WHONET for CAESAR

Manual

Version 2021-1 December 2021

Contents

1 Introduction

1.1 CAESAR data collection

CAESAR collects isolate-based antimicrobial resistance data from the member countries. As opposed to aggregated data that contains only the overall numbers of isolates and the percentages of these that are resistant, intermediate and susceptible, isolate-based data is much more useful for monitoring antimicrobial resistance. Isolate-based data make it possible to add additional patient data, including gender and age, data of hospitalization and other information that makes CAESAR able to conduct analyses that will help give a clearer picture of the antimicrobial resistance situation in the member countries.

Each laboratory contributing to CAESAR collects antimicrobial resistance data and the local data manager sends the data to the national data manager. The national data manager will collect all data from his/her country. Before submitting the data to CAESAR, the national data manager will have to prepare the data and make sure they comply with the CAESAR data file format. When all data has been prepared the national data manager will submit the data to CAESAR and the data will be added to the CAESAR database.

As with any surveillance system, the national data manager needs to perform a number of steps including data collection, data validation and cleaning, data analysis, reporting and feedback. In addition to reporting to CAESAR, it is important to look at local, regional and national trends to inform strategies for the control of antimicrobial resistance. Local data managers should also look at their own data to inform empiric guidelines for treatment in their hospital(s).

1.2 Why electronic data capture and management?

Antimicrobial susceptibility testing is increasing and storing data electronically will make data more accessible. When the amount of data is huge it is difficult to manually analyze data from hand written registers. Data need to be analyzed regularly to monitor trends and check for emergence of resistance. Local resistance patterns are useful for guidance regarding empiric use of antibiotics.

There are several Laboratory Information Management Systems (LIMS) available with different specifications according to the different needs of the laboratory. These LIMS might be costly so not available to every laboratory. WHONET is a free software that can be used to enter data directly into, or transfer electronic data already entered elsewhere, to be able to analyze it. It can also be used to print results to be sent out to clinicians.

2 WHONET and BacLink

2.1 About WHONET and BacLink

WHONET is free software developed by the WHO Collaborating Centre for Surveillance of Antimicrobial Resistance, Brigham and Women's Hospital, Boston USA, for the purpose of laboratory-based surveillance of infectious diseases and antimicrobial resistance.

WHONET is meant to be used in laboratories. It stores the results of antimicrobial resistance tests in its own database, and enables analysis on these data. The program is flexible to fit in the workflow of each laboratory: all entry screens are configurable, the list of pathogens can be modified, as well as the tested antimicrobials. Data are stored as raw values (MIC or diameter), and are interpreted according to guidelines which can easily be updated or edited. WHONET data can be exported to international surveillance systems like GLASS, EARS-Net or CAESAR.

BacLink is software to convert and standardize microbiology data from existing systems or prepared files into WHONET. BacLink is a flexible tool and accepts different data structures and file formats. Installation of WHONET installs BacLink as well.

This WHONET manual has been prepared to facilitate the collection and analysis of AMR data for CAESAR. However, WHONET can also be used to collect and analyze other AMR data from laboratories and hospitals.

In WHONET, there is often more than one way to perform a particular task or to navigate to a particular part of the program. Some examples are given in this brief manual but you will come across further examples as you gain more experience with the software.

2.2 WHONET in surveillance

WHONET has the option to combine data from different laboratories into one data file. This option can be used for national surveillance. The WHONET files from the participating laboratories combined, will give a datafile that can be used to provide national statistics. WHONET can also combine WHONET files into TESSy, CAESAR or GLASS data files.

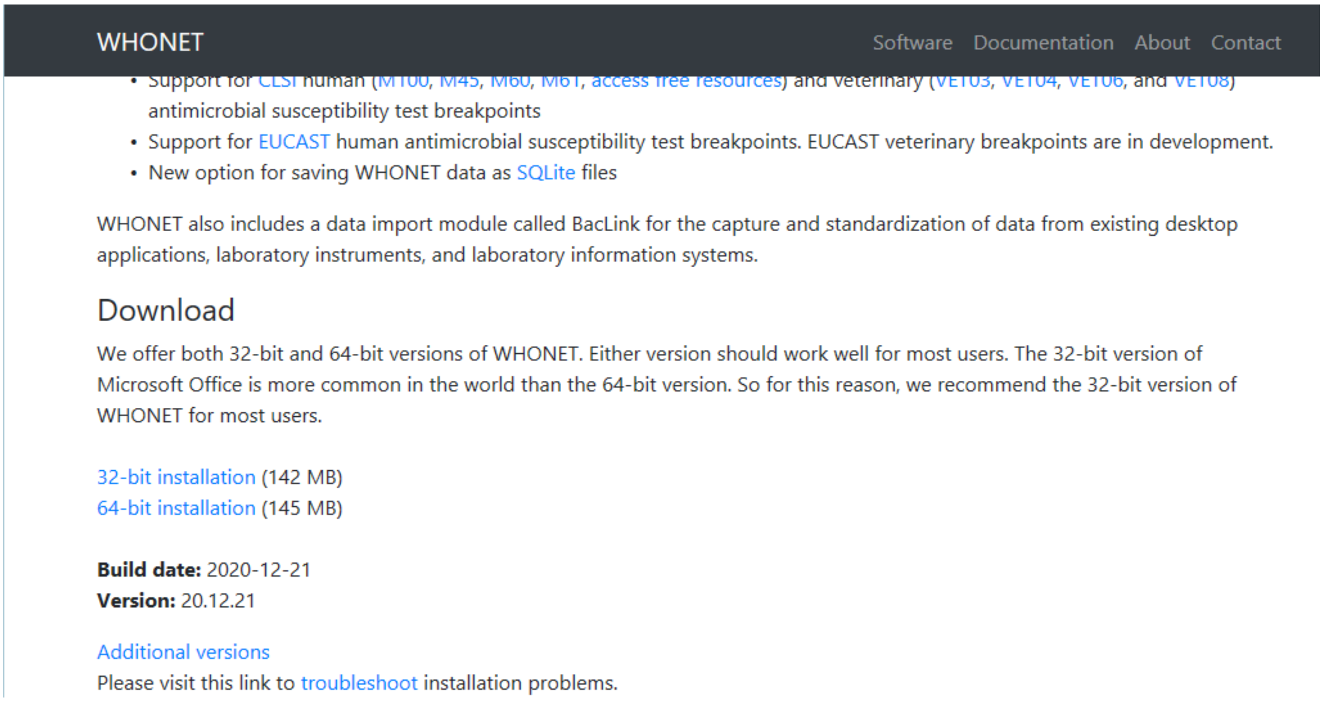
This option is particularly useful if the majority of laboratories use WHONET for data handling. For the laboratories not using WHONET, the data need to be entered into WHONET afterwards. This data entry needs to be done with a separate configuration for each laboratory, making this a time-consuming process. Alternatively, a BacLink conversion could be developed, to translate the data in some other standardized format into WHONET.

2.3 Installing WHONET and BacLink

The software is available from the WHONET website: www.whonet.org. The WHONET installation includes BacLink. There are 2 WHONET versions available: 64 and 32 bit. Both versions have the same functionality, and files are compatible. WHONET has the option to export Excel files, therefore it is recommended to match the version with the version of Microsoft Office on your computer. If you have 64 bit MS-Office installed, also install 64 bit WHONET, otherwise install 32 bit WHONET.

To find your currently installed version of MS-Office: open any MS-Office application (Access, Excel, Word). Choose file, account. Here you find: about Access/Excel/Word. The version is shown.

Choose one of the versions of WHONET, and download. Only one version can be installed on one computer.



- Support for CLSI human (M100, M45, M60, M61, access free resources) and veterinary (VET03, VET04, VET06, and VET08) antimicrobial susceptibility test breakpoints
- Support for EUCAST human antimicrobial susceptibility test breakpoints. EUCAST veterinary breakpoints are in development.
- New option for saving WHONET data as SQLite files

WHONET also includes a data import module called BacLink for the capture and standardization of data from existing desktop applications, laboratory instruments, and laboratory information systems.

Download

We offer both 32-bit and 64-bit versions of WHONET. Either version should work well for most users. The 32-bit version of Microsoft Office is more common in the world than the 64-bit version. So for this reason, we recommend the 32-bit version of WHONET for most users.

32-bit installation (142 MB)
64-bit installation (145 MB)

Build date: 2020-12-21
Version: 20.12.21

Additional versions
Please visit this link to troubleshoot installation problems.

Figure 2.1: WHONET download page.

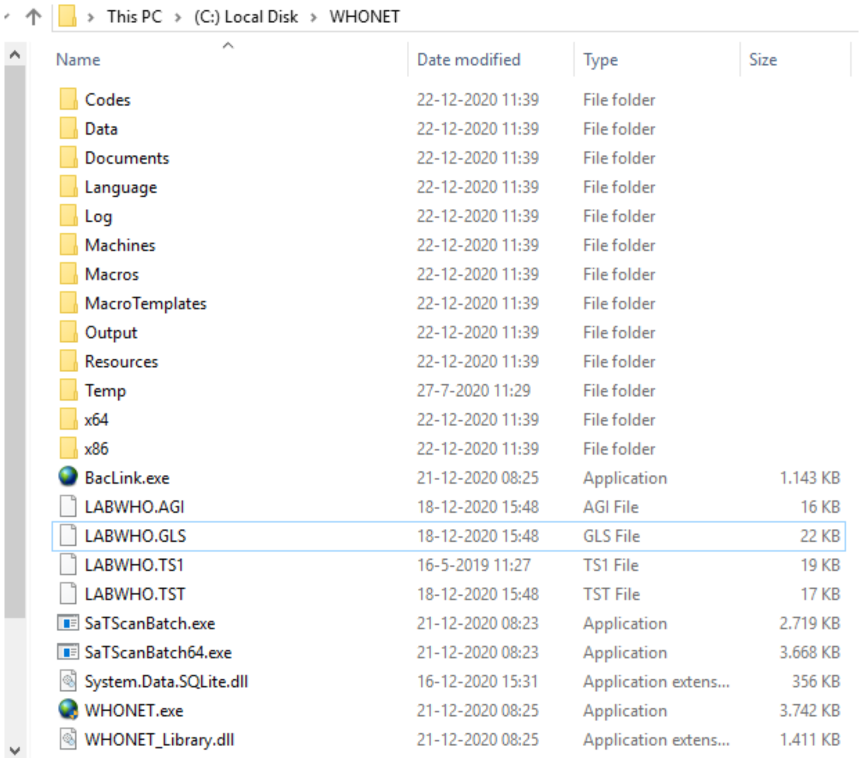
2.3.1 Installing WHONET for the first time

Downloading and installing the latest version of WHONET is simple to do, although you may need to get your IT/computer department to do this for you as often they restrict what users can do in terms of downloading and installing software. To install WHONET, an administrator account for your computer is needed. Sometimes anti-virus software blocks the installation. If this occurs, the protection must be temporarily disabled during the installation. Most antivirus software has the option to disable the protection for a couple of minutes.

Once you have downloaded the installation package, right-click on the downloaded file, and choose ‘Run as administrator’. It is possible that you need to provide an administrator username and password. Follow the instructions on the InstallShield Wizard screen (‘Run’, ‘Next’, ‘Install’, ‘OK’, ‘Finish’).

The default location for the WHONET installation is C:\WHONET (see Figure 2.2). Once WHONET is installed, this folder is where you will find a number of subfolders including ‘Documents’, where you will find comprehensive manuals for both WHONET and BacLink. Two other important subfolders to be aware of are:

- ‘Data’ subfolder, which is the default location for all new data files created (unless the location is specifically changed)
- ‘Output’ subfolder, which is the default location for any new output files created when you analyze your data



Name	Date modified	Type	Size
Codes	22-12-2020 11:39	File folder	
Data	22-12-2020 11:39	File folder	
Documents	22-12-2020 11:39	File folder	
Language	22-12-2020 11:39	File folder	
Log	22-12-2020 11:39	File folder	
Machines	22-12-2020 11:39	File folder	
Macros	22-12-2020 11:39	File folder	
MacroTemplates	22-12-2020 11:39	File folder	
Output	22-12-2020 11:39	File folder	
Resources	22-12-2020 11:39	File folder	
Temp	27-7-2020 11:29	File folder	
x64	22-12-2020 11:39	File folder	
x86	22-12-2020 11:39	File folder	
BacLink.exe	21-12-2020 08:25	Application	1.143 KB
LABWHO.AGI	18-12-2020 15:48	AGI File	16 KB
LABWHO.GLS	18-12-2020 15:48	GLS File	22 KB
LABWHO.TS1	16-5-2019 11:27	TS1 File	19 KB
LABWHO.TST	18-12-2020 15:48	TST File	17 KB
SaTScanBatch.exe	21-12-2020 08:23	Application	2.719 KB
SaTScanBatch64.exe	21-12-2020 08:23	Application	3.668 KB
System.Data.SQLite.dll	16-12-2020 15:31	Application extens...	356 KB
WHONET.exe	21-12-2020 08:25	Application	3.742 KB
WHONET_Library.dll	21-12-2020 08:25	Application extens...	1.411 KB

Figure 2.2: Default location on the C:\ drive for WHONET installation, including Data and Output subfolders and configuration files.

Once you have installed the program you will find icons for both WHONET and BacLink on your desktop (see Figure 2.3). It is from these icons that you can access the program. Alternatively, you can access the program from the Start menu like any other program.

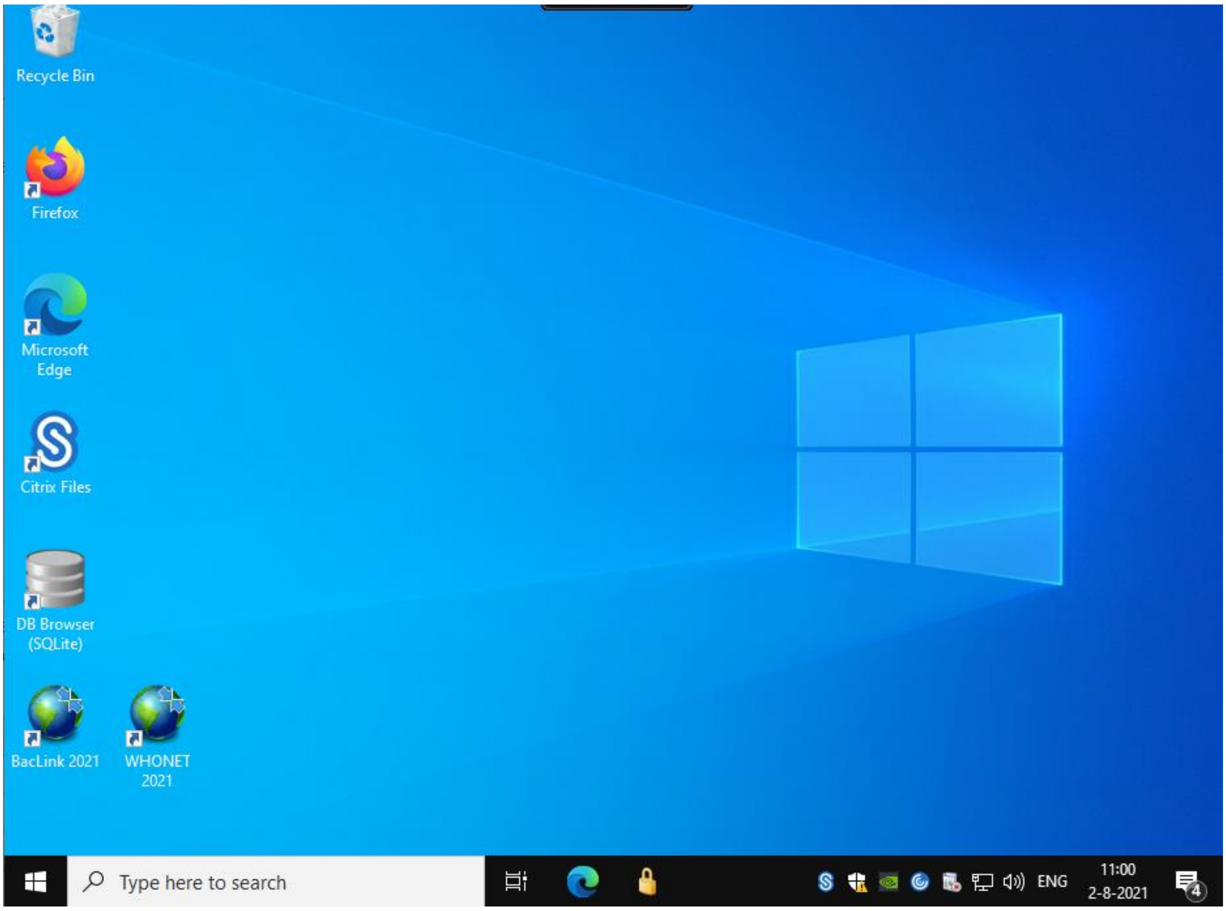


Figure 2.3: Desktop showing icons for WHONET and BacLink 2019.

2.3.2 Updating WHONET software

This section does not apply to users installing WHONET for the very first time.

It is advisable to install the most up to date version of WHONET at least once a year, but preferably mHore often because WHONET gets regular updates. These updates could correct errors in the software, or add new features. The name of the program is usually WHONETyyyy (where yyyy is the current year). This does not mean there is only one version per year, every version has a built date and a version number.

When you are installing the latest version of WHONET, only the program files for the software will be updated: all your configuration and data files will not be changed in any way. This also means that breakpoints are not updated automatically. Updating breakpoints is a manual process for each laboratory configuration. It could be important when interpreting and analyzing data from a specific year, that the breakpoints from that year are used. Updating breakpoints will be covered later in this manual in the section about WHONET configuration.

2.4 WHONET laboratory configuration

WHONET is flexible software. It can be used in microbiology laboratories for human healthcare, but also laboratories working for veterinary care of for food and environment. It supports guidelines from EUCAST, CLSI as well as a lot of national guidelines. The price for this flexibility is that configuration is very important. So before starting to use WHONET in a laboratory the program needs to be configured to fit the procedures and guidelines used in that laboratory. All the settings are stored in a laboratory configuration file: one for each laboratory, for each year of data. The latter because EUCAST as well as CLSI will have updated breakpoints each year, and the breakpoints are part of the laboratory configuration.

In WHONET, there is often more than one way to perform a particular task or to navigate to a particular part of the program. Some examples are given in this manual but you will come across further examples as you gain more experience with the software.

