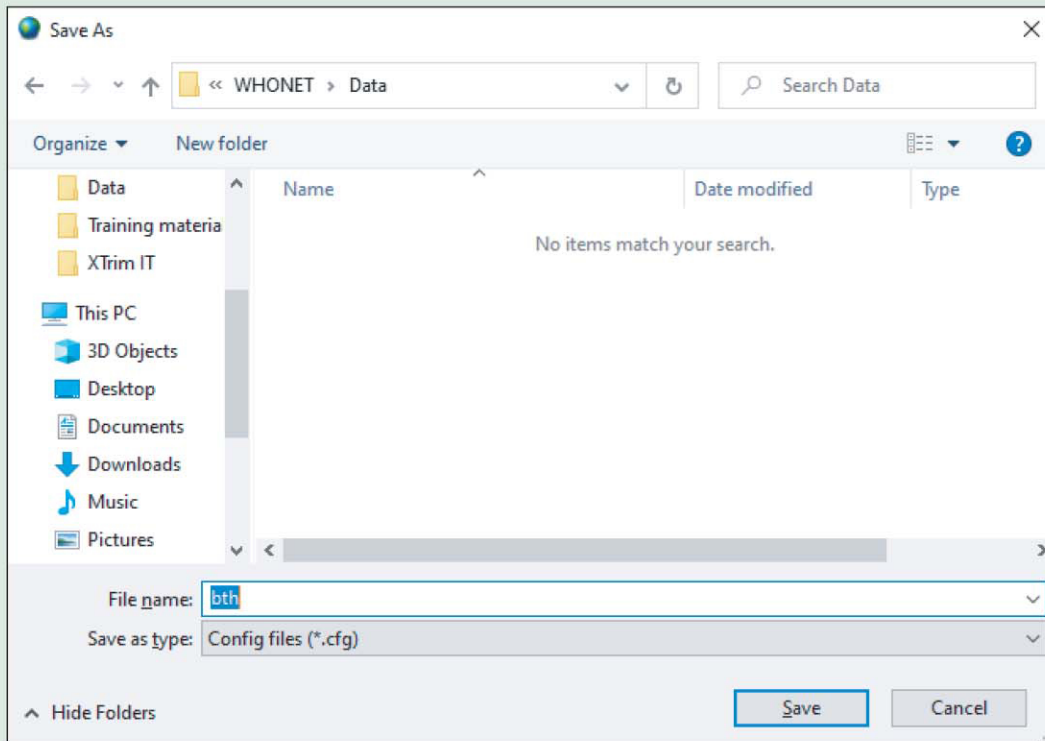


You have now completed all of the required configuration steps. Click on “OK” to return to the file format configuration screen, and “OK” again to return to the main configuration screen.

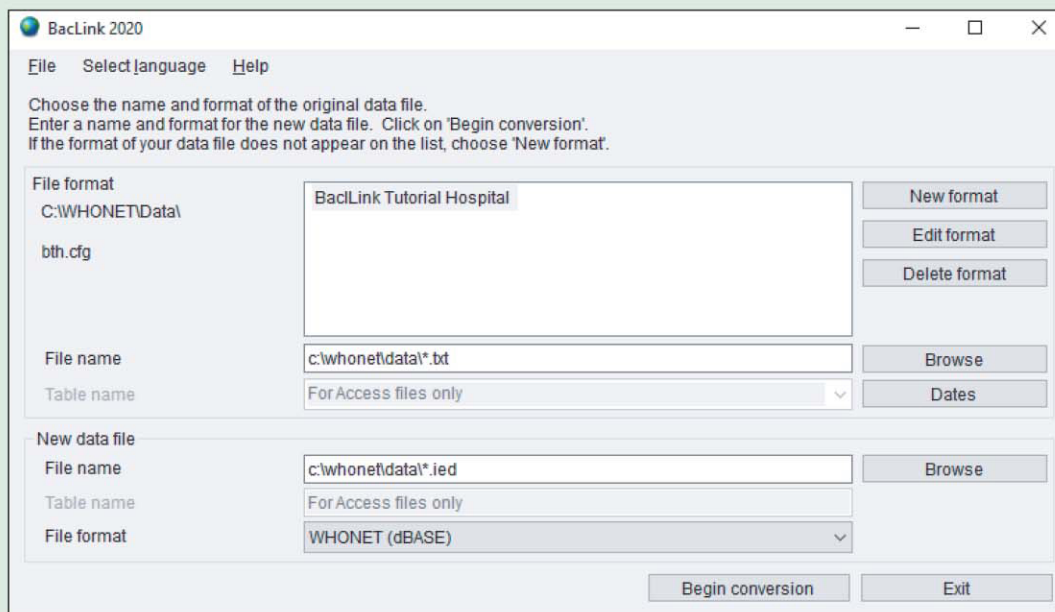
Configuration – Saving the configuration

You should now save all of the work you have been doing in configuration. Click on “Save”. Give a name to the new BacLink configuration, for example: bth.cfg

The filename should end in “.cfg”, but if you do not do this, there is no problem. BacLink will automatically add “.cfg” to the filename that you give.



Then click on “Exit” to leave the configuration area. The new configuration will appear on your list of BacLink file formats: “BacLink Tutorial Hospital” with a filename of bth.cfg.

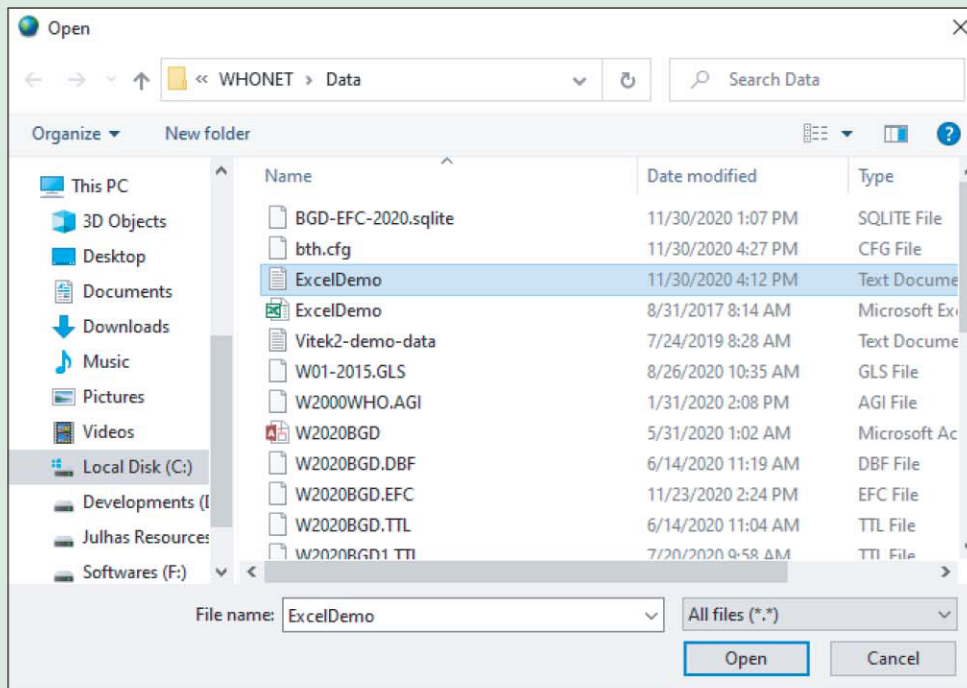


PART 5. RUNNING THE CONVERSION

In Part 4, you configured the import of the sample file. You will now see how to convert the text file to a WHONET file with this new configuration. You will also see how to check whether the configuration is working and define any of your local data codes that WHONET doesn’t recognize.

Starting the conversion

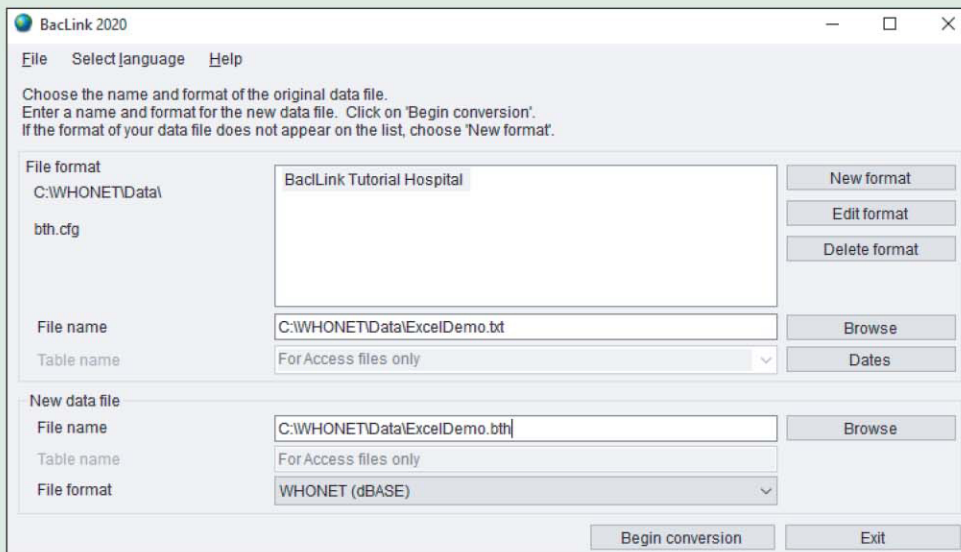
Original data file: Click on the File format for “BacLink Tutorial Hospital” that you configured in the previous step. In the upper box called “File name” click on “Browse” to select the file “ExcelDemo.txt”.