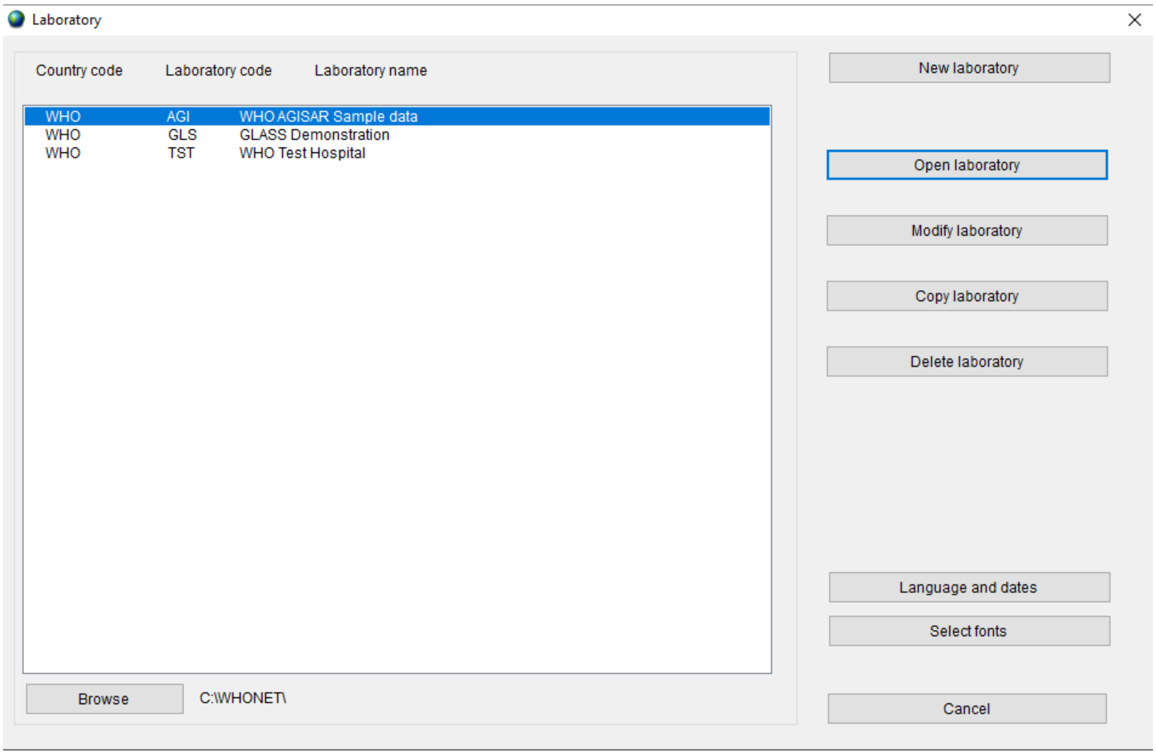
2.4.1 Creating a new laboratory configuration

In WHONET, there are several ways to create a new laboratory configuration, all in the ‘file’ menu. Examples:

- New laboratory, this is the long way. You will have to configure all the fields yourself. This is not dealt with in this manual.
- Create a laboratory from a data file (especially useful for users of BacLink and when you receive a WHONET data file from someone else). The configuration will include the used antibiotics and tests (such as disk or MIC), and also the guideline (CLSI or EUCAST) but it is not possible to see which version of the breakpoints was used to create the file.
- File menu: EARS-Net/CAESAR › New laboratory. This is the easiest way for our purpose. It is still possible to make all modifications, but much of the necessary configuration is already predefined. We will explain this option in detail.

2.4.1.1 Creating a new laboratory for TESSy/CAESAR

If you start WHONET the first time, the screen below will appear. The only laboratory configurations are examples (see Figure 2.4).



Country code	Laboratory code	Laboratory name
WHO	AGI	WHO AGISAR Sample data
WHO	GLS	GLASS Demonstration
WHO	TST	WHO Test Hospital

C:\WHONET\

Figure 2.4: Opening screen.

Since we do not have a laboratory configuration yet, click on ‘Cancel’.

The main WHONET screen appears, this screen is empty, except for 2 menu items (see Figure 2.5 for part of the screen).

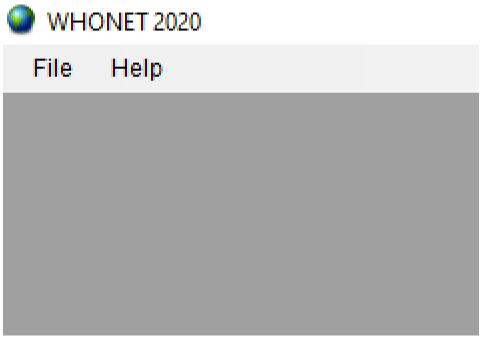


Figure 2.5: Main WHONET screen.

Click ‘File’ and then ‘EARS-Net/CAESAR and ‘New laboratory’ (see Figure 2.6). Note that the following screens refer to TESSY laboratory. TESSy is the name of the database used for EARS-Net.

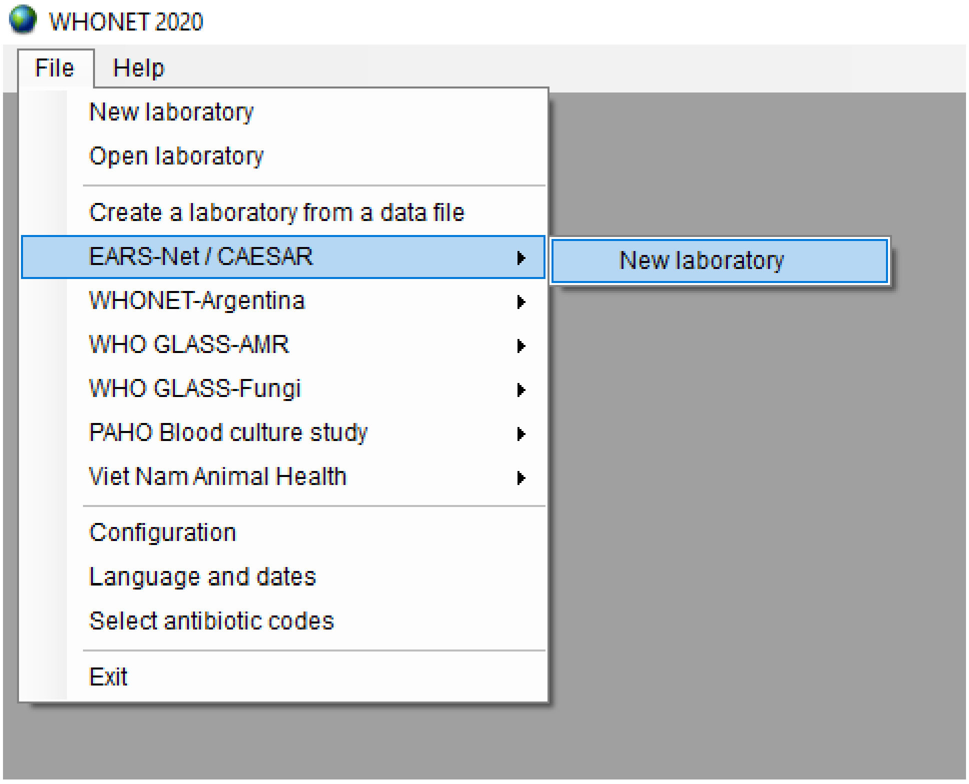
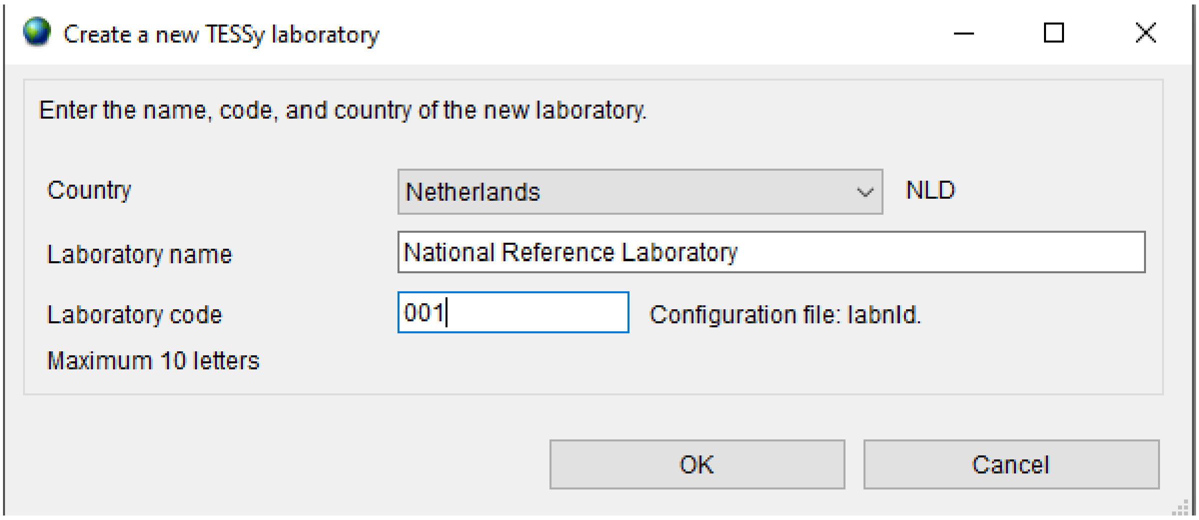


Figure 2.6: Create a new EARS-Net/CAESAR laboratory.

The following screen will appear within the main screen (Figure 2.7):


Create a new TESSy laboratory

Enter the name, code, and country of the new laboratory.

Country: Netherlands NLD

Laboratory name: National Reference Laboratory

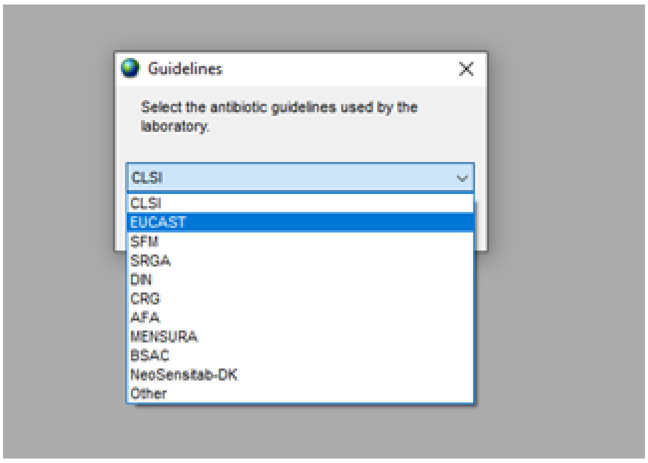
Laboratory code: 001 Configuration file: labnld.

Maximum 10 letters

Figure 2.7: New TESSy laboratory, select country.

Indicate your country, laboratory name and laboratory code (this will be provided by your national data manager and will most likely be a 3-digit numeric code, e.g., 001) and then click 'OK'.

The next screen appears (Figure 2.8):



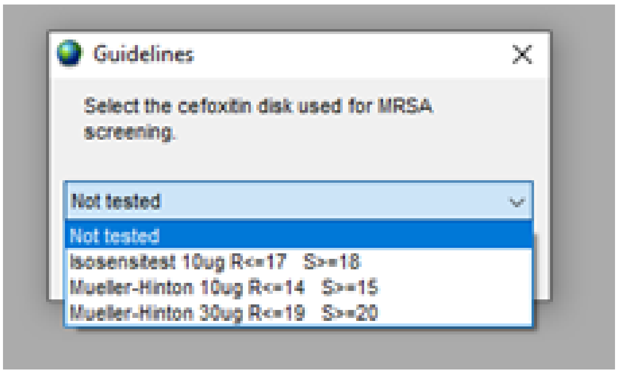
Select the antibiotic guidelines used by the laboratory.

CLSI

Figure 2.8: New TESSy laboratory, select guideline.

Select the guidelines used by the laboratory and click ‘OK’. Note that if you choose EUCAST, afterwards you can still add CLSI tests and vice versa.

Then the following screen will appear (Figure 2.9):



Select the cefoxitin disk used for MRSA screening.

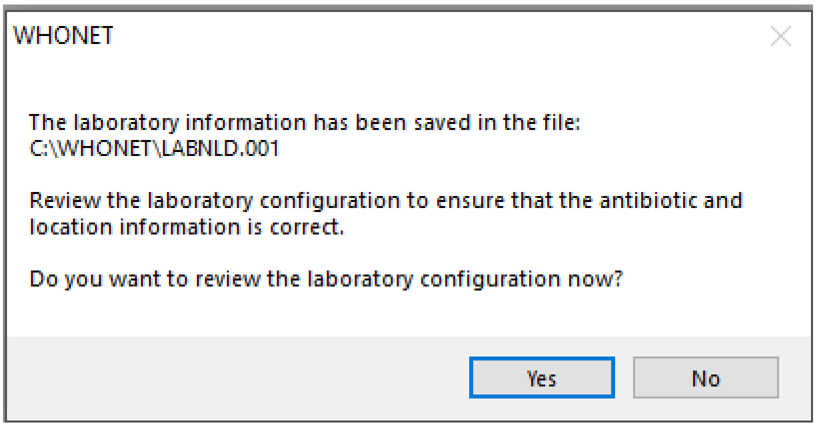
Not tested

Figure 2.9: New TESSy laboratory, select method for MRSA screening.

If you use a cefoxitin disk to screen for MRSA isolates, indicate the medium and disk potency used, which should be in accordance with the guidelines followed. Both CLSI and EUCAST use Mueller-Hinton 30µg. If cefoxitin disk is not used for this purpose, select ‘Not tested.’

Click ‘OK’.

WHONET will create a new laboratory with the recommended set of CAESAR data fields and codes, including the preferred antibiotics. You will then be prompted with the following screen (Figure 2.10):


WHONET

The laboratory information has been saved in the file:
C:\WHONET\LABNLD.001

Review the laboratory configuration to ensure that the antibiotic and location information is correct.

Do you want to review the laboratory configuration now?

Figure 2.10: New TESSy laboratory created.

If you want to review the configuration and make any modifications, click ‘Yes’: it is a good idea to do this as you may want to remove any antibiotics that are not routinely tested in your laboratory, or add antibiotics used that are not pre-configured. If you do not want to configure now, click ‘No’. Configuration can also be done later, using the option ‘modify laboratory’.

WHONET automatically creates a configuration file for the laboratory created with the file name following the format, LABCCC.XXX: where CCC is the country’s 3-letter ISO code (based on the country selected) and XXX is the laboratory’s 3-digit (for CAESAR) laboratory code as provided by the national data manager. In this example, the country code is NLD and the laboratory code is 001, hence the configuration file name is LABNLD.001.

By default, the configuration file is stored in the C:\WHONET directory.

TIP FOR NATIONAL DATA MANAGERS

You may wish to create a ‘national’ laboratory configuration, for example ‘All laboratories’ which could be used for managing/analyzing data from any (combination) of the contributing laboratories in the country.

2.4.2 Configuring antibiotics

Before you configure the antibiotics in your WHONET laboratory configuration, compile a list of antibiotics and the test methods used, e.g. disk diffusion, MICs (including breakpoint methodologies using automated instruments) and/or gradient tests.

For CAESAR, refer to the manual for the list of key antibiotics required for each of the pathogens under surveillance (Table 2 on page 32 of the CAESAR Manual Version 3, 2019).

The ‘WHONET antibiotic list’ appears to the left, while the antibiotics that you select will appear to the right under ‘Local antibiotic list’ (see Figure 2.12).

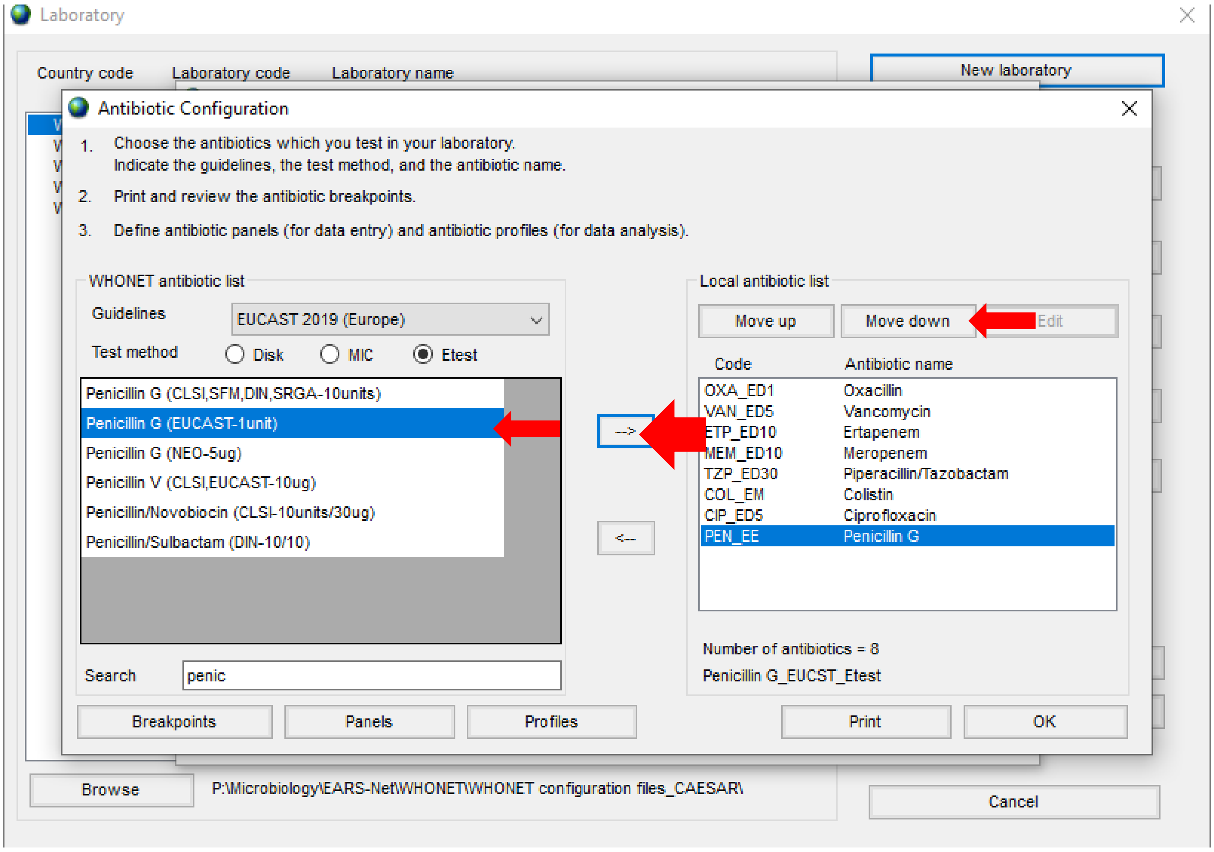
For each combination of antibiotic and test method:Figure 2.11

- select the correct testing guidelines using the dropdown menu (e.g. EUCAST or CLSI; please note: WHONET default is CLSI, but CAESAR recommends EUCAST)

- **AND** click on the correct test method (disk diffusion, MIC, Etest®)

- **AND** select the correct antibiotic (including the **correct** disk potency for the guidelines being followed if the test method is disk diffusion). For MIC or gradient testing, you can choose any disk potency, as it is ignored for MIC/gradient testing.

You can select an antibiotic by double-clicking on it OR by clicking on it once and then clicking the right arrow button '-->'. This will result in the antibiotic being moved across from the 'WHONET antibiotic list' to the 'Local antibiotic list'.



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

Guidelines: EUCAST 2019 (Europe)

Test method: ○ Disk ○ MIC ● Etest

Penicillin G (CLSI,SFM,DIN,SRGA-10units)
Penicillin G (EUCAST-1unit)
Penicillin G (NEO-5ug)
Penicillin V (CLSI,EUCAST-10ug)
Penicillin/Novobiocin (CLSI-10units/30ug)
Penicillin/Sulbactam (DIN-10/10)

Search: penic

Code	Antibiotic name
OXA_ED1	Oxacillin
VAN_ED5	Vancomycin
ETP_ED10	Ertapenem
MEM_ED10	Meropenem
TZP_ED30	Piperacillin/Tazobactam
COL_EM	Colistin
CIP_ED5	Ciprofloxacin
PEN_EE	Penicillin G

Number of antibiotics = 8
Penicillin G_EUCST_Etest

P:\Microbiology\EARS-Net\WHONET\WHONET configuration files_CAESAR\

Figure 2.12: Laboratory configuration, WHONET and local antibiotic list.

Each antibiotic-test combination is given a code (of up to nine characters) in the 'Local antibiotic list' consisting of:

- the three-letter antibiotic code
- a one-letter code indicating the guideline reference (e.g. E=EUCAST; N=CLSI, formerly NCCLS)
- a one-letter code indicating the test method (D=disk diffusion; M=MIC; E= Gradient, Etest®)
- a disk potency (numerical value in µg) disk diffusion tests

For MICs or Etests, this is rather confusing, you choose the correct antibiotic (ignoring the disk potency) and the guideline. For example: to enter Oxacillin MIC according to EUCAST, choose EUCAST, and MIC. Then choose one of the 3 oxacillin disks. It makes no difference, the disk potency and guideline indicated in the list, are not relevant.

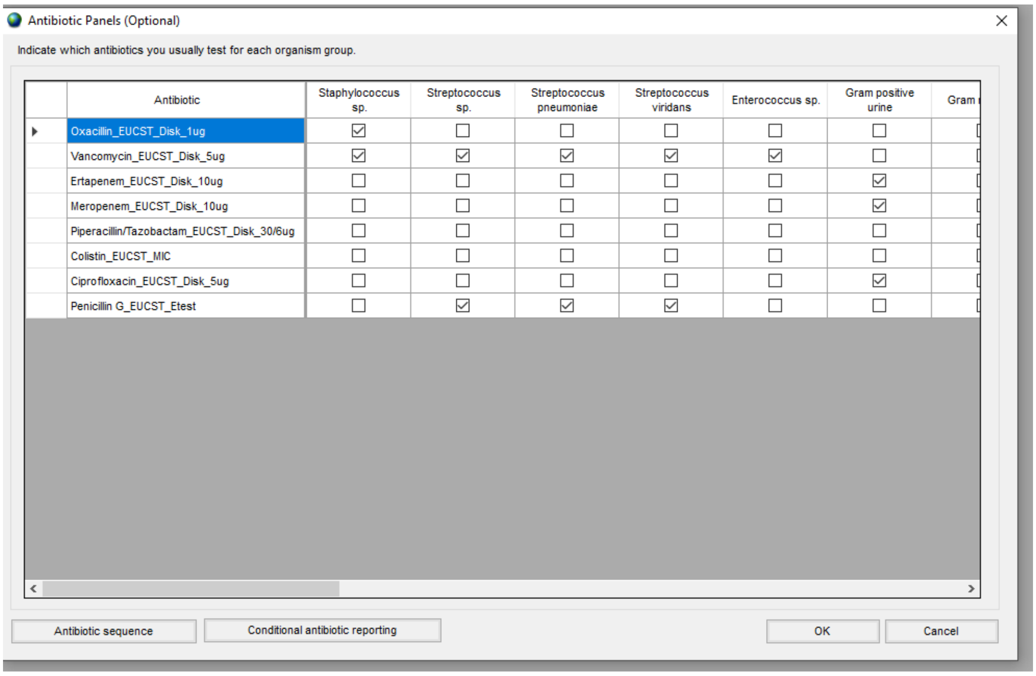
For example, the code GEN_ED10 represents: GEN=gentamicin, E=EUCAST, D=disk diffusion, 10=10µg, while GEN_EM is: gentamicin, EUCAST, MIC.

When you finish entering your antibiotics, review the list and make any needed corrections. To remove an antibiotic from the 'Local antibiotic list', single-click on the antibiotic and hit the left arrow button, '<--'. You may change the sequence of the antibiotics with the 'Move Up' and 'Move Down' buttons.

TIP: It is recommended that you keep the list in alphabetical order for convenience. To do this, highlight the antibiotic you want to move and use the 'Move up' and 'Move down' buttons indicated in the screenshot above.

When you are satisfied with the list, you have the following options:

- 'Breakpoints' to review, modify, and update the antibiotic breakpoints (see section 2.4.3).
- 'Panels' and 'Profiles' are optional: to facilitate data entry, you may wish to use 'Panels' to indicate which antibiotics are tested for each kind of organism (see Figure 2.13). The panels configure which antibiotics will be visible on the entry forms. It is recommended to remove antibiotics not used in your laboratory to prevent data entry errors.
- 'Print': to obtain a printout of your antibiotics and their breakpoints by organism (organism-specific breakpoints). It is recommended that you print out your breakpoints for your review and reference before you start data entry.
- 'OK': to return to the main Laboratory Configuration screen (note: the information has to be saved by clicking on 'Save' in the main Laboratory Configuration screen).



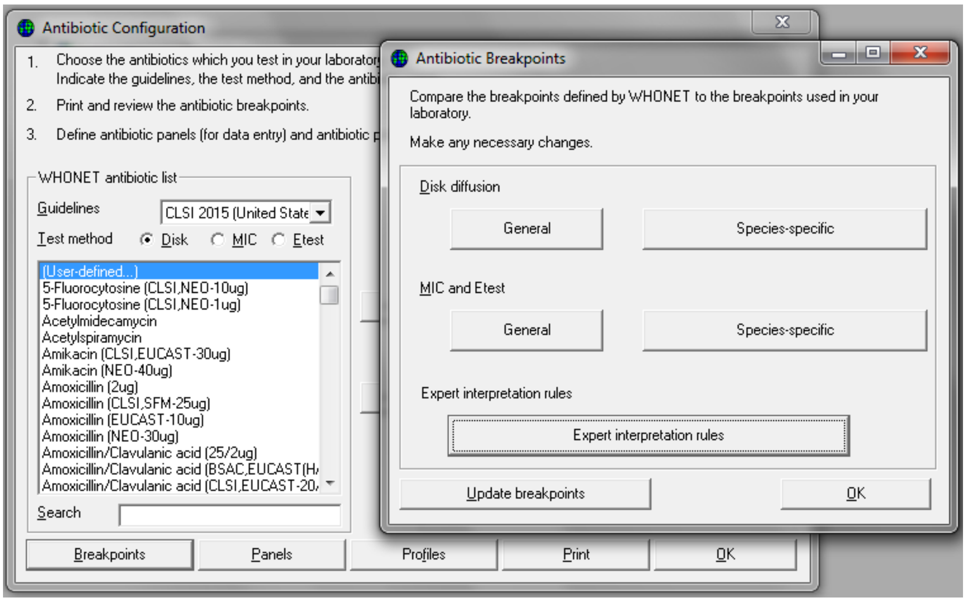
Indicate which antibiotics you usually test for each organism group.

Antibiotic	Staphylococcus sp.	Streptococcus sp.	Streptococcus pneumoniae	Streptococcus viridans	Enterococcus sp.	Gram positive urine	Gram
Oxacillin_EUCST_Disk_1ug	☑	☐	☐	☐	☐	☐	
Vancomycin_EUCST_Disk_5ug	☑	☑	☑	☑	☑	☐	
Ertapenem_EUCST_Disk_10ug	☐	☐	☐	☐	☐	☑	
Meropenem_EUCST_Disk_10ug	☐	☐	☐	☐	☐	☑	
Piperacillin/Tazobactam_EUCST_Disk_30/6ug	☐	☐	☐	☐	☐	☐	
Colistin_EUCST_MIC	☐	☐	☐	☐	☐	☐	
Ciprofloxacin_EUCST_Disk_5ug	☐	☐	☐	☐	☐	☑	
Penicillin G_EUCST_Etest	☐	☑	☑	☑	☐	☐	

Figure 2.13: Antibiotic Panels screen.

2.4.3 Checking and updating antibiotic breakpoints

Checking and updating breakpoints is relevant, because WHONET stores quantitative data, zone diameters and MIC values. Optional you can choose to store only interpretations such as R, I and S. In that case breakpoints are irrelevant to you and you can skip this part. On the first installation, WHONET will automatically load the most recent breakpoints for the antibiotics and guidelines which you have indicated. In certain circumstances, you might want to amend breakpoints to suit local practices, for example, you may have locally agreed breakpoints for antibiotics for which no EUCAST breakpoints are available.


Antibiotic Configuration

1. Choose the antibiotics which you test in your laborator
Indicate the guidelines, the test method, and the antibi
2. Print and review the antibiotic breakpoints.
3. Define antibiotic panels (for data entry) and antibiotic p

WHONET antibiotic list
Guidelines: CLSI 2015 (United State
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)
Amoxicillin (2ug)
Amoxicillin (CLSI,SFM-25ug)
Amoxicillin (EUCAST-10ug)
Amoxicillin (NEO-30ug)
Amoxicillin/Clavulanic acid (25/2ug)
Amoxicillin/Clavulanic acid (BSAC,EUCAST(H
Amoxicillin/Clavulanic acid (CLSI,EUCAST-20

Antibiotic Breakpoints

Compare the breakpoints defined by WHONET to the breakpoints used in your laboratory.

Make any necessary changes.

Figure 2.14: 'Antibiotic Configuration' and 'Antibiotic Breakpoints' screens.

'Update breakpoints': The WHONET antibiotic definition files are updated annually as new recommendations from the reference authorities become available (usually available on the WHONET website in January). When you download a new version of WHONET, usually on an annual basis, the download will include the latest available breakpoints. However, existing laboratory configurations will not automatically have the breakpoints updated for the existing antibiotic list. WHONET does **not** automatically use these new breakpoints for your existing antibiotic list. You have to click on 'Update breakpoints' to replace the breakpoints currently set for your laboratory with the latest antibiotic breakpoints to be found in the most recent antibiotic definition files. If you have more laboratory configurations, you have to update breakpoints for each configuration.

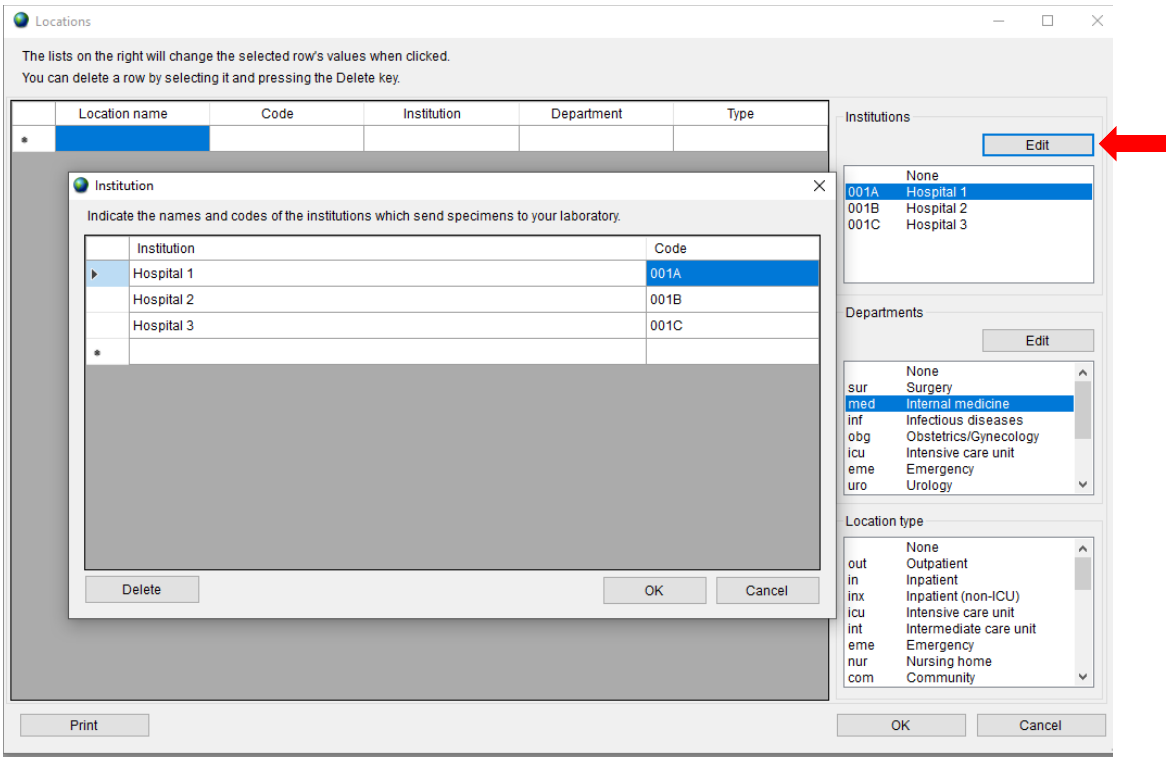
'Expert interpretation rules': These are not required for CAESAR data. See the main WHONET manual for more details.

'OK': When you finish reviewing and/or modifying the antibiotic breakpoints, selecting 'OK' will return you to the 'Antibiotic Configuration' screen.

2.4.4 Locations and hospitals

This configuration screen allows you to add or edit hospital codes. Note that hospital code is named 'Institution' in WHONET. Use this configuration to add codes for all hospitals that send samples to your laboratory. See Figure 2.15.

It is also possible to enter named locations here. This option is optional (i.e. is not a requirement for CAESAR), but is of value if you would like to keep track of the patient locations and medical services from which samples are taken., please refer to the main WHONET manual for a more detailed description.



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

Indicate the names and codes of the institutions which send specimens to your laboratory.

Institution	Code
Hospital 1	001A
Hospital 2	001B
Hospital 3	001C

	None
001A	Hospital 1
001B	Hospital 2
001C	Hospital 3

	None
sur	Surgery
med	Internal medicine
inf	Infectious diseases
obg	Obstetrics/Gynecology
icu	Intensive care unit
eme	Emergency
uro	Urology

	None
out	Outpatient
in	Inpatient
inx	Inpatient (non-ICU)
icu	Intensive care unit
int	Intermediate care unit
eme	Emergency
nur	Nursing home
com	Community

Figure 2.15: Locations screen.

2.4.5 Modifying data fields for CAESAR

A set of standard data fields is defined automatically by WHONET, including: identification number (i.e. patient ID or Medical Record Number/MRN), last name, first name, date of birth, sex, patient ward, specimen number, specimen date, specimen type, organism, etc. All EARS-Net/CAESAR fields are present.

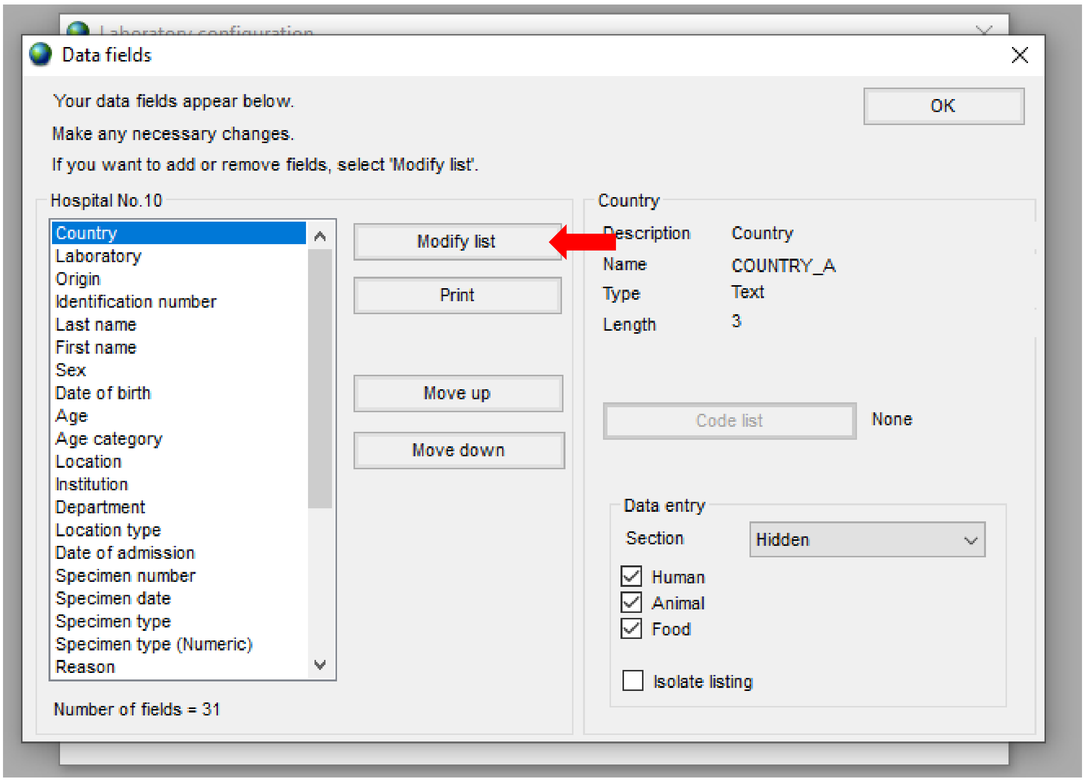
Some of these standard fields can be removed.

To combine other surveillance activities with the CAESAR data collection, you may want to add some additional data fields.

TIP FOR NATIONAL DATA MANAGERS: Ask local laboratories not to include patient names when sending their data files.

2.4.5.1 Example: Adding ‘Diagnosis’ to the laboratory configuration

For antibiotic stewardship it might be interesting to add the diagnosis of the patient to the surveillance. This can be done easily. From the main ‘Laboratory configuration’ screen, click the button for ‘Data Fields’ which will then bring up the ‘Data fields’ screen (see Figure 2.16); then click on ‘Modify list’. You will see the ‘Modify list’ screen similar to the one in Figure 2.17. On the top left panel of the screen (Figure 2.17 label A), you can see the list of ‘Data categories’ that are available in WHONET, including clinical information, infection control, microbiology, etc. Below this in the bottom left panel (Figure 2.17 label B) is the list of 'Data fields' that appears for the data category selected above: for Clinical Information, there are many data fields available, including 'Diagnosis'. Select this field, and the right arrow to add this field.



Your data fields appear below.
Make any necessary changes.
If you want to add or remove fields, select 'Modify list'.