New data file

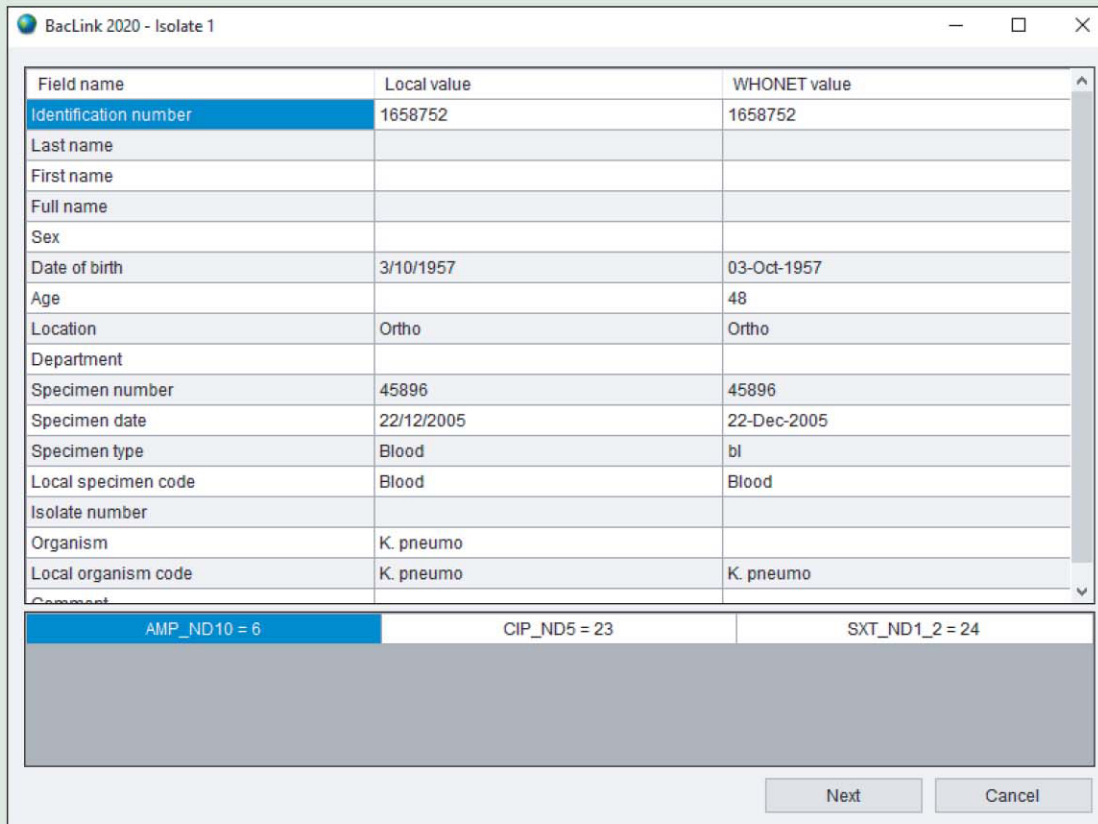
In the lower box, you need to indicate the name of the new WHONET file that you are about to create. For this tutorial, give the file the name: “ExcelDemo.bth”. You can give the new file any name that you like, but it will be convenient for your data file management if all of your data files end with the three-letter code that you gave to your laboratory, in this tutorial “bth”.

If you did these steps properly, your screen should look like the following.



Inspecting the conversion

Click on “Begin conversion”. BacLink will display for you results from the conversion of the first three isolates in the original data file. The purpose is to allow you to visually inspect the accuracy of the conversion. On the below screen, you see results from the first isolate. First focus on the middle column to see whether BacLink is reading the data values correctly, and check the final column to see whether BacLink is converting the data values correctly.



Field name	Local value	WHONET value
Identification number	1658752	1658752
Last name		
First name		
Full name		
Sex		
Date of birth	3/10/1957	03-Oct-1957
Age		48
Location	Ortho	Ortho
Department		
Specimen number	45896	45896
Specimen date	22/12/2005	22-Dec-2005
Specimen type	Blood	bl
Local specimen code	Blood	Blood
Isolate number		
Organism	K. pneumo	
Local organism code	K. pneumo	K. pneumo
Comment		
AMP_ND10 = 6	CIP_ND5 = 23	SXT_ND1_2 = 24

Next Cancel

For this first isolate, there seems to be no problem with Identification number, Location, Date of birth, and Specimen number. There also appears to be no problem with Specimen date – you should always check the reformatting of the date to ensure that you have selected the correct date format (D/M/Y, M/D/Y, MMDDYYYY, Y-M-D, etc.). You will also notice that BacLink calculates the patient’s age using the date of birth and specimen date fields.

For Organism, you will notice that there are two similar rows: “Organism” and “Local organism code”. The first of these is intended for the WHONET organism code, while the second is intended to save the original organism code from your data file without modification. Since you have not yet defined the correspondence between your local code and the WHONET code, the first of these two rows is blank. The situation with Specimen type is similar. In the row “Specimen type”, BacLink leaves the WHONET field blank because it does not know what the corresponding WHONET code is for “Blood”. In the row “Local specimen code”, the original entry is copied over. Finally, in the lower box, you will see that BacLink was able to transfer the antibiotic results correctly.

So from this first record, we can conclude that BaLink is reading the data file correctly, and is saving most of the information into the new WHONET file accurately. However, BaLink has difficulty with the organism and specimen type fields because the codes have not yet been defined. If you think you may have made a mistake in your configuration, click “Cancel” and return to “Edit format” to make the correction. Otherwise, click on “Next” to proceed with the second isolate.

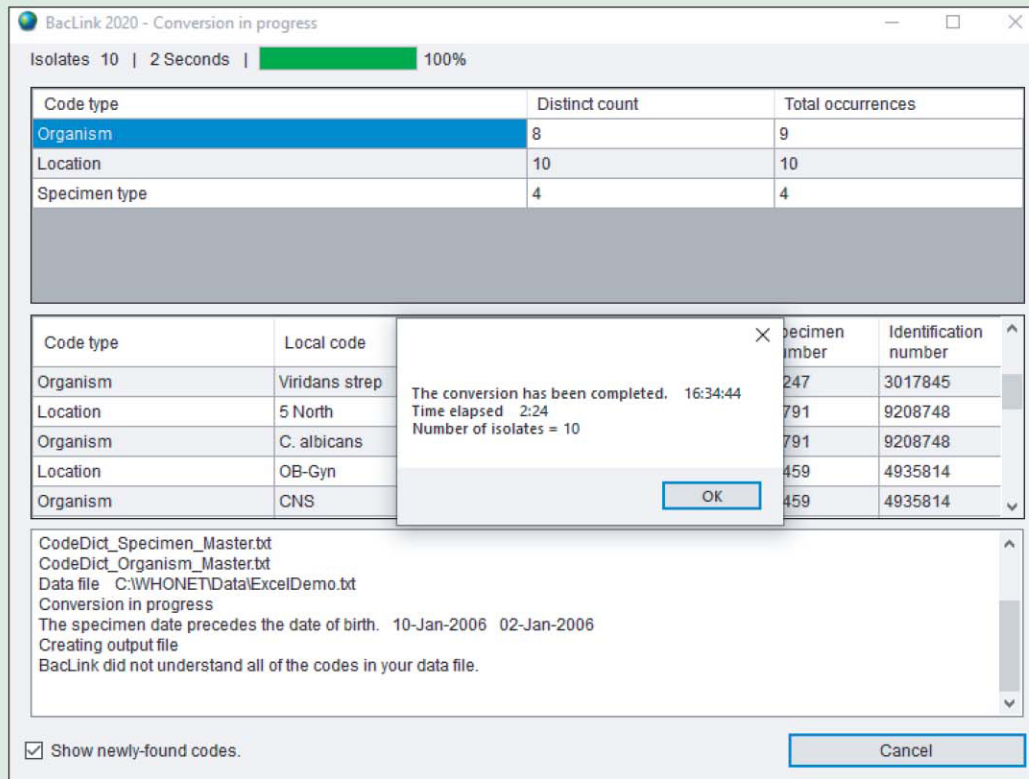
In the second isolate, you will notice a small problem that did not appear with the first isolate. The location code “Medicine 1” has been abridged to “medici”. This is because the default length of the location field is 6 characters. This will be easy to fix later by changing the field length to a larger value.

Isolates			
	Field name	ExcelDemo.txt	ExcelDemo.bth
	Identification number	4689314	4689314
	Last name		
	First name		
	Full name		
	Sex		
	Date of birth	15/3/1980	15-Mar-1980
	Age		25
▶	Location	Medicine1	medici
	Department		
	Specimen number	32047	32047
	Specimen date	7/1/2006	07-Jan-2006
	Specimen type	Urine	
	Local specimen code	Urine	Urine
	Organism	S. aureus	
	Local organism code	S. aureus	S. aureus

Antibiotics	
AMP_ND10	22
CIP_ND5	10
SXT_ND1_2	18

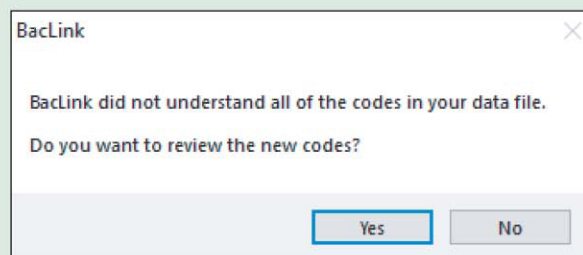
Click on “Next” to see the third isolate, and then “Next” again. BaLink will now proceed to finish the conversion of the rest of the data file. BaLink will tell you how many isolates it converted – 10 isolates in this tutorial. Click on “OK” to continue.

You do not need to enter an exhaustive list. Just indicate the most common or important responses for purposes of standardizing data entry.