Hospital No.10

Country
Laboratory
Origin
Identification number
Last name
First name
Sex
Date of birth
Age
Age category
Location
Institution
Department
Location type
Date of admission
Specimen number
Specimen date
Specimen type
Specimen type (Numeric)
Reason

Number of fields = 31

Country

Description	Country
Name	COUNTRY_A
Type	Text
Length	3

None

Data entry

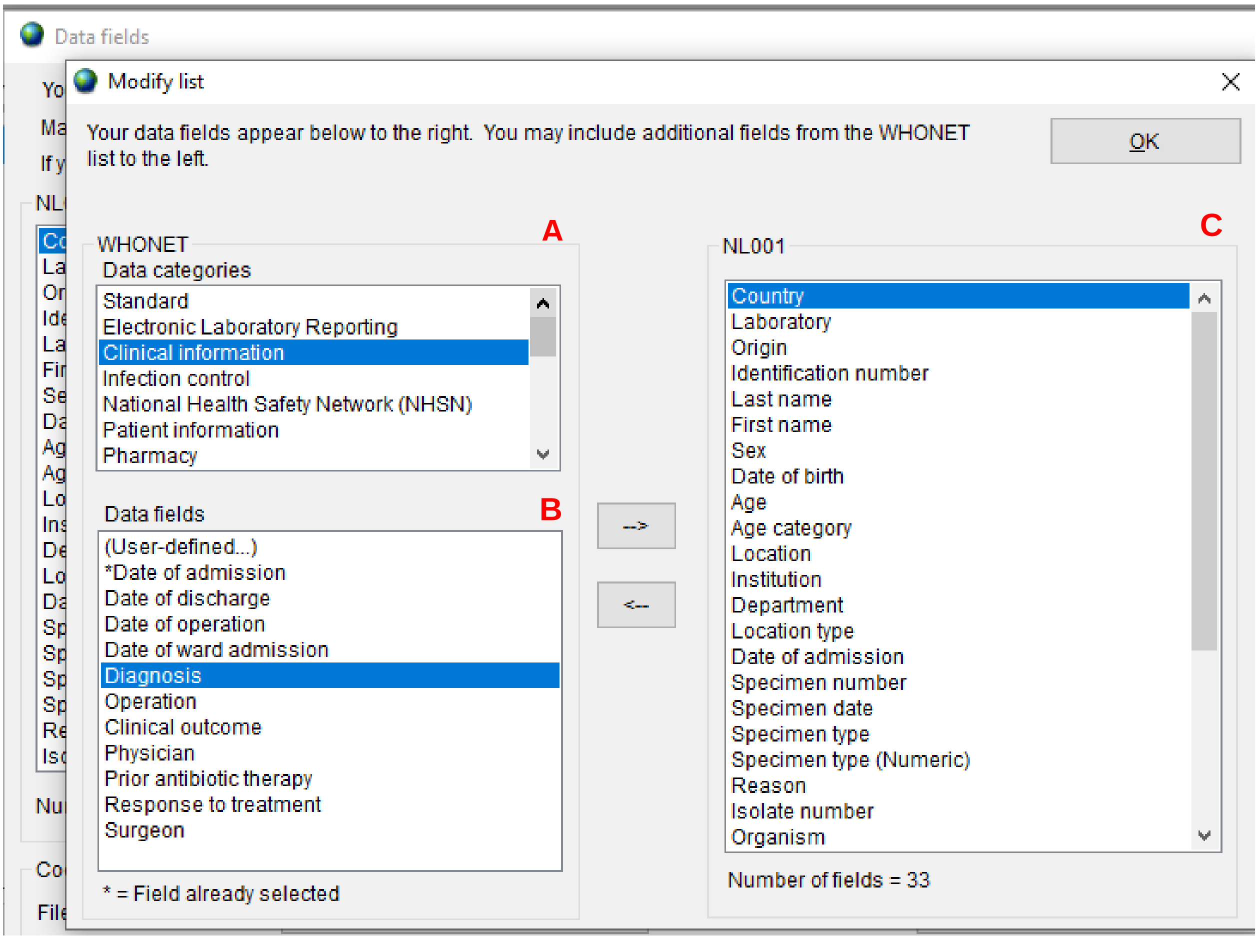
Section: Hidden

☑ Human
☑ Animal
☑ Food

☐ Isolate listing

Figure 2.16: Data fields screen.

An asterisk appears before the data field name (Figure 2.17 label B) once it has been added to the laboratory configuration for this laboratory.


Your data fields appear below to the right. You may include additional fields from the WHONET list to the left.

* = Field already selected

Number of fields = 33

Figure 2.17: Modify list screen.

Once you have added any other additional fields, click ‘OK’ to bring you back to the ‘Data fields’ screen and then click ‘OK’ again to bring you back to the ‘Laboratory configuration’ screen. Finally click on ‘Save’ to save any changes to this lab configuration.

2.4.6 Changing file locations

The default locations for all new laboratory configurations and data/output files created is on the local C:\ drive of the computer on which WHONET is installed:

Laboratory configuration files are stored in:	C:\WHONET
Data files are stored in:	C:\WHONET\Data
Output files are stored in:	C:\WHONET\Output

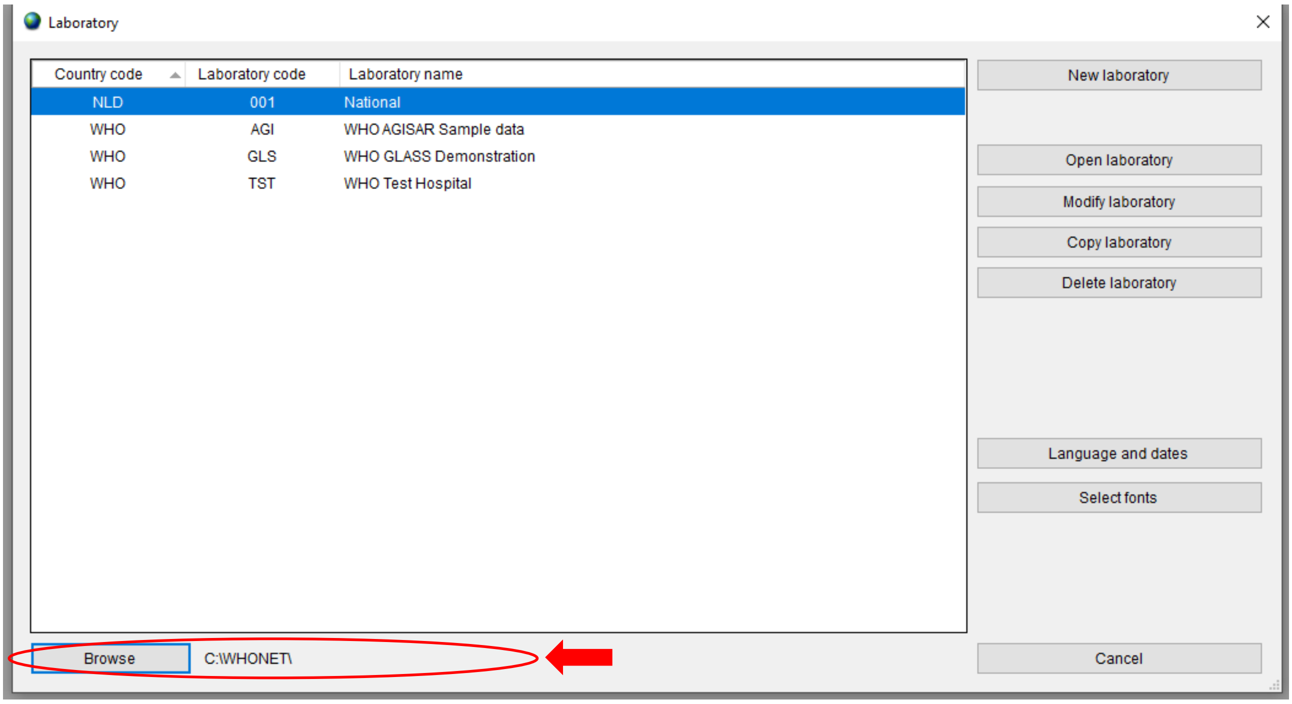
Macros are stored in: C:\WHONET\Macros

If your laboratory has a computer network, it is **not** recommended to keep any files on the local C:\ drive. If this computer crashes then all these files could be lost if the data have not been backed up. By keeping files on a network drive it is possible to share the configuration and data/output files between computers and there is a better chance that all the latest files will have been backed up (of course, this depends on the local IT policies).

1. To change the location of configuration files:

When you open up WHONET, you will see the 'Laboratory' screen (Figure 2.18) showing the list of laboratories available. The red arrow indicates the exact location or pathway to the laboratory configuration files.

TIP: Always change file locations to a drive on your computer network (if you have one).



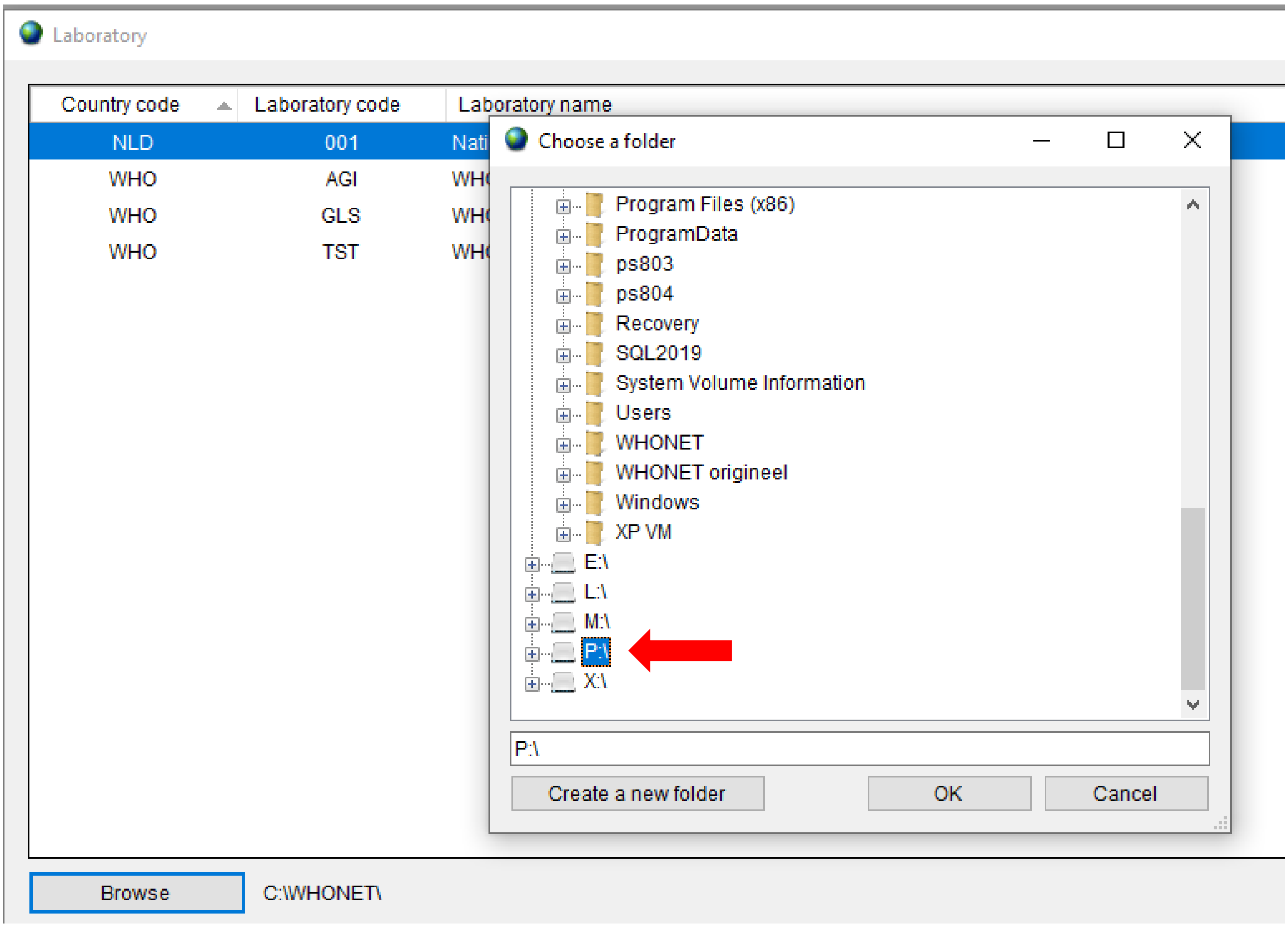
Country code	Laboratory code	Laboratory name
NLD	001	National
WHO	AGI	WHO AGISAR Sample data
WHO	GLS	WHO GLASS Demonstration
WHO	TST	WHO Test Hospital

Browse C:\WHONET\

Figure 2.18: Laboratory screen.

Click on the 'Browse' button to the left of this pathway in order to change this location. This brings up another screen that allows you to 'Select file location'. To change from the C:\ drive to a network drive, in the example below P:\ (Figure 2.19), click on the dropdown menu at the bottom of this screen and navigate to the new location. You may want to create a folder in this location called 'Networked WHONET configuration files'.

Once you have re-set the location of your laboratory configuration files, you will have to move any configuration files from the old location (C:\WHONET5) to the new location.



Country code	Laboratory code	Laboratory name
NLD	001	Nati
WHO	AGI	WH
WHO	GLS	WH
WHO	TST	WH

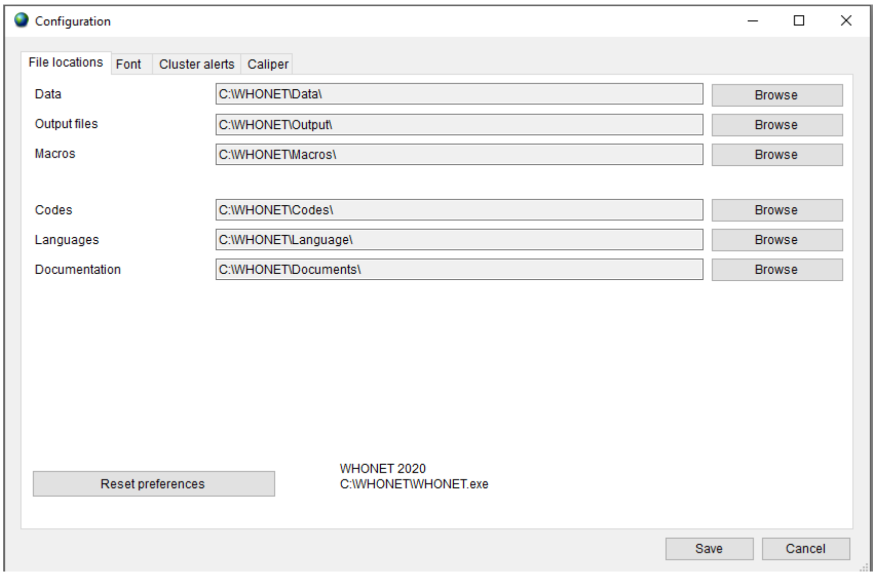
P:\

C:\WHONET\

Figure 2.19: 'Browse For Folder' screen: this allows you to select the folder on your network where laboratory configuration files will be placed.

2. To change the file locations for data, output and macro files:

Go to the WHONET main menu. Click on 'File', then 'Configuration' to bring up the File locations ('Configuration') screen (see Figure 2.20).



Data C:\WHONET\Data\
Output files C:\WHONET\Output\
Macros C:\WHONET\Macros\
Codes C:\WHONET\Codes\
Languages C:\WHONET\Language\
Documentation C:\WHONET\Documents\

WHONET 2020
C:\WHONET\WHONET.exe

Figure 2.20: Change file locations.

Click on the 'Browse' button to the right of 'Data' and 'Output files' pathways above and navigate to the new location on a network drive where you want to store these files.

You may want to create a folder, or folders, in this location, e.g. called 'Networked WHONET data files' and/or 'Networked WHONET output files', respectively.

Once you have re-set the location of data and output files, you will have to move any files already created from the old location (i.e. C:\WHONET\Data and C:\WHONET\Output) to the new location(s).

2.5 WHONET data format

2.5.1 dBase vs SQLite

Traditionally WHONET stored data in dBase format. This is a long existing format. Using the same format has the advantage of compatibility. Older WHONET files can be read with newer versions of the program. But the format has limitations in file size and in the number of columns. Moreover, problems are reported with newer Windows versions in handling this format. With WHONET 2020 a new data format was introduced: SQLite. SQLite is a modern platform, used on many operating systems, contrary to dBase which is only supported in Windows. dBase can still be used in WHONET, but it is recommended to use the newer SQLite format. It is to be expected that in the near future dBase will be abandoned. The reason is that SQLite enables innovations that were not possible in dBase because of its limitations.

2.5.2 Viewing WHONET files in other programs

Excel and Access can open dBase files. Saving a dBase file is not possible in recent Excel versions. Opening SQLite files in Excel is not (yet?) possible. Opening SQLite can be done in the freeware program DB Browser (SQLite). This program has the option to export tables as CSV files. These CSV files can be opened in many programs, including Excel.

2.5.3 Converting dBase into SQLite

WHONET has the option to convert existing dBase files into SQLite (see Figure 2.21). The original files will be kept in a backup folder.

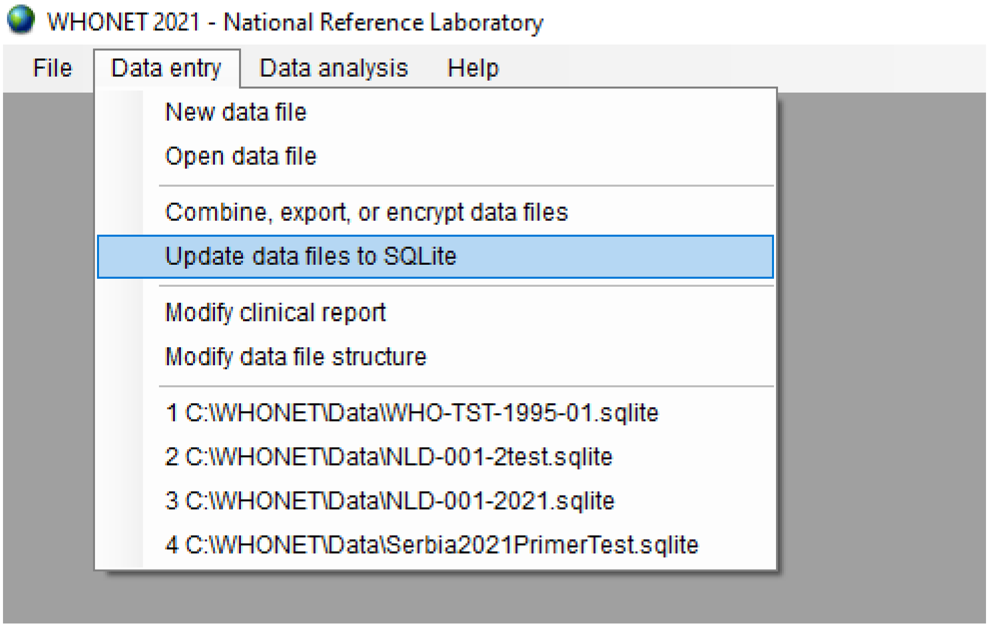
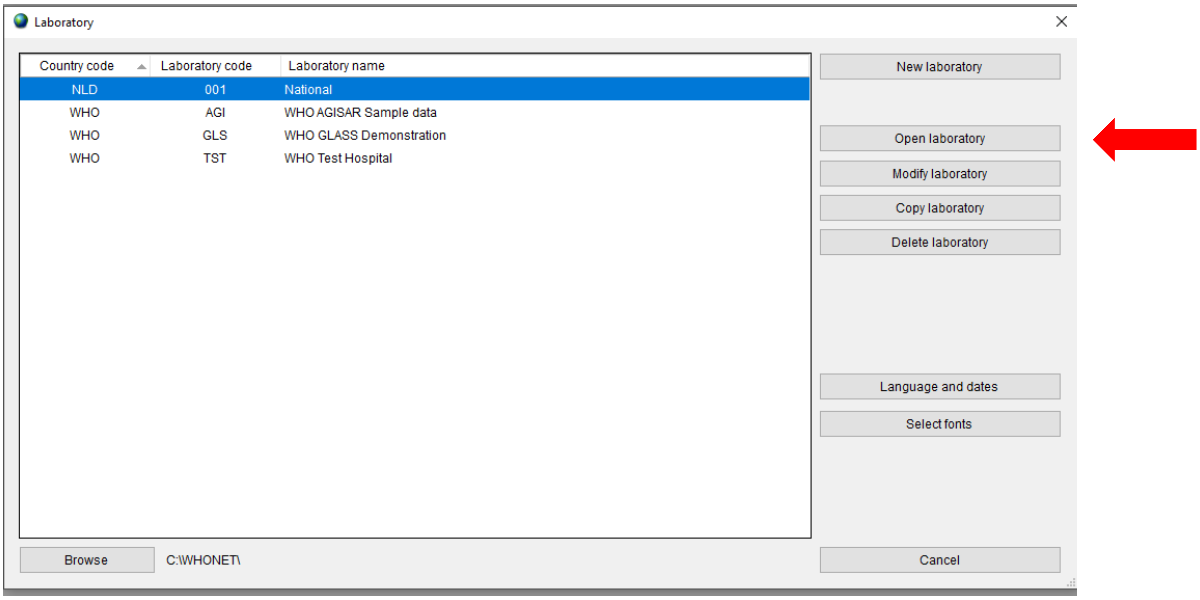


Figure 2.21: Converting DBase to SQLite.