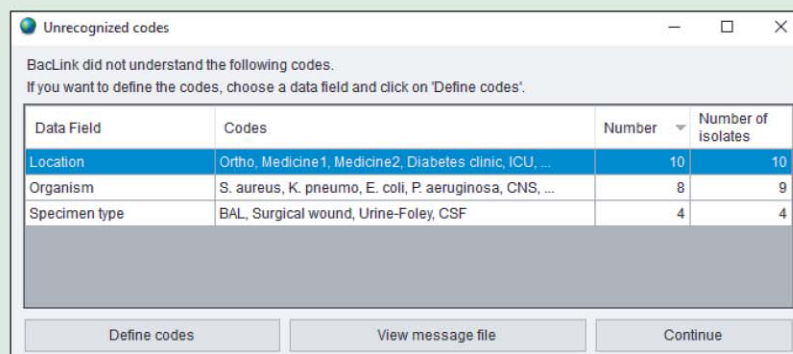


Defining unrecognized codes

When the conversion is finished, BacLink may alert you that it encountered some codes that it did not recognize. In this tutorial, you should see the below message. Click “Yes”.



BacLink will show you a summary of all of the different codes that it did not recognize, as in the below screen.



In this tutorial, BacLink indicates that there are unrecognized locations, organisms, and specimen types. We won't worry about the locations at this point until the problem with the field lengths is fixed (from six characters to a larger value).

Click on the row "Organism". Now click on "Define codes" to see the following screen with a list of all of the unrecognized organism codes/text.

Local organism code	WHONET code	Name
K. pneumo	kpn	Klebsiella pneumoniae

Search: K pneumo

WHONET code	Name
kpn	Klebsiella pneumoniae
koz	Klebsiella pneumoniae ss. ozaenae
kpn	Klebsiella pneumoniae ss. pneumoniae
kpn	Klebsiella pneumoniae ss. rhinoscleromatis

MRSA: [dropdown]
 VRE: [dropdown]
 Beta-lactamase: [dropdown]
 ESBL: [dropdown]

Inducible clindamycin resistance: [dropdown]
 Carbapenemase: [dropdown]
 BLNAR H. influenzae: [dropdown]
 AmpC production: [dropdown]

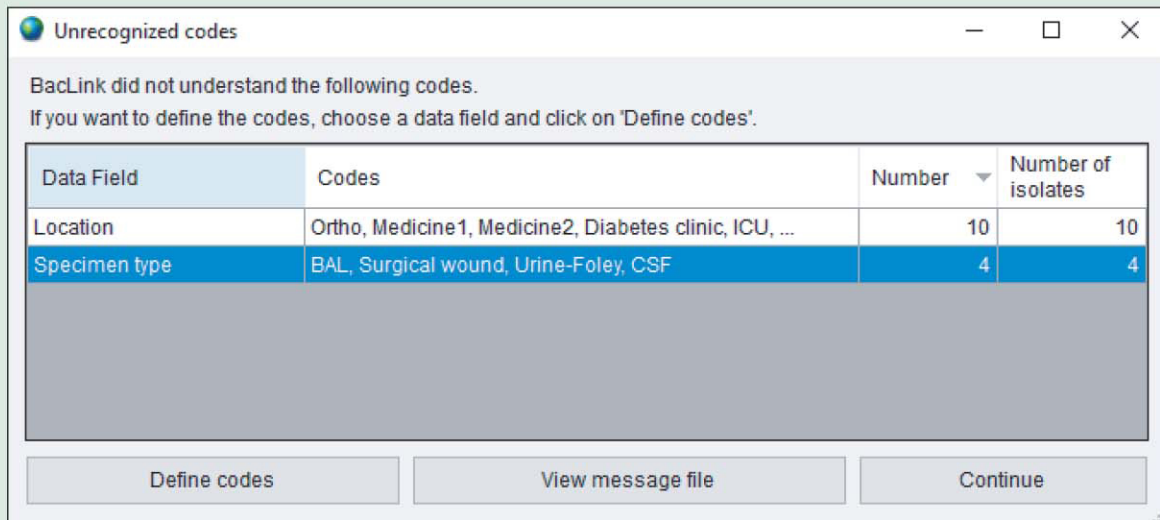
OK Cancel

Click on the first organism "K pneumo" and "Define code". BacLink will now suggest a number of possible matches for this organism. If you see the correct match, click on the organism and click "OK".

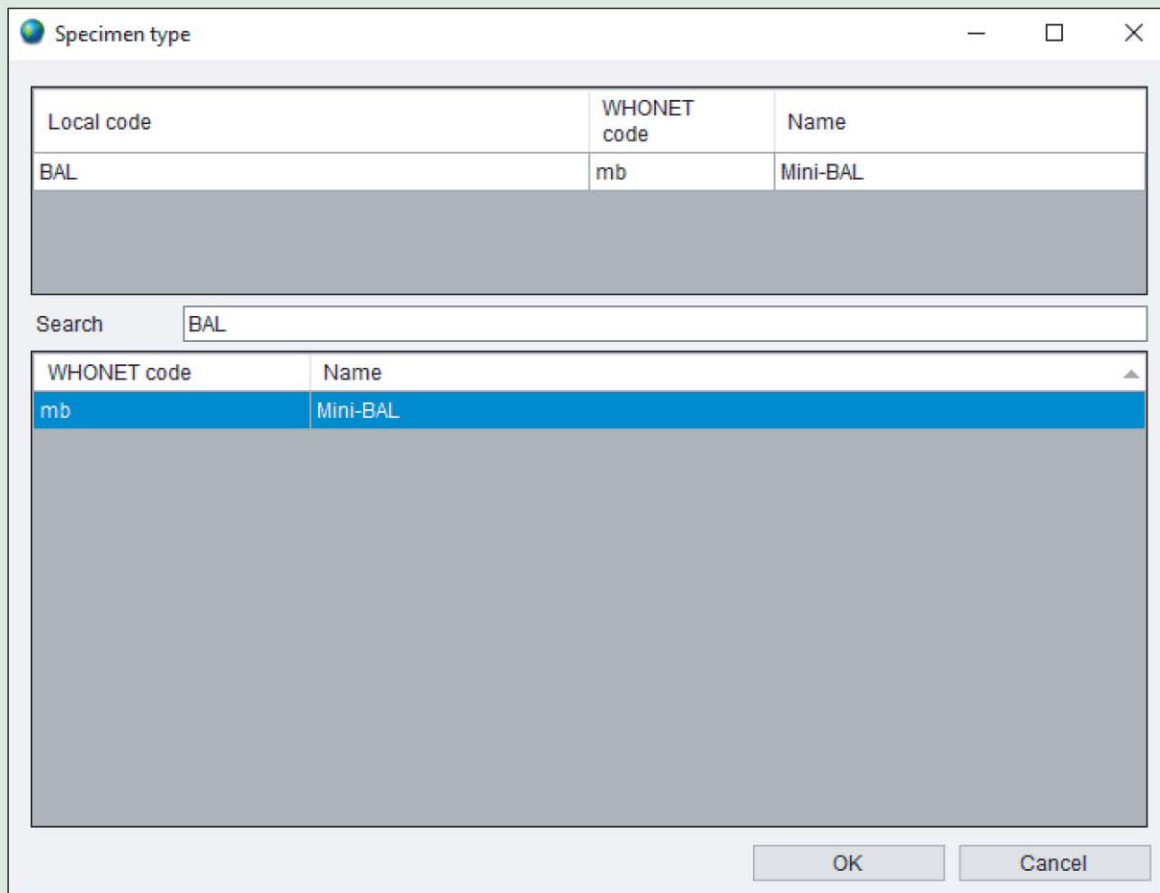
If you do not see the organism listed, then use the search box to look for the correct organism. For example, instead of "CNS" or "Coagulase-negative staphylococci", WHONET has an entry "Staphylococcus, coagulase-negative". To search for an organism, type one or more letters of the genus name and one or more letters of the species name, for example type "Staph coag" to find possible matches for "CNS". For "GC", you should do a search for something similar to "Neiss gon".

After you match the first organism, continue to match all of the rest of the organisms. If you cannot find an appropriate match, you can call the organism "Other" or you can leave it undefined. Then click, "OK" to return to the list with the other undefined codes. You will see that the organism row has disappeared because all of the organisms have been defined.

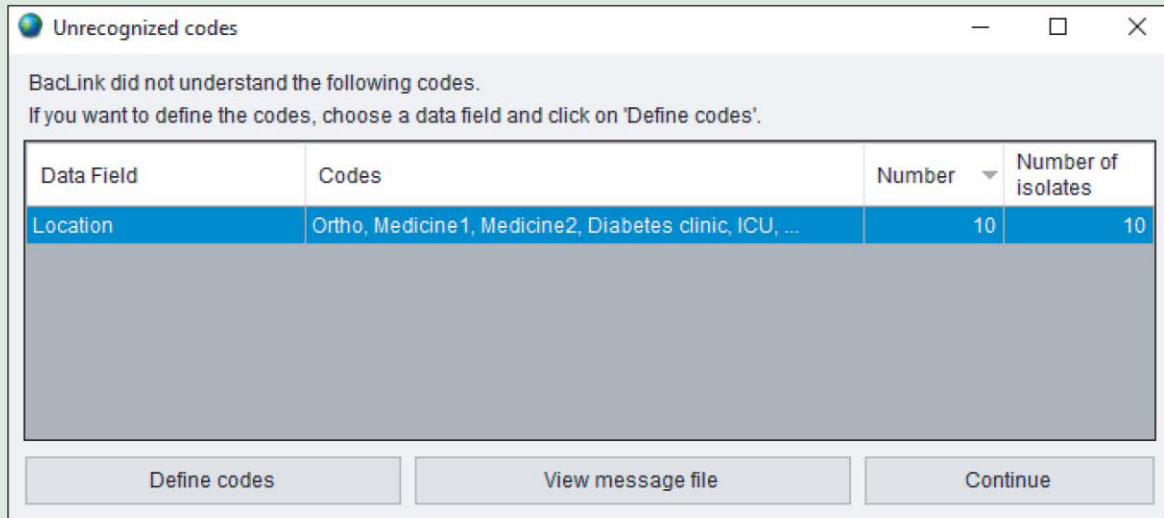
Note: If you have a very long list of codes, there is no need to define all of them. Begin with the most common or important ones. If you do not define a code, WHONET will leave the corresponding WHONET field blank, but will still save the original organism code in the column "Local organism code".



Click on the row for “Specimen type” and “Define codes”.



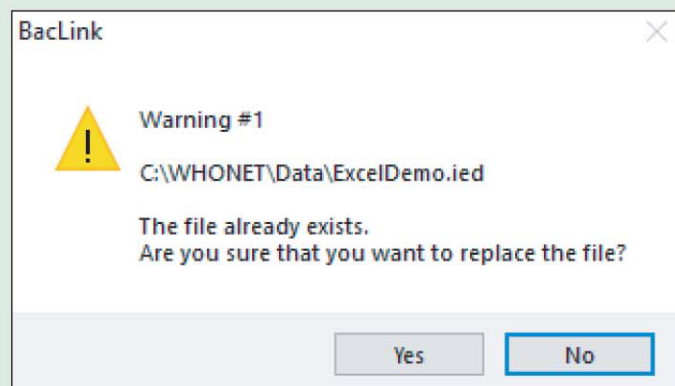
Define the specimen types one at a time, finding the closest match on the WHONET list. When you finish matching the specimen types, click “OK” to return to the remaining list of unrecognized codes.



Since we will define the locations later, click “Continue”. BacLink then warns that you have defined some additional codes that were not included during the conversion. Click “OK” to return to the main BacLink screen.

Running the conversion again...

Now that you have matched some of your codes with the appropriate WHONET codes, run the conversion again. Click on “Begin conversion”. BacLink will give you a warning (Warning #1) that the WHONET file that you want to create already exists, and asks whether you want to replace it. Answer “Yes”, since the first time was just an initial test.



BacLink will then ask again (Warning #2) just to make sure that you read the question. Answer “Yes” again.

You will now see the first isolate again, but this time with the appropriate WHONET organism and specimen type codes indicated. So this conversion is more complete than during your first attempt.

BacLink 2020 - Isolate 1

Field name	Local value	WHONET value
Identification number	1658752	1658752
Last name		
First name		
Full name		
Sex		
Date of birth	3/10/1957	03-Oct-1957
Age		48
Location	Ortho	Ortho
Department		
Specimen number	45896	45896
Specimen date	22/12/2005	22-Dec-2005
Specimen type	Blood	bl
Local specimen code	Blood	Blood
Isolate number		
Organism	K. pneumo	kpn
Local organism code	K. pneumo	K. pneumo
Comment		

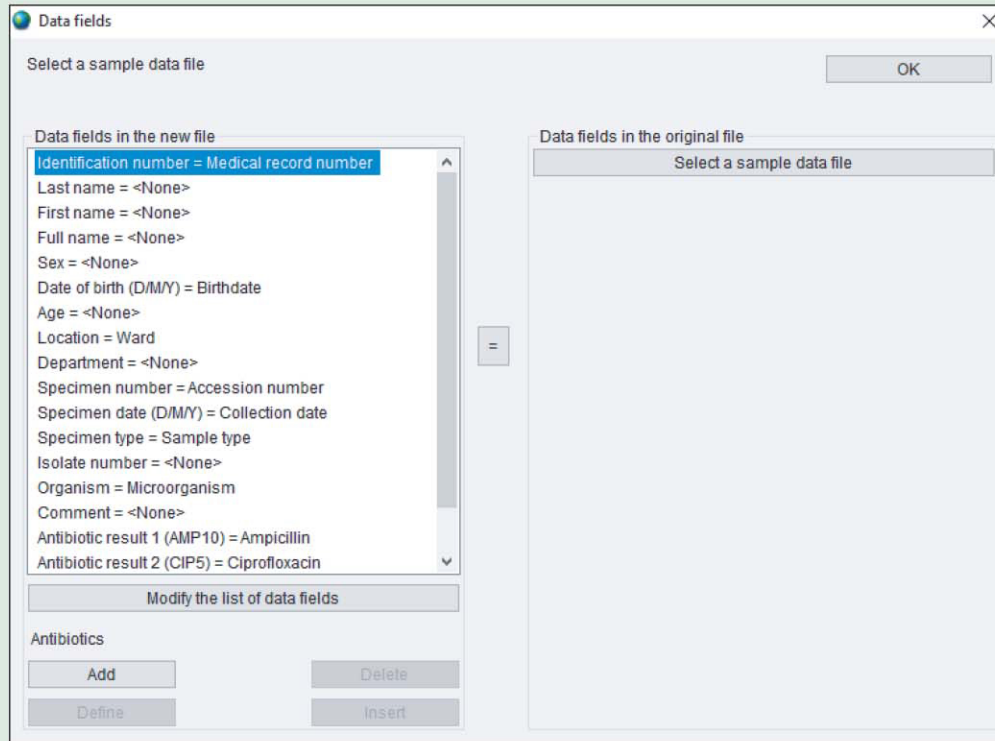
AMP_ND10 = 6	CIP_ND5 = 23	SXT_ND1_2 = 24
--------------	--------------	----------------

Next Cancel

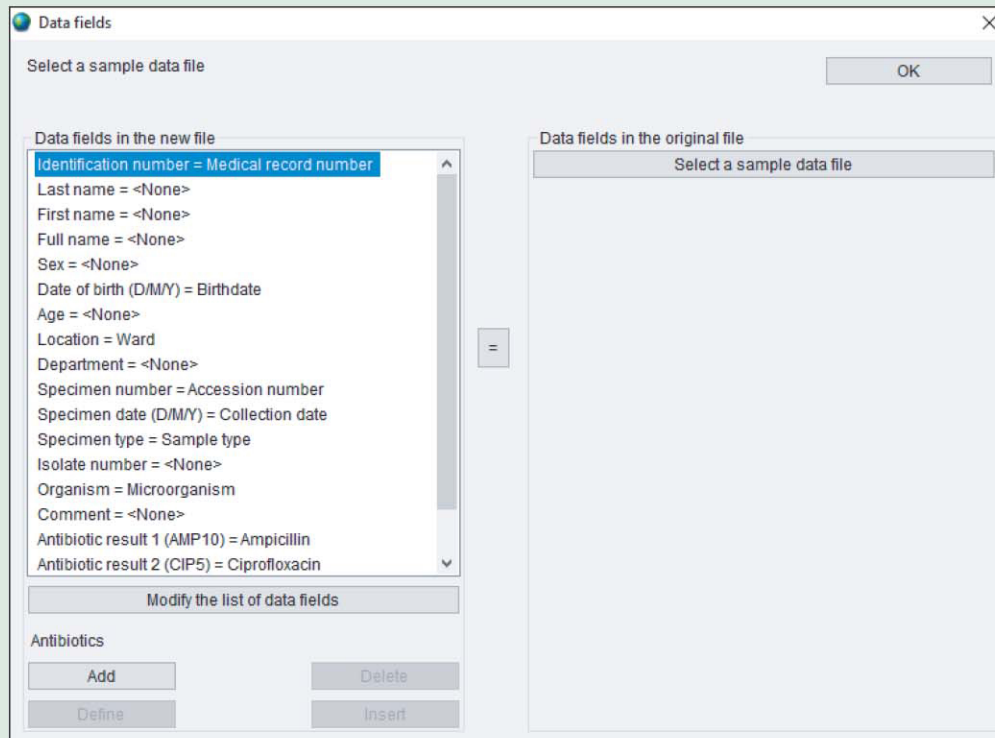
Click “Next isolate”, and you will see that the problem with the length of the location code field still persists (“medici” instead of “medicine 1”). Click “Next” and “Next” again to finish the conversion. BacLink indicates that it converted ten isolates. Click “OK”, and answer “Yes” to the question about the unrecognized codes. This time, you will see that the list of unrecognized codes is much shorter than before. Only the locations remain to be defined. Click on “Continue” to return to the main BacLink screen.

Editing the configuration

The conversion is working in most respects with the exception of the location codes which are being shortened to six characters. This is easy to fix. Click on “Edit format” from the main BacLink screen to return to the configuration part of BacLink. Click on “File format” and “Data fields”. This will return you to the screen in which you defined the matches between the fields in the Excel data file and in WHONET.



Click on “Modify the list of data fields”. You will see the following screen. From this screen, you can configure the current fields, add additional ones to the list, and delete fields that you do not need. Click on the option “Location”. On the right side of the screen, you will see that this length of this field is set to 6 characters. Change this to 20.



Then click “OK”, “OK”, “OK”, “Save”, and “Exit”. This should return you to the main BacLink screen.

Running the conversion again...

Click on “Begin conversion”. Answer “Yes” and “Yes” again to replace the current WHONET file. BacLink will show you the first isolate, but this is unchanged from before. Click on “Next’ to see the second isolate. You will now notice that the location “Medicine 1” is being correctly being saved as “medicine 1”.