2.6 WHONET data entry

First you must open the appropriate laboratory configuration before you can start entering data:

- Open WHONET
- Select the appropriate laboratory and click on ‘Open laboratory’ (see Figure 2.22)



Country code	Laboratory code	Laboratory name
NLD	001	National
WHO	AGI	WHO AGISAR Sample data
WHO	GLS	WHO GLASS Demonstration
WHO	TST	WHO Test Hospital

C:\WHONET\

Figure 2.22: WHONET opening screen, Open laboratory.

OR

- Go to the main menu and click on ‘File’, then ‘Open laboratory’ (see Figure 2.23)
- Select the appropriate laboratory and click on ‘‘Open laboratory’

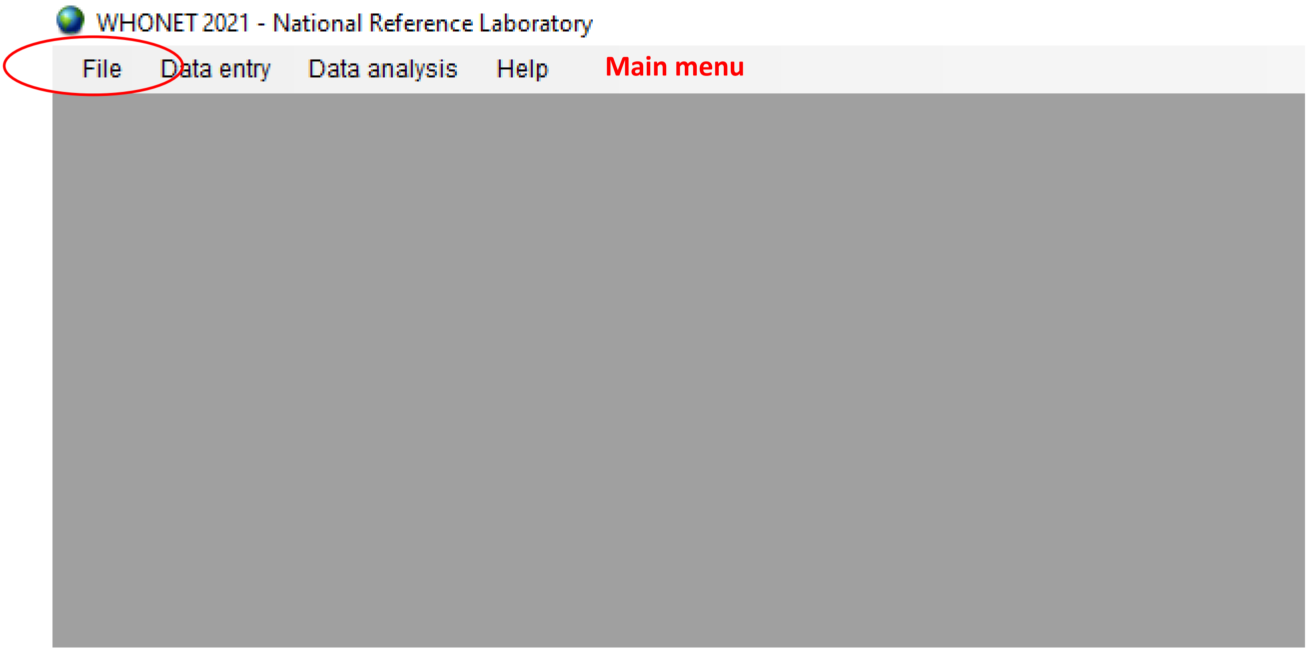


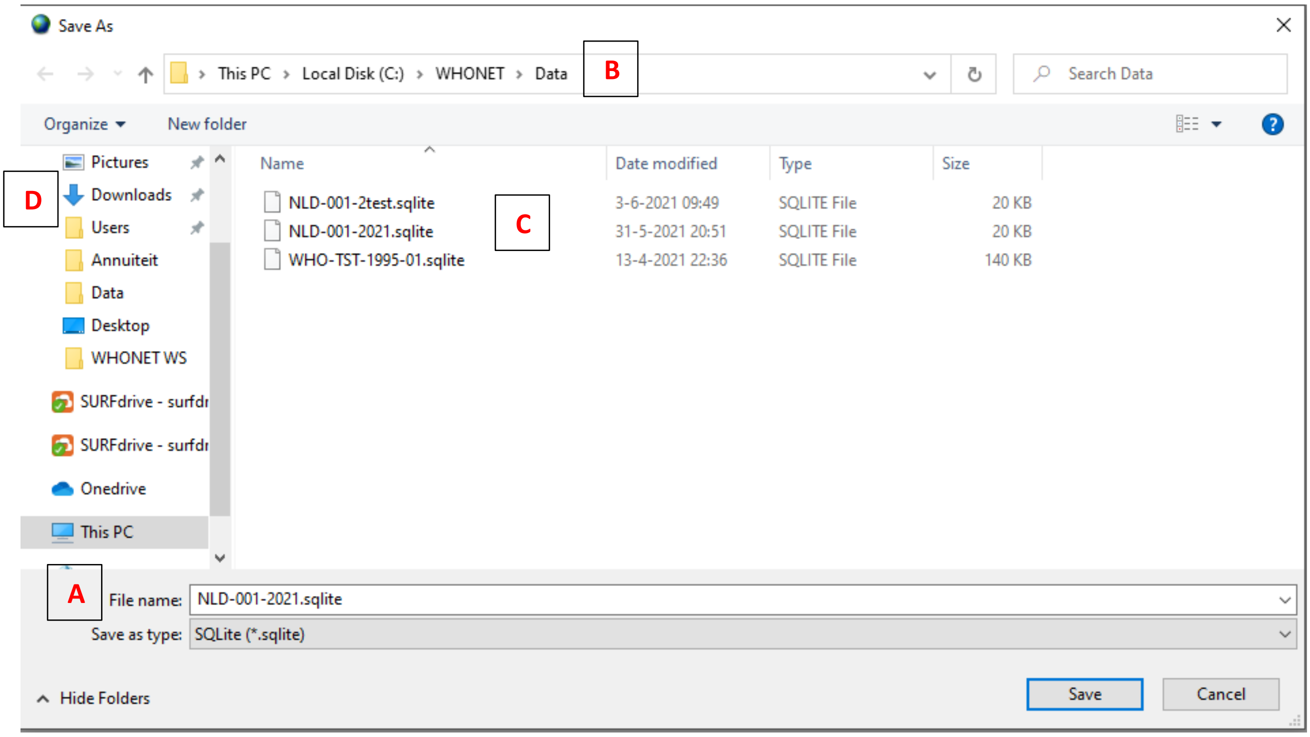
Figure 2.23: WHONET main screen: Open laboratory.

You can select a new data file or you can open an existing file.

To create a new file:

- Go to the main menu and click on ‘Data entry’, then ‘New data file’

The following screen appears (Figure 2.24):



Name	Date modified	Type	Size
NLD-001-2test.sqlite	3-6-2021 09:49	SQLITE File	20 KB
NLD-001-2021.sqlite	31-5-2021 20:51	SQLITE File	20 KB
WHO-TST-1995-01.sqlite	13-4-2021 22:36	SQLITE File	140 KB

File name: NLD-001-2021.sqlite
Save as type: SQLite (*.sqlite)

Figure 2.24: Create a name for the data file.

- You have to enter the name of the new file you want to create at the bottom of this screen (labelled A), for example NLD-001-2021.sqlite (see Tip below)

  Note: The current location where data files are stored is marked B (you will need to click on this in order to see the full pathway); Other files stored in this location are indicated by C; if you want to change the pathway, first change the drive (if required) marked D, then browse or navigate to get the correct pathway

TIP: It is recommend that you devise a sensible and consistent nomenclature/naming system for your data files that will allow you to identify exactly what data the file contains:

e.g. W121NLD.001 where W stands for WHONET, the first 1 represents the quarter number, 21 represents the year, NLD represents your country code and .001 is the file extension which allows WHONET to identify that this file is associated with the correct laboratory configuration for CAESAR General Hospital (LABNLD.001).

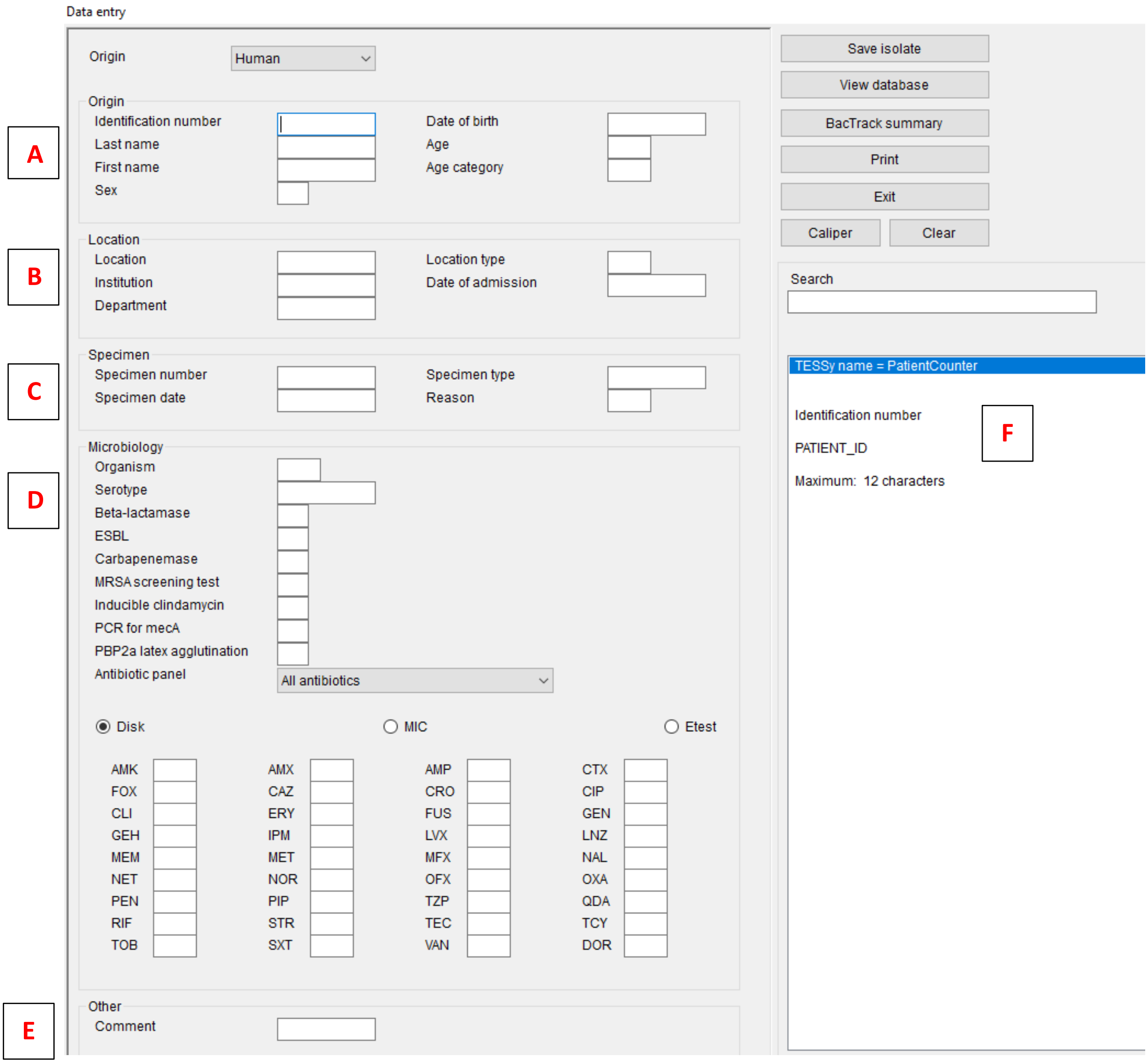
Other examples: 2021_urines.001; 2021Jan_wounds.001; 2021Q3_screening.001

TIP: BE CONSISTENT

TIP: we recommend that you do NOT store your data files in C:\WHONET5\data, which is the default folder for newly created files in WHONET unless otherwise stated. It is preferable and safer to store ALL data files in a network folder that is backed up regularly (if your organisation has a computer network). If not available make sure to regularly save backup copies elsewhere as well.

Once you have given the new data file its name, click ‘Save’.

WHONET will then create the file and open up the data entry screen (see Figure 2.25).



Origin: Human

Antibiotic panel: All antibiotics

● Disk

TESSy name = PatientCounter

Identification number

PATIENT_ID

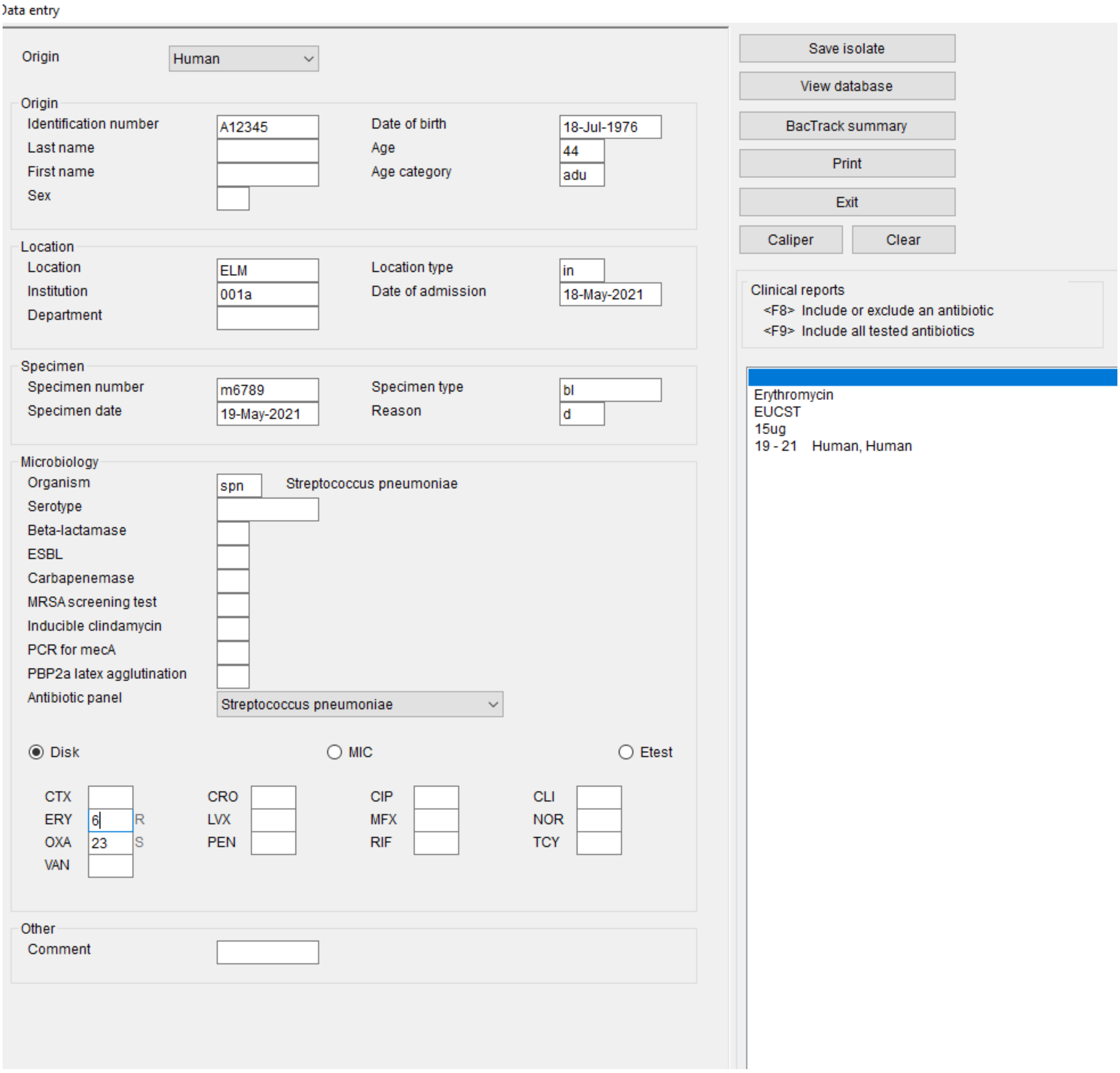
Maximum: 12 characters

Figure 2.25: Data entry form.

- The data entry form appears in the left side of the screen and is a divided into a number of sections:
    - **Origin** (**A**) = Patient-level details
    - **Location** (**B**) = Location of the patient in terms of location type (e.g. inpatient, outpatient), hospital/institution (e.g. 065A, 065B etc. refer to different hospitals and institutions), ward name (e.g. Oak ward; Ward No.1, etc.) and speciality (e.g. ICU, surgery, medical, ob/gyn, etc.)

- **Specimen** (**C**) = Specimen-level details
  - **Microbiology** (**D**) = Organism name and its associated antibiogram
  - **Other** (**E**) = Comment and other optional data fields as configured locally
- By clicking on each of the data fields in turn, a brief outline of the data options for that field (instructions and recommended data codes) appear in the lower right of the screen **(F)**

TIP: You can only enter data for one isolate of an organism at a time: if a specimen has more than one isolate (or strain) of a particular organism or multiple isolates of different organisms, subsequent strains and organisms must be entered separately.



Origin: Human

Origin
Identification number: A12345
Last name:
First name:
Sex:
Date of birth: 18-Jul-1976
Age: 44
Age category: adu

Location
Location: ELM
Institution: 001a
Department:
Location type: in
Date of admission: 18-May-2021

Specimen
Specimen number: m6789
Specimen date: 19-May-2021
Specimen type: bl
Reason: d

Microbiology
Organism: spn Streptococcus pneumoniae
Serotype:
Beta-lactamase:
ESBL:
Carbapenemase:
MRSA screening test:
Inducible clindamycin:
PCR for mecA:
PBP2a latex agglutination:
Antibiotic panel: Streptococcus pneumoniae

● Disk ○ MIC ○ Etest

CTX		CRO		CIP		CLI	
ERY	6 R	LVX		MFX		NOR	
OXA	23 S	PEN		RIF		TCY	
VAN							

Other
Comment:

Clinical reports
<F8> Include or exclude an antibiotic
<F9> Include all tested antibiotics

Erythromycin
EUCST
15ug
19 - 21 Human, Human

Figure 2.26: Entering data.

- After entering data in one field, there are four ways of moving to the next field:

  - press the <Enter> key; or
  - press the <Tab> key; or
  - press the arrow keys; or
  - use the mouse
- You should enter **dates** in the same format as the default format on your computer, namely as day/month/year or month/day/year or year/month/day. When you have entered a date and moved to the next field, check that the date has been interpreted correctly: WHONET automatically converts the numeric date to the name of the month. When entering a date, the year can be entered as a 2- or 4-digit date. The numbers indicating day, month and year must be separated by a '/' or a '–' or a space

TIP: Be careful with dates before 1950, e.g. if you enter a date of birth 01/01/49, this will appear as 01/01/**20**49. So for dates before 1950, enter the full 4-digit year.