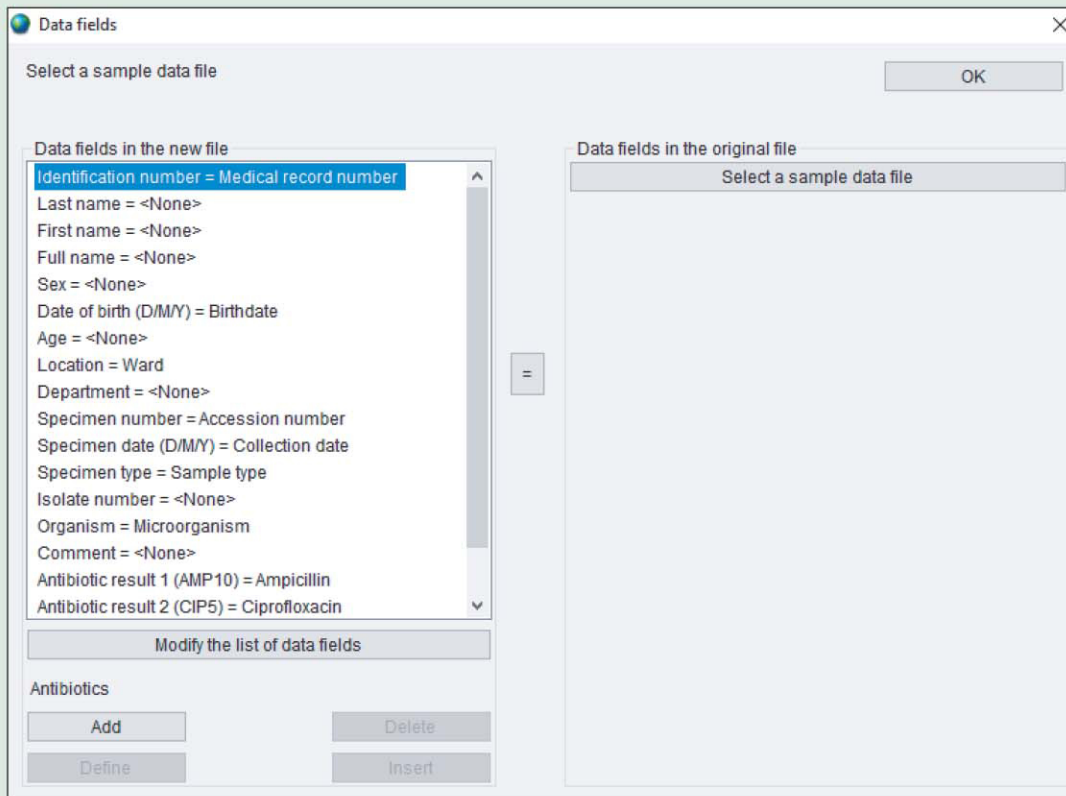
The screenshot shows a window titled "BacLink 2020 - Isolate 2" with a table comparing local and WHONET values. The table has three columns: Field name, Local value, and WHONET value. The "Identification number" field is highlighted in blue. Below the table, there are three fields: AMP_ND10 = 22, CIP_ND5 = 10, and SXT_ND1_2 = 18. At the bottom right, there are "Next" and "Cancel" buttons.

Field name	Local value	WHONET value
Identification number	4689314	4689314
Last name		
First name		
Full name		
Sex		
Date of birth	15/3/1980	15-Mar-1980
Age		25
Location	Medicine1	Medicine1
Department		
Specimen number	32047	32047
Specimen date	7/1/2006	07-Jan-2006
Specimen type	Urine	ur
Local specimen code	Urine	Urine
Isolate number		
Organism	S. aureus	sau
Local organism code	S. aureus	S. aureus
Comment		

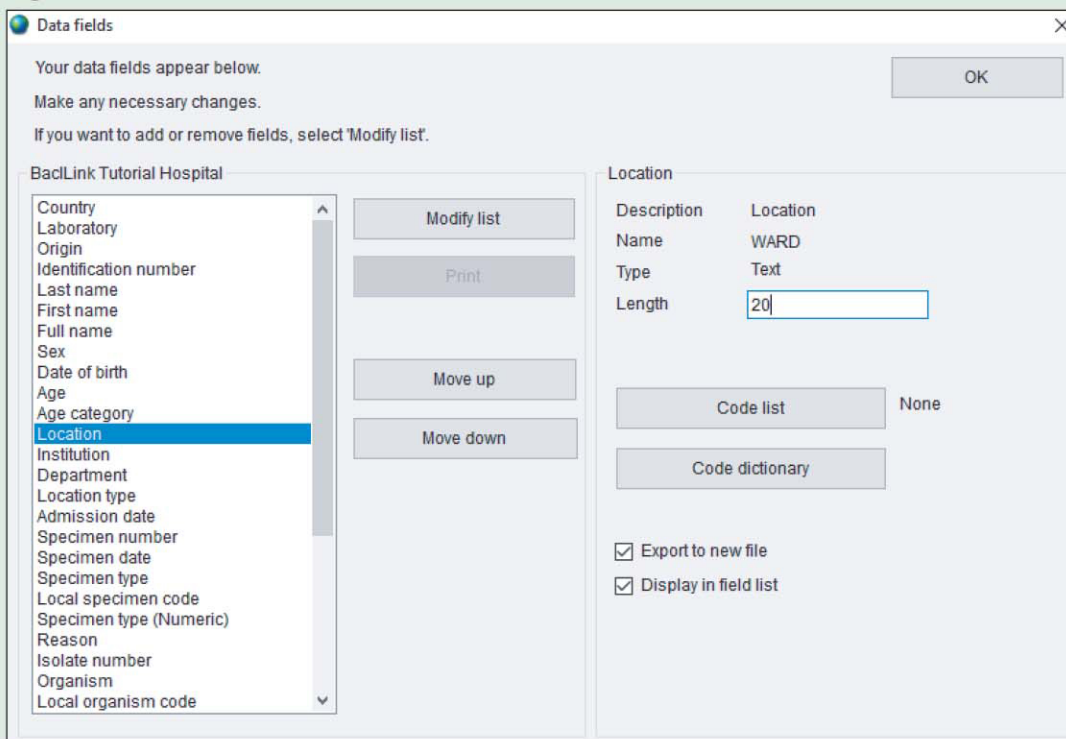
AMP_ND10 = 22 CIP_ND5 = 10 SXT_ND1_2 = 18

Next Cancel

Then continue with the rest of the conversion until you see the list of unrecognized codes. Click on “Location” and “Define codes”.



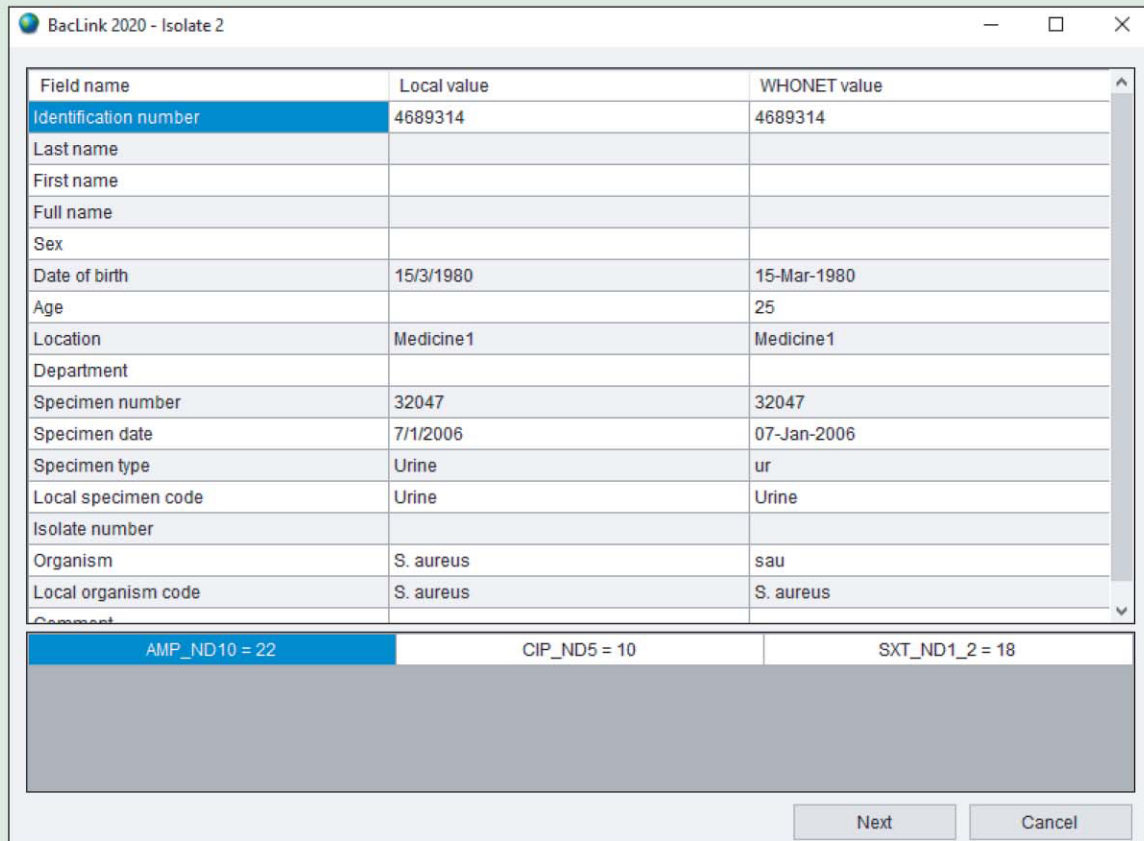
Click on “Modify the list of data fields”. You will see the following screen. From this screen, you can configure the current fields, add additional ones to the list, and delete fields that you do not need. Click on the option “Location”. On the right side of the screen, you will see that this length of this field is set to 6 characters. Change this to 20.



Then click “OK”, “OK”, “OK”, “Save”, and “Exit”. This should return you to the main BacLink screen.

Running the conversion again...

Click on “Begin conversion”. Answer “Yes” and “Yes” again to replace the current WHONET file. BacLink will show you the first isolate, but this is unchanged from before. Click on “Next’ to see the second isolate. You will now notice that the location “Medicine 1” is being correctly being saved as “medicine 1”.



The screenshot shows a window titled "BacLink 2020 - Isolate 2" with a table comparing local and WHONET values. The table has three columns: "Field name", "Local value", and "WHONET value". The "Identification number" field is highlighted in blue. Below the table, there are three buttons: "Next" and "Cancel".

Field name	Local value	WHONET value
Identification number	4689314	4689314
Last name		
First name		
Full name		
Sex		
Date of birth	15/3/1980	15-Mar-1980
Age		25
Location	Medicine1	Medicine1
Department		
Specimen number	32047	32047
Specimen date	7/1/2006	07-Jan-2006
Specimen type	Urine	ur
Local specimen code	Urine	Urine
Isolate number		
Organism	S. aureus	sau
Local organism code	S. aureus	S. aureus
Comment		

AMP_ND10 = 22 CIP_ND5 = 10 SXT_ND1_2 = 18

Next Cancel

Then continue with the rest of the conversion until you see the list of unrecognized codes. Click on “Location” and “Define codes”.

BacLink did not understand the following codes.
Click on a code and select 'Define code'.

Location

- 5 North
- Diabetes clinic
- ER
- HC5
- ICU
- Medicine1
- Medicine2
- NICU
- OB-Gyn
- Ortho

Define code

View code list

View code dictionary

Save list

Print

OK

For the first item on the list, click on “Define code” to get the following screen.

Local code: 5 North

WHONET code: 5 north

Institution: bth bth BacLink Tutorial Hosp: ▾

Department: ▾

Location type: ▾

OK Cancel

You will notice that defining location codes is different from defining organism, specimen, and antibiotic codes. For the latter three, WHONET has a standard list of codes used by all laboratories with WHONET. For location codes, WHONET simply uses the same code that your laboratory uses.

Defining your location codes serves a different purposes – it allows you to describe the details about the location to BacLink, for example which department/specialty, whether the location is in an inpatient or outpatient area, etc

For the first location, “5 North”, choose a department of “med=Medicine” and a location type of “inx = Inpatient (non-ICU)”. Then click “OK”.

Continue defining the other location codes in the manner using the following suggestions:

Location	Institution	Department	Location type
Diabetes clinic	bth	med	out
ER	bth	eme	eme
HC5	oth	out	out
ICU	bth	icu	icu
Medicine 1	bth	med	inx
Medicine 2	bth	med	inx
NICU	bth	neo	icu
OB-Gyn	bth	obg	inx
Ortho	bth	sur	in

In this example, HC5 represents a “Health Center #5”, an outpatient clinic outside the hospital.

Defining locations has two important benefits: 1. at the local level, hospital staff will be able to analyze easily data at the level of the ward, department, or inpatient/outpatient status, even if the original data file only had the ward information; and 2. at the national level, defining the location codes permits standardization for purposes of national comparisons and analyses.

After defining all of the location codes, return to the main BaLink screen.

Running the conversion again... for the last time!

Click on “Begin conversion”, and replace the previous WHONET file. Look at the conversion for the first isolate. You will notice that for the location “Ortho”, BaLink is now putting the department equal to “sur=Surgery” because of the location matchings you defined in the previous step.

Field name	ExcelDemo.txt	ExcelDemo.bth
Identification number	1658752	1658752
Last name		
First name		
Full name		
Sex		
Date of birth	3/10/1957	03-Oct-1957
Age		48
Location	Ortho	ortho
Department		sur
Specimen number	45896	45896
Specimen date	22/12/2005	22-Dec-2005
Specimen type	Blood	bl
Local specimen code	Blood	Blood
Organism	K. pneumo	kpn
Local organism code	K. pneumo	K. pneumo

Antibiotics	
AMP_ND10	6
CIP_ND5	23
SXT_ND1_2	24

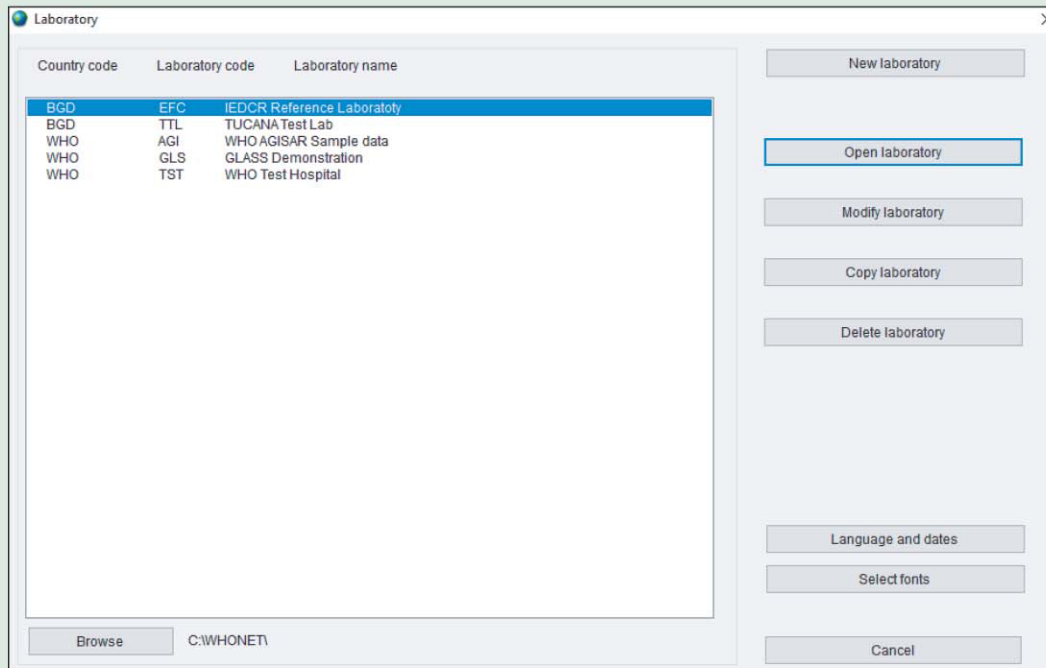
Then click “Next” and finish the rest of the conversion. When the conversion is finished, BaLink will return you immediately to the main BaLink screen because all of the undefined codes have now been defined.

Congratulations! You have successfully finished a BaLink configuration, defined all of the codes needed by WHONET, and converted a sample data file (ExcelDemo.xls) to WHONET format (ExcelDemo.bth). You can then proceed to WHONET to analyze this file. Click on “Exit” to leave BaLink.

The configuration that you made will be useful for any file that has this same structure. For example, if use your January data file to define your BaLink configuration and codes matches, you can use the same configuration to convert your February, March, etc. data. If BaLink encounters some new codes in the following months, you can define them as they arise over time.

PART 6. GETTING STARTED WITH WHONET

Now that you have created a valid WHONET file using BaLink, you can proceed to WHONET. Double-click on your WHONET icon to begin WHONET.

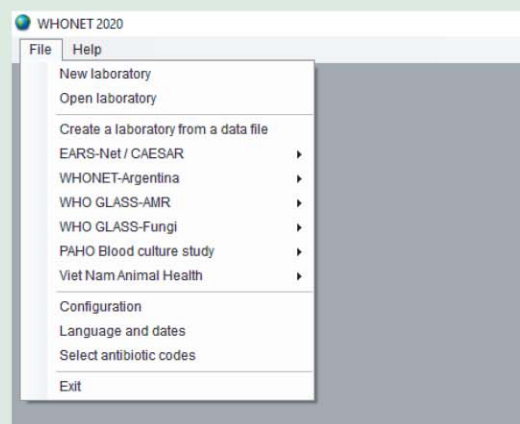


You will notice that the “BacLink Tutorial Hospital” that we are using in this tutorial does not yet appear on the WHONET list of laboratories. Before you can begin analyzing the sample data file, you will need to create a laboratory configuration

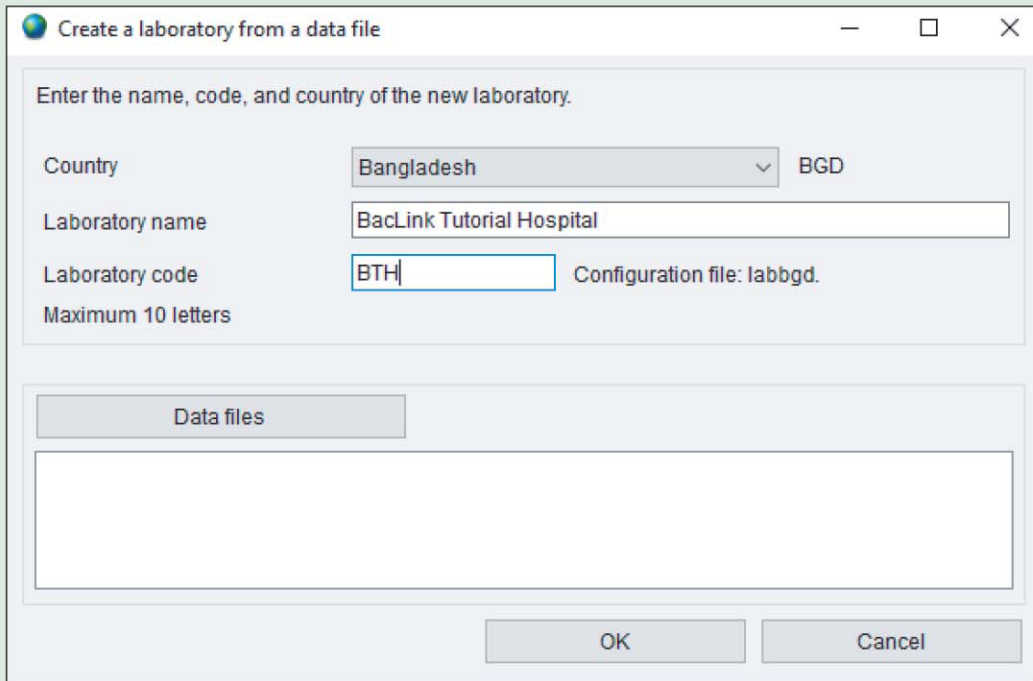
Creating a laboratory configuration

To create a WHONET laboratory configuration, one option would be to use the “New laboratory” option on this screen. You would need to enter the laboratory name and code, the list of antibiotics, locations, etc. But fortunately, there is a faster way.