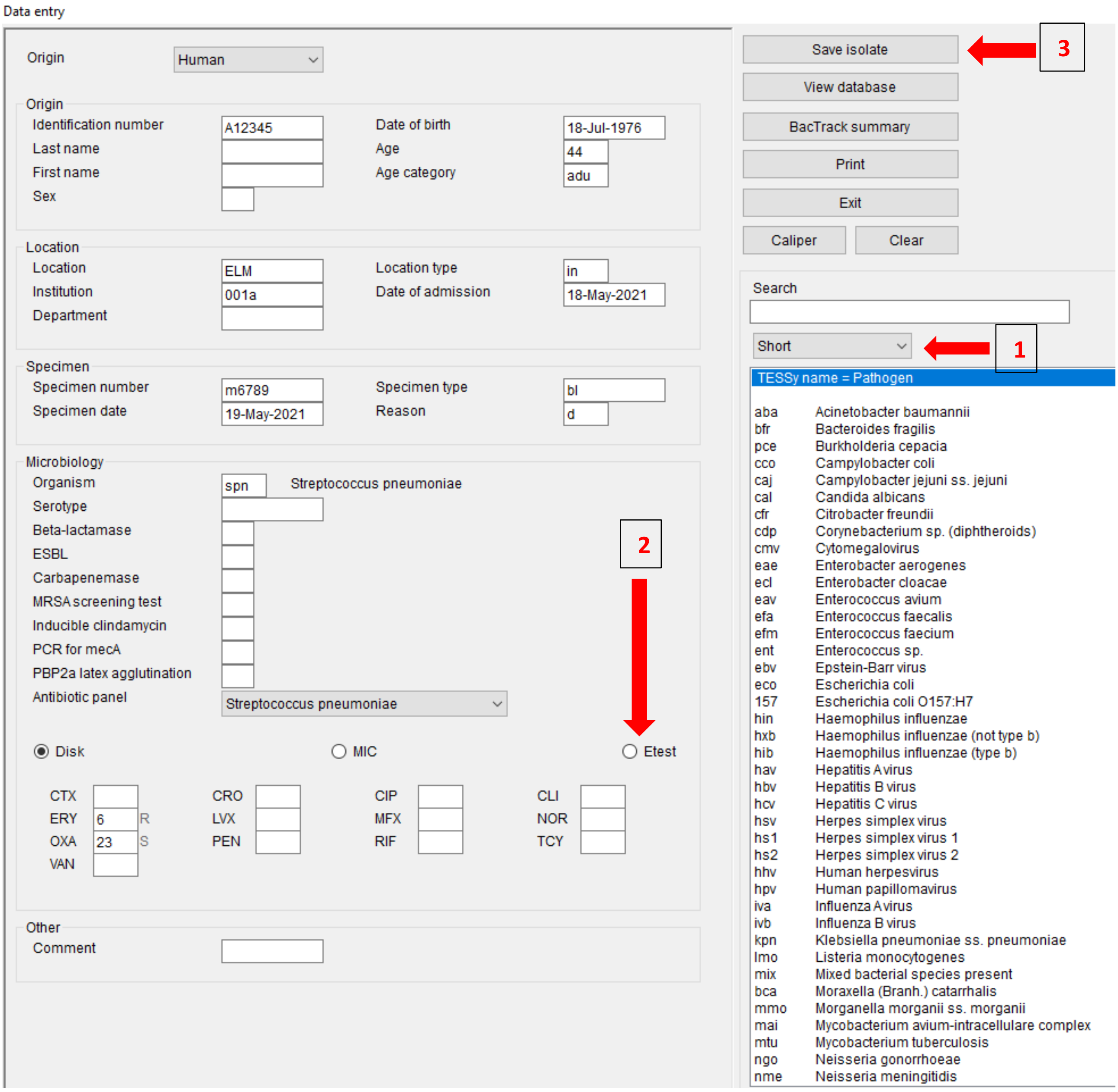
Field specific comments:

Age

You have the option of entering the patient's age. However, if you have entered the patient's date of birth, their age and age category will automatically be calculated and inserted in the age and age category fields, respectively, when you enter the specimen date (otherwise the age will be calculated using the date of data entry if no specimen date is available).

Organism

The 3-character WHONET organism code should be entered here, or selected from the list on the right half of the screen. By default, only the most common organism codes ('Short' list) are listed. To view the full list, select 'Extended' from the dropdown (see Figure 2.27 label 1).



Data entry

Origin: Human

Origin

Identification number: A12345
Last name:
First name:
Sex:
Date of birth: 18-Jul-1976
Age: 44
Age category: adu

Location

Location: ELM
Institution: 001a
Department:
Location type: in
Date of admission: 18-May-2021

Specimen

Specimen number: m6789
Specimen date: 19-May-2021
Specimen type: bl
Reason: d

Microbiology

Organism: spn Streptococcus pneumoniae
Serotype:
Beta-lactamase:
ESBL:
Carbapenemase:
MRSA screening test:
Inducible clindamycin:
PCR for mecA:
PBP2a latex agglutination:
Antibiotic panel: Streptococcus pneumoniae

● Disk ○ MIC ○ Etest

CTX		CRO		CIP		CLI	
ERY	6 R	LVX		MFX		NOR	
OXA	23 S	PEN		RIF		TCY	
VAN							

Other

Comment:

Search:

Short

TESSy name = Pathogen

aba	Acinetobacter baumannii
bfr	Bacteroides fragilis
pce	Burkholderia cepacia
cco	Campylobacter coli
caj	Campylobacter jejuni ss. jejuni
cal	Candida albicans
cfr	Citrobacter freundii
cdp	Corynebacterium sp. (diphtheroids)
cmv	Cytomegalovirus
eae	Enterobacter aerogenes
ecl	Enterobacter cloacae
eav	Enterococcus avium
efa	Enterococcus faecalis
efm	Enterococcus faecium
ent	Enterococcus sp.
ebv	Epstein-Barr virus
eco	Escherichia coli
157	Escherichia coli O157:H7
hin	Haemophilus influenzae
hxb	Haemophilus influenzae (not type b)
hib	Haemophilus influenzae (type b)
hav	Hepatitis A virus
hbv	Hepatitis B virus
hcv	Hepatitis C virus
hsv	Herpes simplex virus
hs1	Herpes simplex virus 1
hs2	Herpes simplex virus 2
hhv	Human herpesvirus
hpv	Human papillomavirus
iva	Influenza A virus
ivb	Influenza B virus
kpn	Klebsiella pneumoniae ss. pneumoniae
lmo	Listeria monocytogenes
mix	Mixed bacterial species present
bca	Moraxella (Branh.) catarrhalis
mmo	Morganella morganii ss. morganii
mai	Mycobacterium avium-intracellulare complex
mtu	Mycobacterium tuberculosis
ngo	Neisseria gonorrhoeae
nme	Neisseria meningitidis

Figure 2.27: Entering susceptibility results.

Susceptibility results and the list of antibiotics

To enter susceptibility results, first click on the appropriate test method: Disk (for disk diffusion), MIC or Etest (see Figure 2.27 label 2). The list of antibiotics which you defined for that test method should appear immediately below.

Each time you enter a result and press <Enter> (or <Tab>), the cursor jumps to the next antibiotic.

If antibiotic panels have been configured: for example, if you are entering results for *Staphylococcus aureus* (organism code 'sau'), you will be asked for the Gram-positive drugs only. If you change the panel to 'All antibiotics', then you may select from any of the antibiotics in the laboratory's antibiotic list.

TIP: In the laboratory configuration, the order of antibiotics should be alphabetical or some other logical way to ensure ease of data entry: the order should never be random!

Entering susceptibility results

WHONET allows the entry of quantitative results (e.g. 13mm, 64µg/ml) or qualitative results (R = resistant, I = intermediate, S = susceptible).

The lowest possible zone diameter is 6mm. If you enter 0mm (indicating no inhibition), WHONET automatically changes this to 6mm.

For off-scale MIC values you may enter, for example, <=.5, >64.

If you are entering MIC results from the test of a drug combination, enter the result of the first (or principal) agent only:

trimethoprim/sulfamethoxazole	>4/76: then enter >4
piperacillin/tazobactam	<=4/4: then enter <=4

Note: MIC concentrations usually follow the 1, 2, 4, 8 … doubling-dilution series.

Saving the isolate information

- When you have entered all the data for an isolate, click on 'Save Isolate' (see Figure 2.27 label 3), or press Alt-S. WHONET will then ask you whether you want to:
    - Save the isolate
    - Save and continue with the same specimen (all the details for Origin, Location and Specimen will be automatically filled in based on the previous entry, but not Microbiology or Other)
    - Save and continue with the same patient (all the details for Origin and Location will be automatically filled in based on the previous entry, but not Specimen, Microbiology or Other)
- Click on one of these options as appropriate and then 'OK' (the data will be saved to disk and the Data Entry screen will be cleared so that the data for the next isolate can be entered) **OR** if you decide not to save the record click 'Cancel'

Exiting data entry

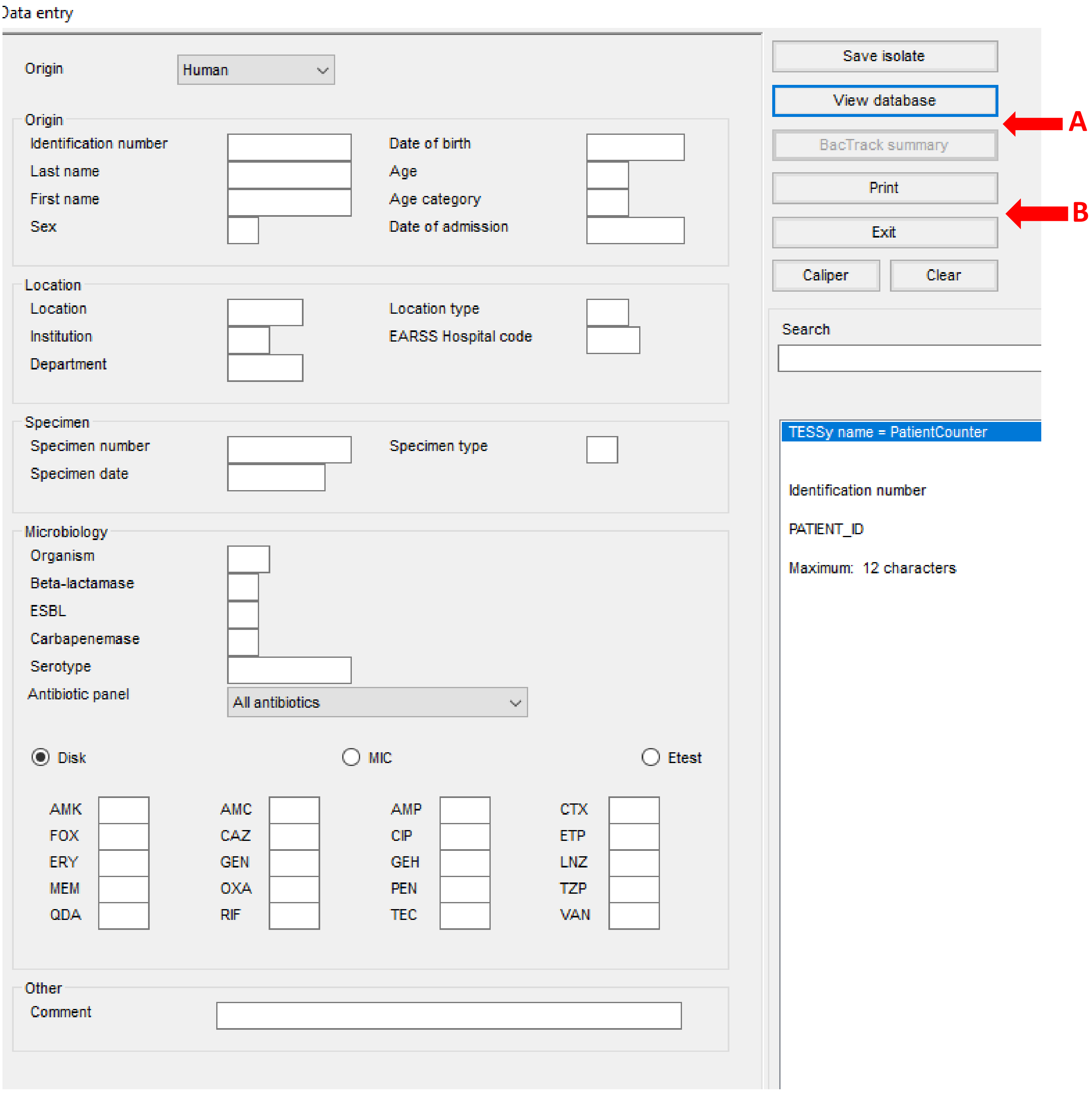
- Once you are finished entering data, click on 'Exit' on the Data entry screen to return to the main menu of WHONET

To open an existing data file, view the database and edit the data

- From the main menu, go to 'Data entry', then 'Open data file'

- Select the data file and click on 'Open', or alternatively just double-click on the data file to be opened

- To look at the database, containing all the records entered so far, click on 'View database' (see Figure 2.28 label A)



Origin: Human

Antibiotic panel: All antibiotics

● Disk ○ MIC ○ Etest

TESSy name = PatientCounter

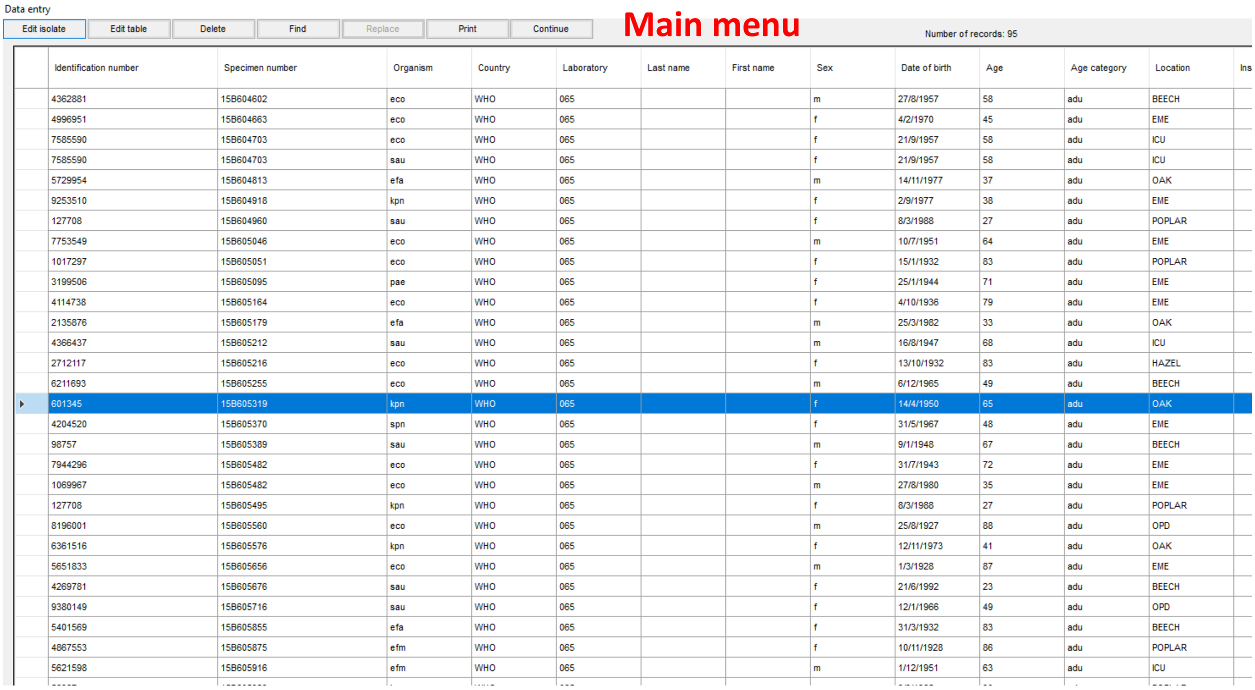
Identification number

PATIENT_ID

Maximum: 12 characters

Figure 2.28: Data entry screen.

- The Database View screen below appears:



Number of records: 95

	Identification number	Specimen number	Organism	Country	Laboratory	Last name	First name	Sex	Date of birth	Age	Age category	Location	Ins
	4362881	15B604602	eco	WHO	065			m	27/8/1957	58	adu	BEECH	
	4996951	15B604663	eco	WHO	065			f	4/2/1970	45	adu	EME	
	7585590	15B604703	eco	WHO	065			f	21/9/1957	58	adu	ICU	
	7585590	15B604703	sau	WHO	065			f	21/9/1957	58	adu	ICU	
	5729954	15B604813	efa	WHO	065			m	14/11/1977	37	adu	OAK	
	9253510	15B604918	kpn	WHO	065			f	2/9/1977	38	adu	EME	
	127708	15B604960	sau	WHO	065			f	8/3/1988	27	adu	POPLAR	
	7753549	15B605046	eco	WHO	065			m	10/7/1951	64	adu	EME	
	1017297	15B605051	eco	WHO	065			f	15/1/1932	83	adu	POPLAR	
	3199506	15B605095	pae	WHO	065			f	25/1/1944	71	adu	EME	
	4114738	15B605164	eco	WHO	065			f	4/10/1936	79	adu	EME	
	2135876	15B605179	efa	WHO	065			m	25/3/1982	33	adu	OAK	
	4366437	15B605212	sau	WHO	065			m	16/8/1947	68	adu	ICU	
	2712117	15B605216	eco	WHO	065			f	13/10/1932	83	adu	HAZEL	
	6211693	15B605255	eco	WHO	065			m	6/12/1965	49	adu	BEECH	
▶	601345	15B605319	kpn	WHO	065			f	14/4/1950	65	adu	OAK	
	4204520	15B605370	spn	WHO	065			f	31/5/1967	48	adu	EME	
	98757	15B605389	sau	WHO	065			m	9/1/1948	67	adu	BEECH	
	7944296	15B605482	eco	WHO	065			f	31/7/1943	72	adu	EME	
	1069967	15B605482	eco	WHO	065			m	27/8/1980	35	adu	EME	
	127708	15B605495	kpn	WHO	065			f	8/3/1988	27	adu	POPLAR	
	8196001	15B605560	eco	WHO	065			m	25/8/1927	88	adu	OPD	
	6361516	15B605576	kpn	WHO	065			f	12/11/1973	41	adu	OAK	
	5651833	15B605656	eco	WHO	065			m	1/3/1928	87	adu	EME	
	4269781	15B605676	sau	WHO	065			f	21/6/1992	23	adu	BEECH	
	9380149	15B605716	sau	WHO	065			f	12/1/1966	49	adu	OPD	
	5401569	15B605855	efa	WHO	065			f	31/3/1932	83	adu	BEECH	
	4867553	15B605875	efm	WHO	065			f	10/11/1928	86	adu	POPLAR	
	5621598	15B605916	efm	WHO	065			m	1/12/1951	63	adu	ICU	

Figure 2.29: Database View screen.

- If you want to sort any column, click once on that column heading (e.g. single clicking on Date of birth will sort the dates from oldest to newest; similarly single-clicking on Location will sort the locations (in this example, ward names) alphabetically
- It is possible to make changes to either (1) individual isolates or (2) directly to the database:
    - To make changes to a single isolate, click on 'Edit isolate' at the top of the screen. This will bring you back to the data entry screen, from where you can make the changes. Click on 'Save Isolate' to save any changes
    - To make changes directly to the database, click on 'Edit table' from the Main menu at the top of the screen (see Figure 2.29). Click on 'Find' (also from Main menu) to search for a particular id number, organism, specimen date, etc (see Figure 2.30)
      This is particularly useful if you are editing the same field in multiple isolates, e.g. adding ESBL results to all *E. coli* isolates.