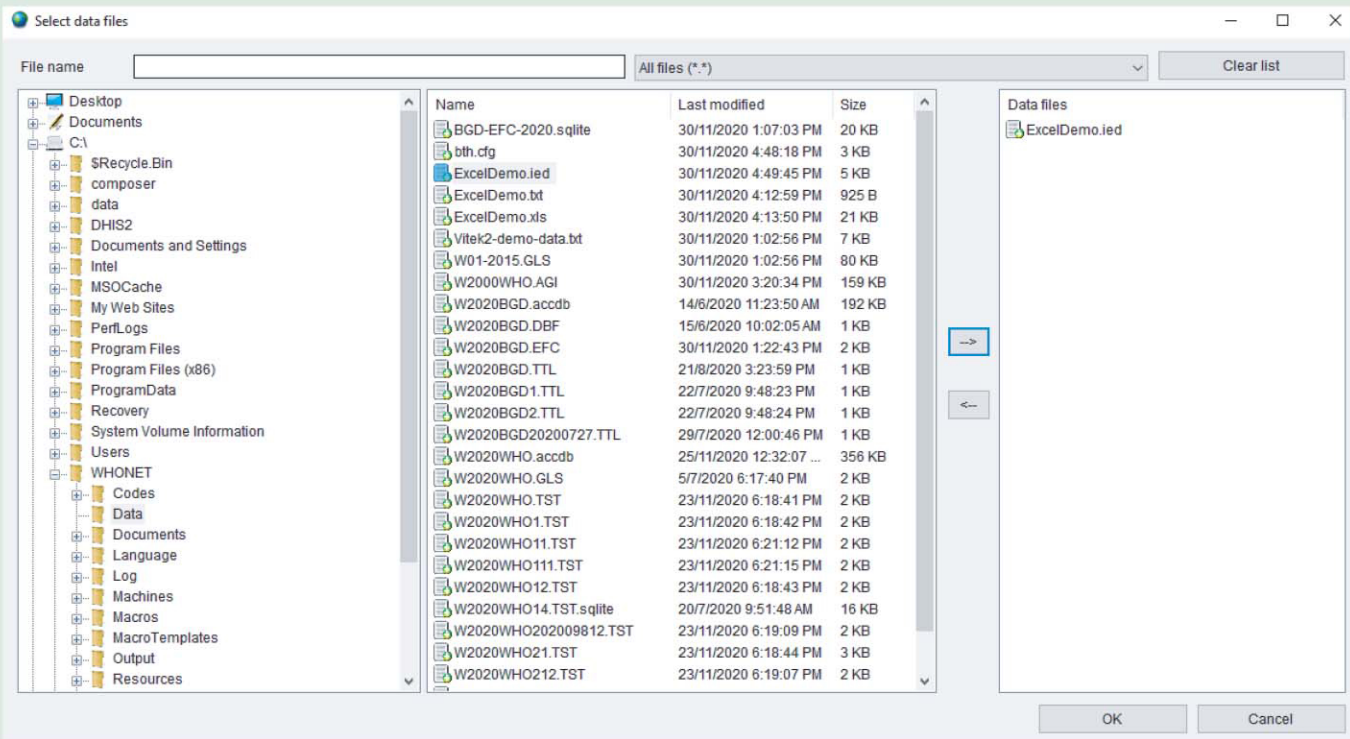
Click on “Cancel” to go to the main WHONET menu. Click on “File”. You will notice an option called “Create a laboratory from a data file”. Click on this option



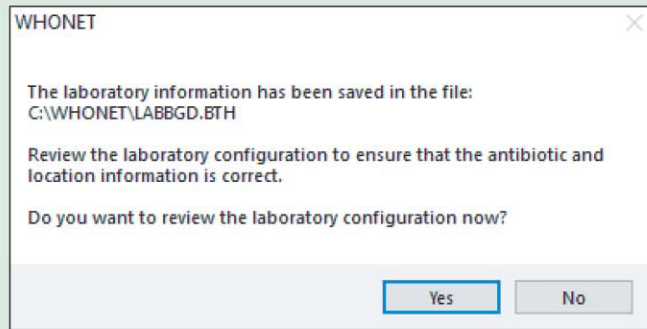
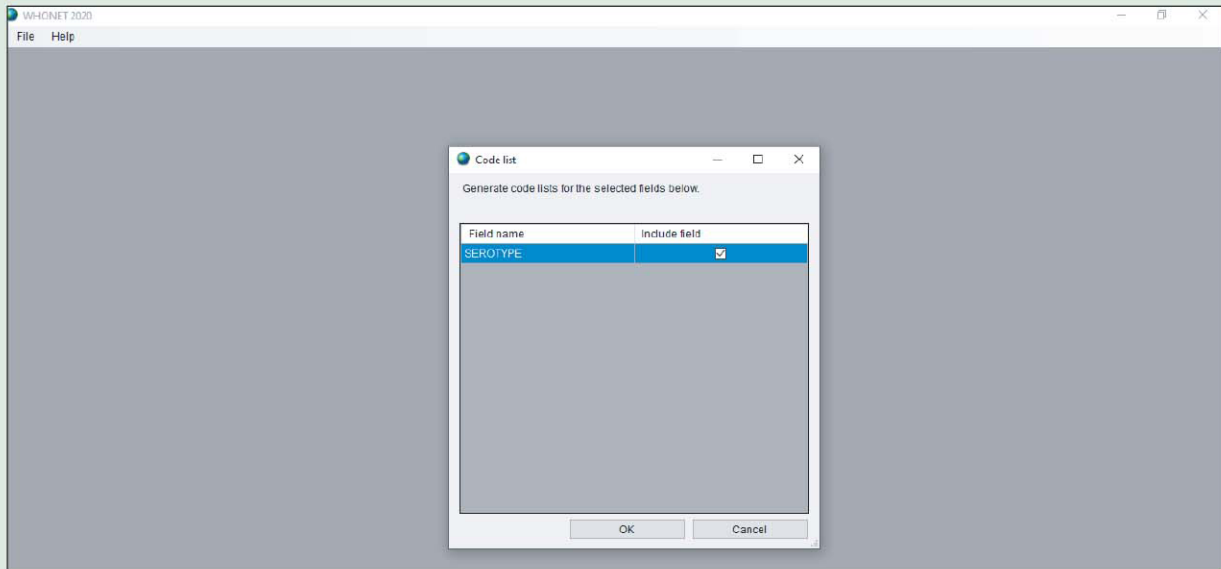
Enter the country “Bangladesh”, laboratory = “BacLink Tutorial Hospital”, and laboratory code = “BTH”. Click “OK”.



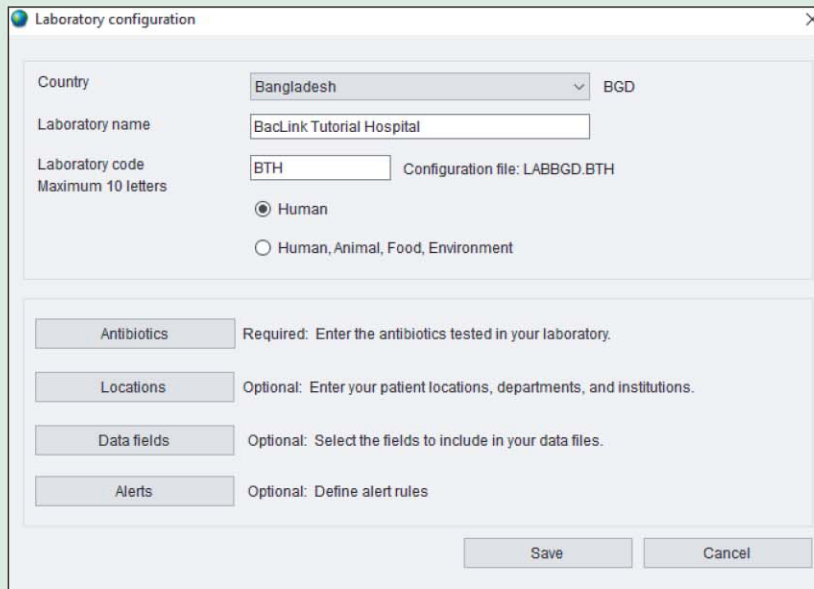
On the next screen, WHONET will ask you to select an example of a data file from this laboratory. Choose the file “ExcelDemo.bth” that you created with this BacLink tutorial, and click “Open”.



WHONET will now examine the file “ExcelDemo.ied” – what antibiotics are present, what data fields, locations, etc. With this information WHONET can create a matching laboratory configuration. When WHONET finishes, the program will ask if you want to review the new configuration. Answer “Yes”.



WHONET will then show you the laboratory configuration that it prepared.



If you click on “Antibiotics”, you will see that WHONET has the three antibiotics present in the original Excel file. You can also check the antibiotic breakpoints, and configure the panels and profiles if you wish.

Antibiotic Configuration

- Choose the antibiotics which you test in your laboratory. Indicate the guidelines, the test method, and the antibiotic name.
- Print and review the antibiotic breakpoints.
- Define antibiotic panels (for data entry) and antibiotic profiles (for data analysis).

WHONET antibiotic list

Guidelines:

Test method: Disk MIC Etest

(User-defined...)

- 5-Fluorocytosine (CLSI,NEO-10ug)
- 5-Fluorocytosine (CLSI,NEO-1ug)
- Acetylmidecamycin
- Acetylspiramycin
- Amikacin (CLSI,EUCAST-30ug)
- Amikacin (NEO-40ug)
- Amikacin/Fosfomycin (CLSI)
- Amoxicillin (20ug)
- Amoxicillin (2ug)

Search:

Breakpoints Panels Profiles

Local antibiotic list

Move up Move down Edit

Code	Antibiotic name
AMP_ND10	Ampicillin
CIP_ND5	Ciprofloxacin
SXT_ND1.2	Trimethoprim/Sulfamethoxazole

Number of antibiotics = 3

Print OK

If you click on "Locations", you will see the list of locations from the original file.

Locations

The lists on the right will change the selected row's values when clicked. You can delete a row by selecting it and pressing the Delete key.

Location name	Code	Institution	Department	Type
5 North	5 North			
Diabetes clinic	Diabetes clinic			
ER	ER			
HC5	HC5			
ICU	ICU			
Medicine1	Medicine1			
Medicine2	Medicine2			
NICU	NICU			
OB-Gyn	OB-Gyn			
Ortho	Ortho			

Institutions Edit

IED None IED

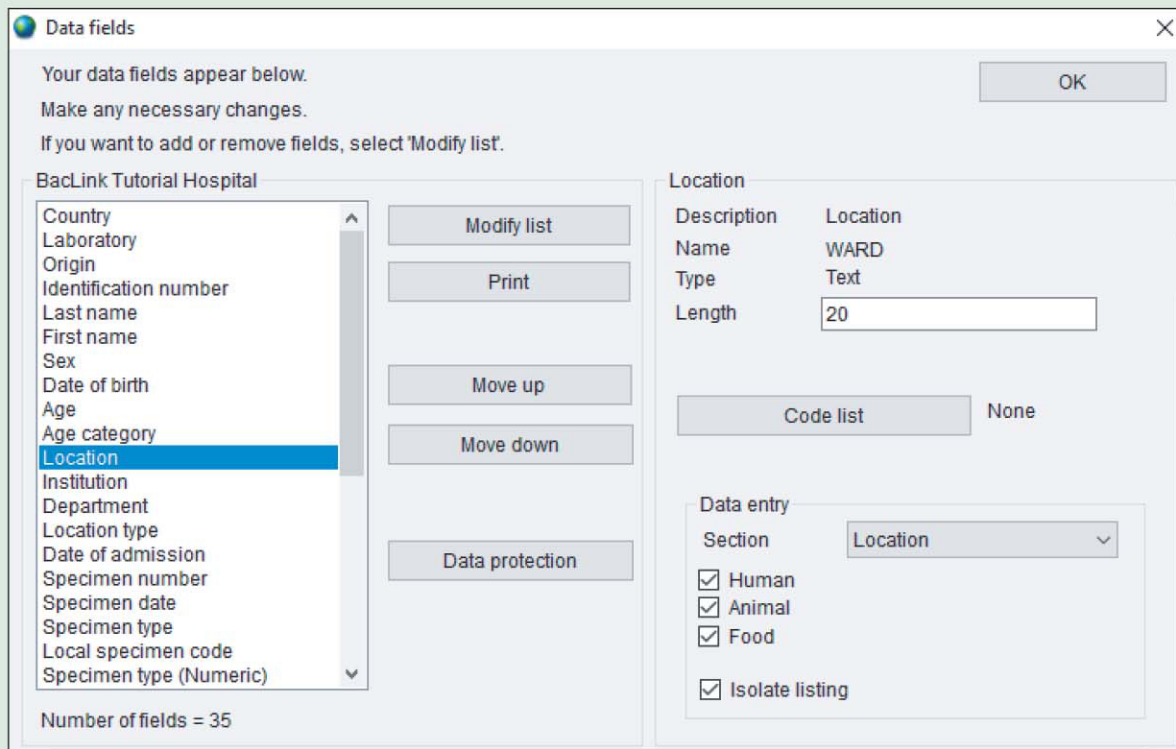
Departments Edit

med None
sur Medicine
tran Surgery
tran Transplant service
trm Traumatology
icu Intensive care unit
aicu Adult intensive care unit

Location type

out None
in Outpatient
in Inpatient
inx Inpatient (non-ICU)
icu Intensive care unit
int Intermediate care unit
eme Emergency

If you click on "Data fields", you will see that the location field has a length of 20 characters, rather than the usual default of 6 characters.



After you explore these screens, click on “Save” to leave the configuration program.

Note: After creating the configuration utilizing the shortcut described here, you can make any further edits, such as any modifications to the antibiotic breakpoints and profiles, with Modify laboratory in the same way as any WHONET laboratory configuration.

Inspecting the data file

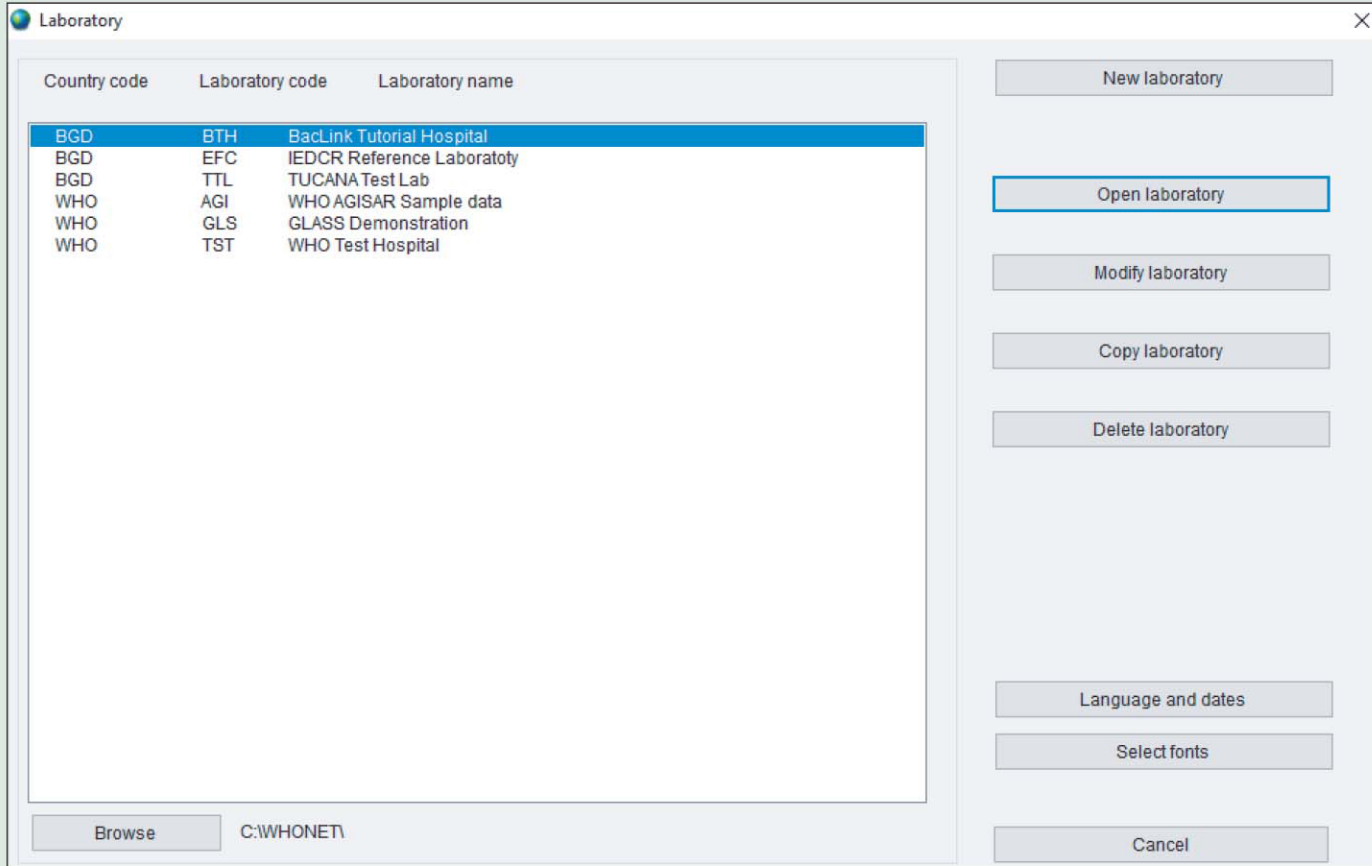
As a final step, click on “Data entry”, “Open data file”, and choose the file “ExcelDemo.ied”. You will now be in the Data entry program. Click on “View database” to see the following screen.

Identification number	Specimen number	Organism	Country	Laboratory	Origin	Last name	First name	Sex	Date of birth	Age	Age category	Location	Institution	Department	Location type
1658752	45896	kpn	BGD	IED					3/10/1957	48	adu	Ortho	IED		
4689314	32047	sau	BGD	IED					15/3/1980	25	adu	Medicine1	IED		
7584301	14658	eco	BGD	IED					2/2/1940	65	adu	Medicine2	IED		
4865921	76481	pae	BGD	IED					10/1/2006			Diabetes clinic	IED		
5481023	16594	sau	BGD	IED					20/6/1924	81	adu	ICU	IED		
4935814	68459	cnv	BGD	IED					6/2/1992	13	ped	OB-Gyn	IED		
9208748	28791	cal	BGD	IED					26/7/2004	1	ped	5 North	IED		
3017845	30247	svi	BGD	IED					30/11/2001	4	ped	HC5	IED		
4869704	45076	gct	BGD	IED					11/8/1952	53	adu	ER	IED		
5904720	48692	xxx	BGD	IED					18/12/1986	19	adu	NICU	IED		

WHONET is now showing you the complete contents of the data file created by BacLink. Inspect this file to see if there are any possible errors – in the dates, codes, antibiotic results, etc. This will also help to familiarize you with the structure and contents of a WHONET data file.

When you finish, click on “Continue” and “Exit” to return to the main WHONET screen. Then “File”, “Exit” to leave WHONET completely.

The next time that you enter WHONET, you will see your new laboratory configuration for the “BaLink Tutorial Hospital” on the list. You can then select this laboratory for laboratory configuration, data entry, or data analysis.



Summary: You have learned how to convert data from common desktop softwares, such as Excel, and text files exported from laboratory information systems. The steps were: 1. configuration – which only needs to be accomplished once; and 2. running the conversion – which you can repeat as you continue to collect additional data.

You then set up a new WHONET configuration for this laboratory. With this configuration, you can now analyze your data with WHONET. If needed, you could also use WHONET for manual data entry of supplemental information that you did not have in your original data file.

You can find additional tutorials on BaLink from the following links:

AMRTRACKER: <http://amrtracker.com/whonet/baclink.html#collapseLBP2>

WHONET: <https://whonet.org/documentation.html>

Live Support: <http://amrtracker.com/public/support>

References:

1. <https://whonet.org/documentation.html>
2. DAI FF Pakistan - WHONET User Manual