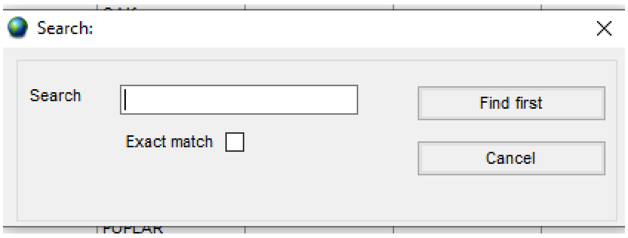
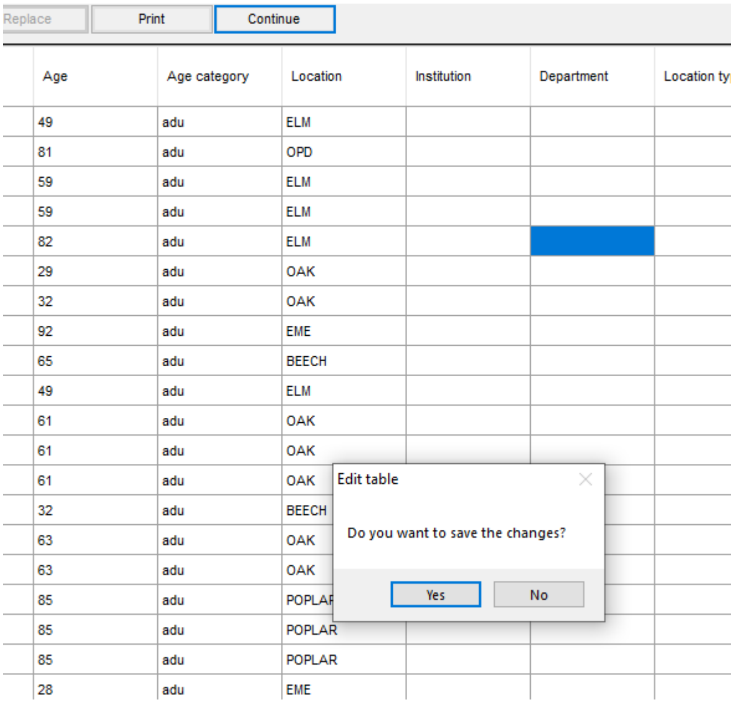


Figure 2.30: Search function.

Make the necessary changes to the table or database

To leave this screen above, click on 'Continue' to bring you back to the Data entry screen. You will be asked 'Do you want to save the changes?' Click 'Yes' (or 'No')



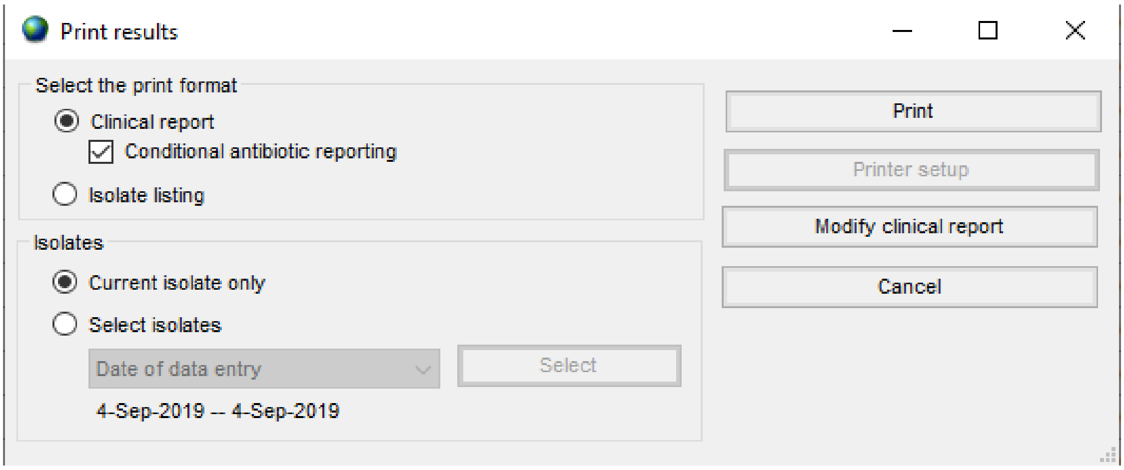
Age	Age category	Location	Institution	Department	Location ty
49	adu	ELM			
81	adu	OPD			
59	adu	ELM			
59	adu	ELM			
82	adu	ELM			
29	adu	OAK			
32	adu	OAK			
92	adu	EME			
65	adu	BEECH			
49	adu	ELM			
61	adu	OAK			
61	adu	OAK			
61	adu	OAK			
32	adu	BEECH			
63	adu	OAK			
63	adu	OAK			
85	adu	POPLAF			
85	adu	POPLAR			
85	adu	POPLAR			
28	adu	EME			

Edit table

Do you want to save the changes?

Figure 2.31: Database view: Save Changes?

- To delete an isolate, highlight the appropriate isolate and click on ‘Delete’ (see Figure 2.29)
- From either the Data entry screen or the Database View screen, it is possible to print all the details for a particular isolate/record by clicking on ‘Print’ (see Figure 2.28 label B OR Figure 2.29) to bring up the Print results screen (see Figure 2.32) [note: this screen allows you to play around with the format of what is to be printed] and click on ‘Print’

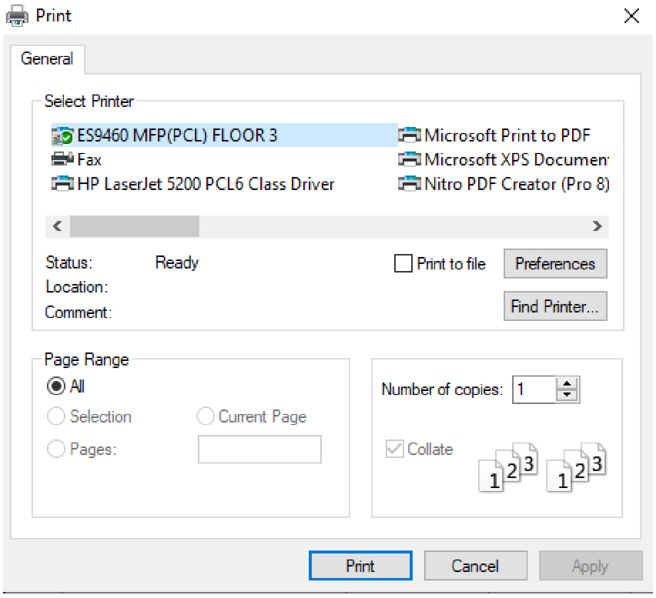

Print results

Select the print format
● Clinical report
☑ Conditional antibiotic reporting
○ Isolate listing

Isolates
● Current isolate only
○ Select isolates
Date of data entry
4-Sep-2019 -- 4-Sep-2019

Figure 2.32: Print results screen.

Finally click on ‘Print’ on the subsequent Print screen (see Figure 2.33) [note: this screen allows you to select a printer from your network where you want the report to be printed]



Status: Ready

Location:

Comment:

☐ Print to file

● All

Number of copies: 1

☑ Collate

Figure 2.33: Printer selection screen.

- From the data entry screen, click on ‘Exit’ to bring you back to the main menu of WHONET

3 WHONET data analysis

WHONET provides a useful ‘Data analysis’ package for analysing your data.

The ‘Data analysis’ screen is divided into a number of different sections (see Figure 3.1).

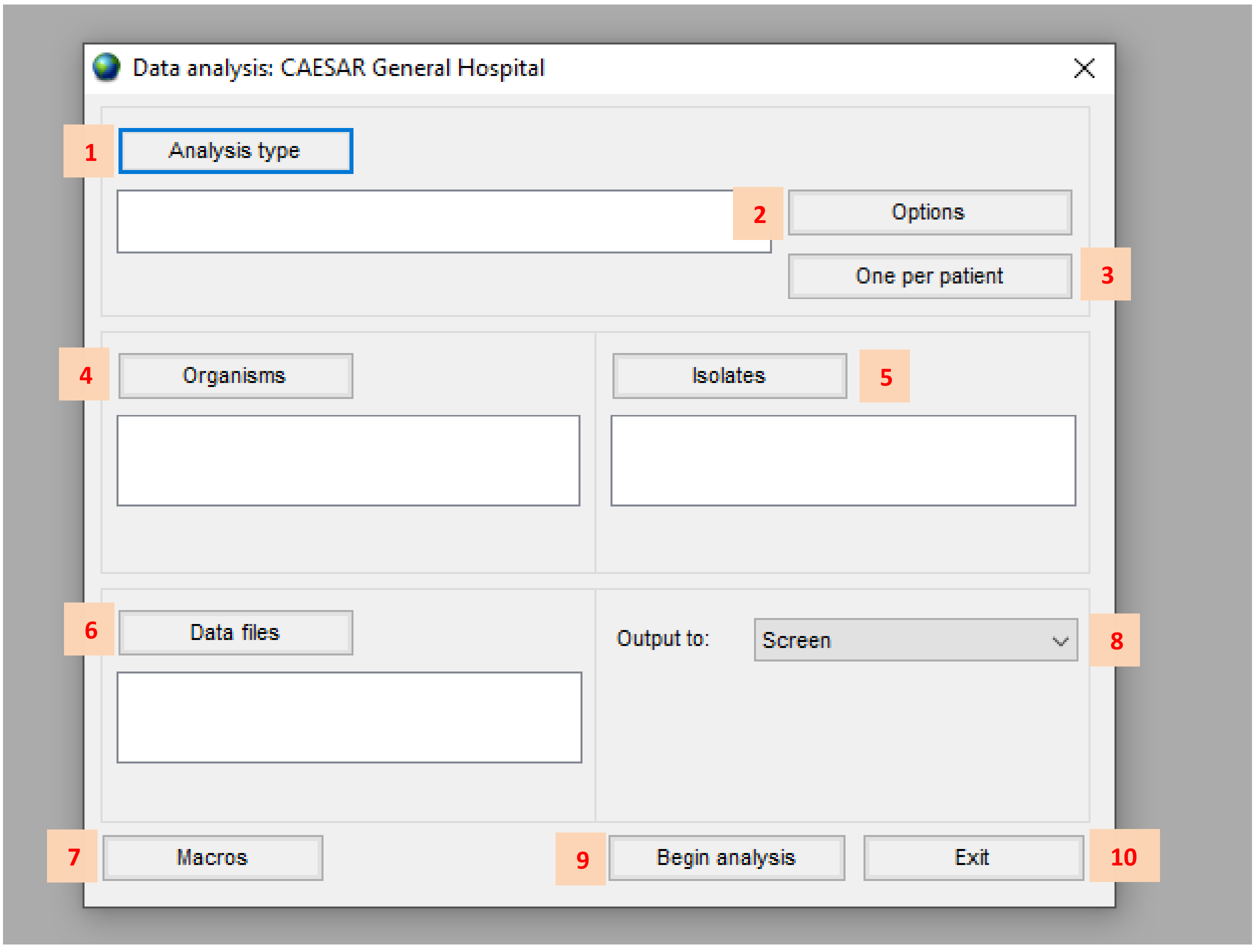
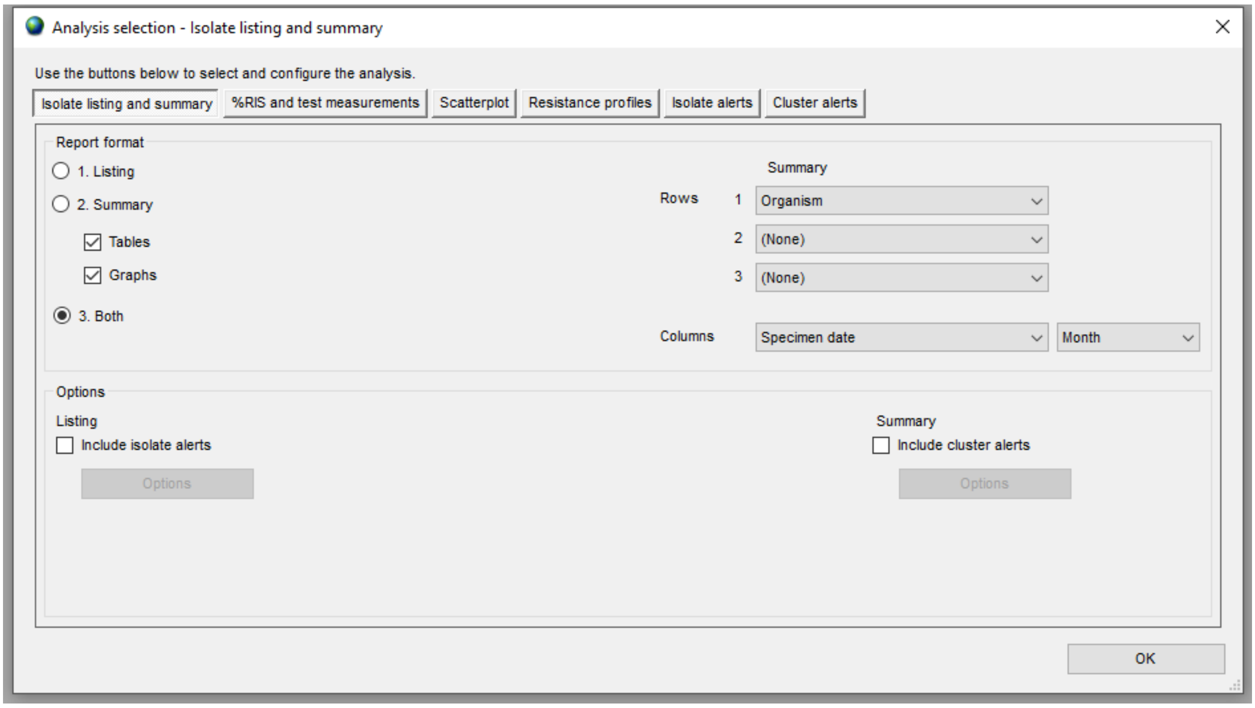


Figure 3.1: Data analysis screen.

Click on the ‘Analysis type’ button (Figure 3.1 label 1) to see the 6 analysis type options currently available:

1. Isolate listing and summary
2. %RIS and test measurements
3. Scatterplot (Not covered in this manual)
4. Resistance profiles
5. Isolate alerts - previously called Bactrack in WHONET 5.6 (Not covered in this manual)
6. Cluster alerts (Not covered in this manual)



Analysis selection - Isolate listing and summary

Use the buttons below to select and configure the analysis.

Report format

○ 1. Listing

○ 2. Summary

☑ Tables

☑ Graphs

● 3. Both

Summary

Rows 1 Organism

2 (None)

3 (None)

Columns Specimen date Month

Options

Listing

☐ Include isolate alerts

Summary

☐ Include cluster alerts

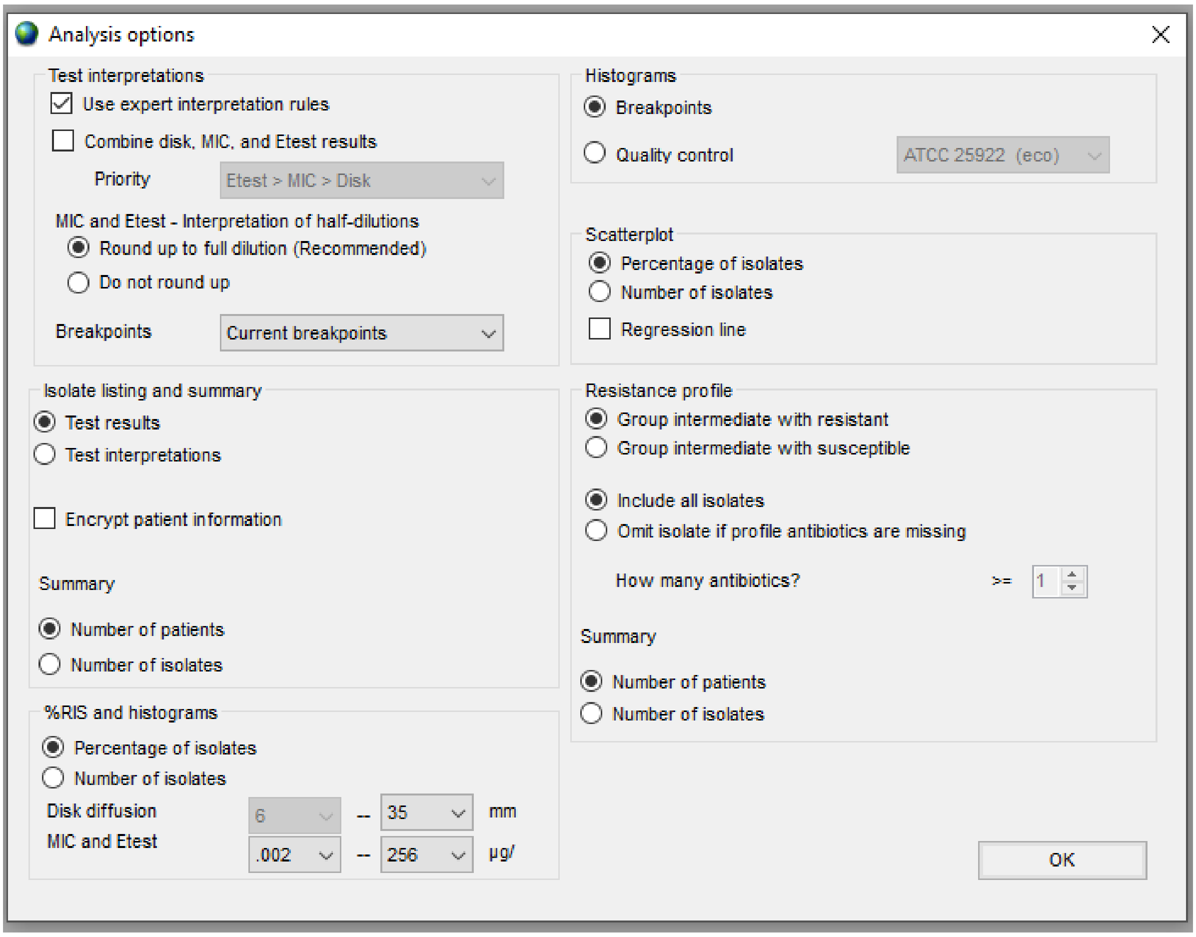
Figure 3.2: Isolate listing and summary.

Click on the ‘Options’ button (Figure 3.1 label 2) to see the options that are available (see Figure 3.2). The ‘Analysis options’ screen is arranged into 6 sections, each of which has different parameters that can be amended to suit the needs of the analysis being undertaken:

- Test interpretations (these are general options that apply to all analysis types)
- Isolate listing and summary
  Please note: the option to ‘Encrypt patient information’ does not provide particularly strong encryption
- %RIS and histograms
- Histograms
- Scatterplot
- Resistance profile

Click on the ‘One per patient?’ button (Figure 3.1 label 3) to see the options that are available (see Figure 3.3). These options allow analysis by:

- Isolate – this is the default and ALL isolates in the file(s) will be included in the analysis
- Patient – this allows you to select the first isolate per patient with antibiotic results
- Time interval – this allows you to select the first isolate per patient with antibiotic results over a specific time period that you select, e.g. 30 days, which means a 2nd isolate from the same patient will only be counted 30 days after the 1st one


Analysis options

Test interpretations
☑ Use expert interpretation rules
☐ Combine disk, MIC, and Etest results
Priority: Etest > MIC > Disk
MIC and Etest - Interpretation of half-dilutions
● Round up to full dilution (Recommended)
○ Do not round up
Breakpoints: Current breakpoints

Isolate listing and summary
● Test results
○ Test interpretations
☐ Encrypt patient information
Summary
● Number of patients
○ Number of isolates

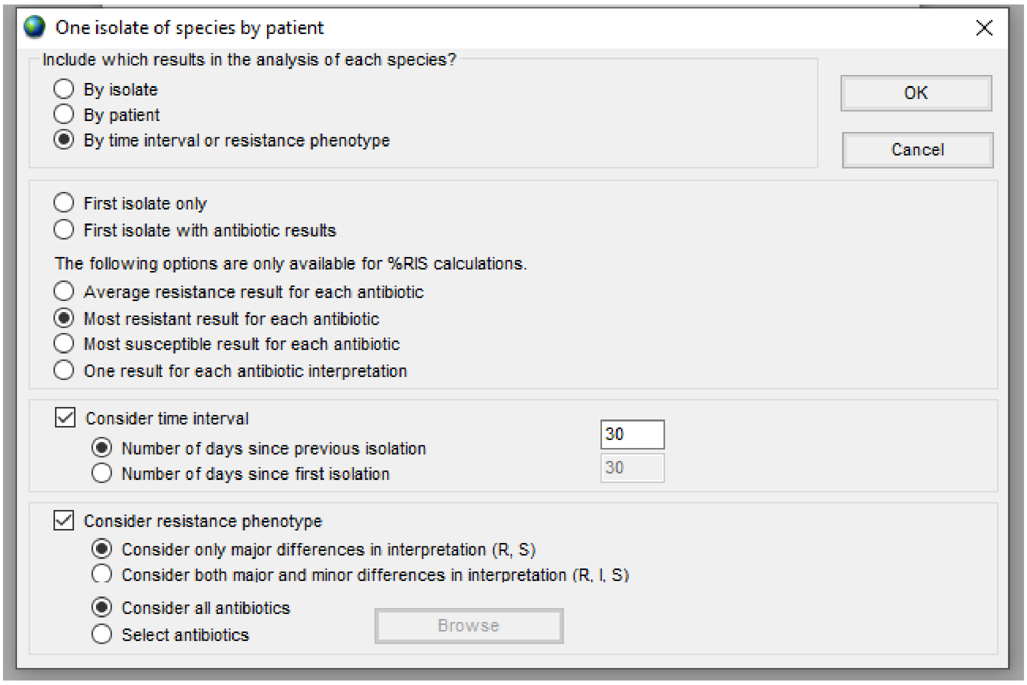
%RIS and histograms
● Percentage of isolates
○ Number of isolates
Disk diffusion: 6 -- 35 mm
MIC and Etest: .002 -- 256 µg/

Histograms
● Breakpoints
○ Quality control: ATCC 25922 (eco)

Scatterplot
● Percentage of isolates
○ Number of isolates
☐ Regression line

Resistance profile
● Group intermediate with resistant
○ Group intermediate with susceptible
● Include all isolates
○ Omit isolate if profile antibiotics are missing
How many antibiotics? >= 1
Summary
● Number of patients
○ Number of isolates

Figure 3.3: Analysis options screen.



One isolate of species by patient

Include which results in the analysis of each species?

○ By isolate
○ By patient
● By time interval or resistance phenotype

○ First isolate only
○ First isolate with antibiotic results

The following options are only available for %RIS calculations.

○ Average resistance result for each antibiotic
● Most resistant result for each antibiotic
○ Most susceptible result for each antibiotic
○ One result for each antibiotic interpretation

☑ Consider time interval
- ● Number of days since previous isolation: 30
- ○ Number of days since first isolation: 30

☑ Consider resistance phenotype
- ● Consider only major differences in interpretation (R, S)
- ○ Consider both major and minor differences in interpretation (R, I, S)
- ● Consider all antibiotics
- ○ Select antibiotics

Figure 3.4: Options for 'One (isolate) per patient'.

Click on the 'Organisms' button (Figure 3.1 label 4) to select the species or groups (e.g. all Gram-negatives or Enterobacteriaceae). WHONET uses 3 letter codes for organisms and organism groups. The relevant organisms and codes for CAESAR are in Table 1:

Table 1: WHONET codes for CAESAR organisms.

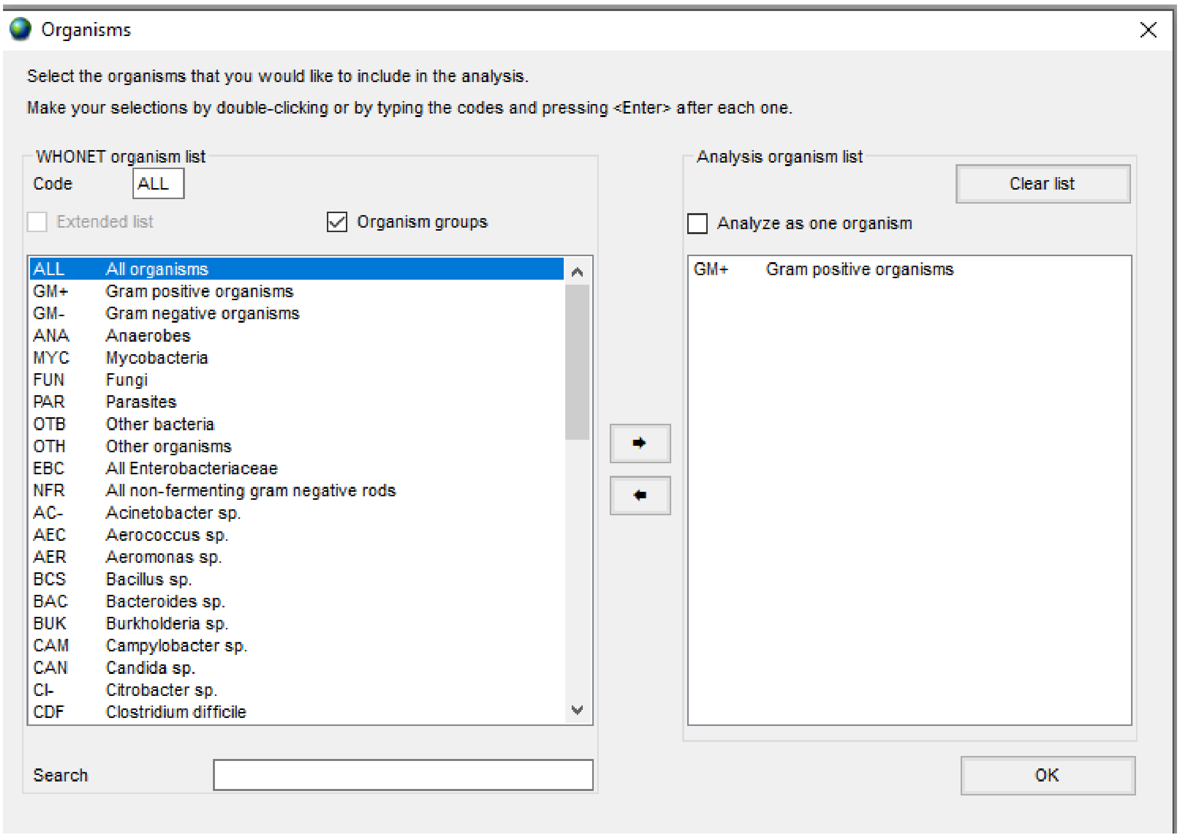
Organism	**WHONET code**
S. aureus	sau
S. pneumoniae	spn
E. coli	eco
E. faecalis	efa
E. faecium	efm
K. pneumoniae	kpn
P. aeruginosa	pae
Salmonella spp.	sal
Acinetobacter spp.	ac-

*Note: The code AC- (upper case) will bring back all Acinetobacters regardless of the species

If you want to analyse all organisms in the file(s), then use the organism code 'ALL'.

Note: 'All' will include all the results in your data file even if these were no growth/no pathogens isolated if your file includes all the laboratory results.

The full list of organisms and groups appears on the left side of the window (see Figure 3.4), the panel on the right side is the list of organisms/groups to be analysed. Use the Search field to find the organism(s) to be included in the analysis, highlight the organism using your mouse (it will be highlighted in blue) and then double (left) click your mouse or single click on the left-pointing arrow between the two panels to bring the organism across to the panel on the right. Click 'OK' when the list is complete.



Organisms

Select the organisms that you would like to include in the analysis.
Make your selections by double-clicking or by typing the codes and pressing <Enter> after each one.

WHONET organism list

Code: ALL

☐ Extended list ☑ Organism groups

ALL	All organisms
GM+	Gram positive organisms
GM-	Gram negative organisms
ANA	Anaerobes
MYC	Mycobacteria
FUN	Fungi
PAR	Parasites
OTB	Other bacteria
OTH	Other organisms
EBC	All Enterobacteriaceae
NFR	All non-fermenting gram negative rods
AC-	Acinetobacter sp.
AEC	Aerococcus sp.
AER	Aeromonas sp.
BCS	Bacillus sp.
BAC	Bacteroides sp.
BUK	Burkholderia sp.
CAM	Campylobacter sp.
CAN	Candida sp.
CI-	Citrobacter sp.
CDF	Clostridium difficile

Search

Analysis organism list

☐ Analyze as one organism

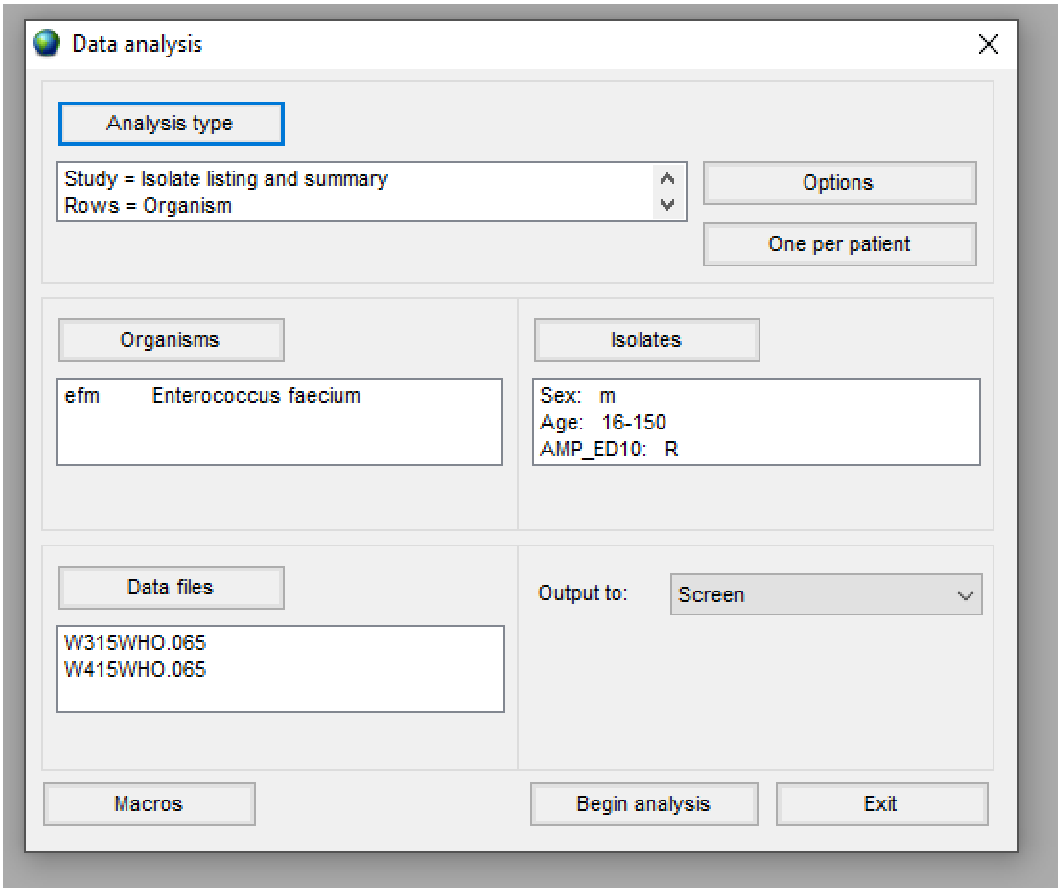
GM+	Gram positive organisms

Figure 3.5: Organism options.

Click on the 'Isolates' button (Figure 3.1 label 5) to restrict the analysis to include (or exclude) patients and/or isolates matching a certain criteria, e.g. only males aged between 16 and 40 years and/or isolates that are non-susceptible to a particular antibiotic (see Figure 3.6).

Highlight the field of interest and double click to bring up the options available for narrowing down the analysis (see Figure 3.7).

It is possible to include isolates that meet all the selection criteria (default option) or at least one of the selection criteria.



Study = Isolate listing and summary
Rows = Organism

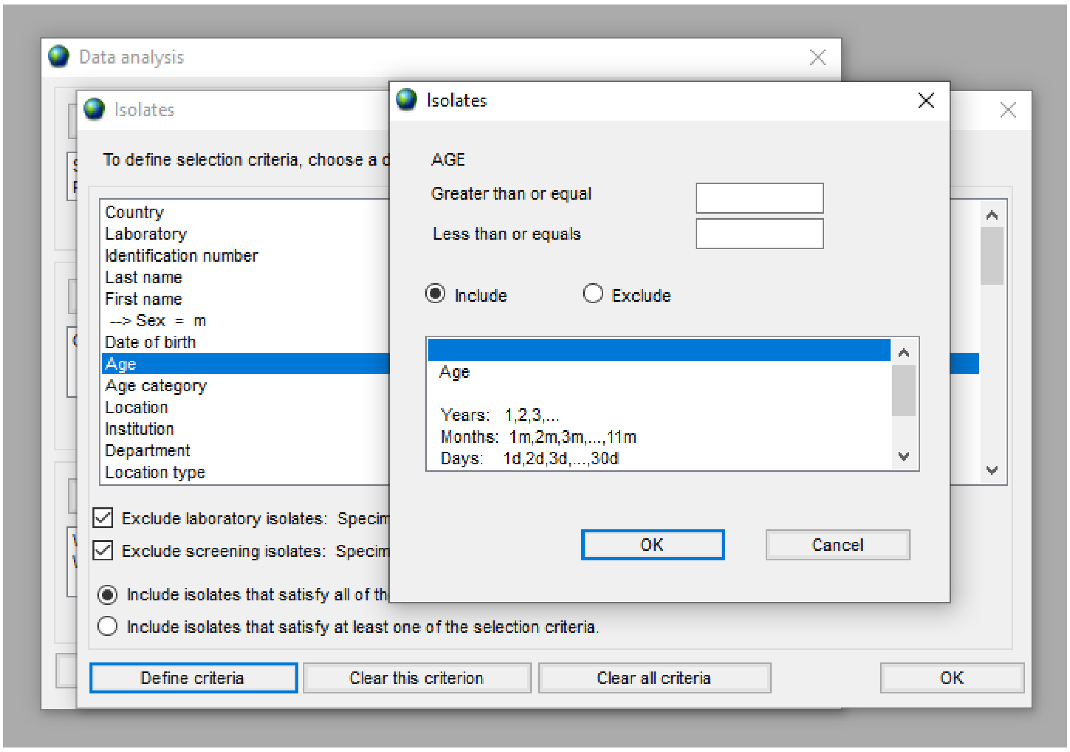
efm Enterococcus faecium

Sex: m
Age: 16-150
AMP_ED10: R

W315WHO.065
W415WHO.065

Output to: Screen

Figure 3.6: 'Isolates' options 1.



To define selection criteria, choose a d

Country
Laboratory
Identification number
Last name
First name
--> Sex = m
Date of birth
Age
Age category
Location
Institution
Department
Location type

☑ Exclude laboratory isolates: Specim
☑ Exclude screening isolates: Specim

● Include isolates that satisfy all of th
○ Include isolates that satisfy at least one of the selection criteria.

AGE
Greater than or equal
Less than or equals

● Include ○ Exclude

Age

Years: 1,2,3,...
Months: 1m,2m,3m,...,11m
Days: 1d,2d,3d,...,30d

Figure 3.7: 'Isolates' options 2.

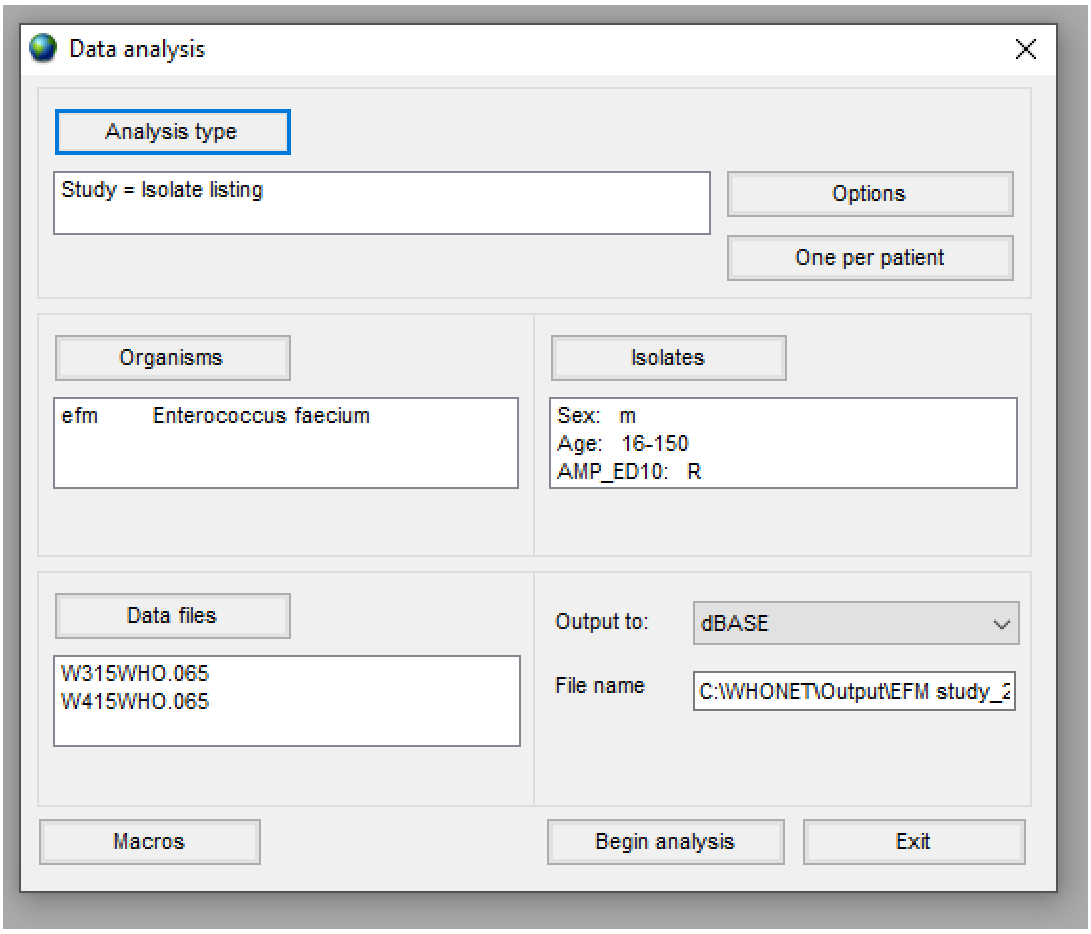
Click on the ‘Data files’ button (Figure 3.1 label 6) to select the file(s) to be analysed. WHONET will automatically look in the default ‘Data files’ folder (if previously selected under ‘File locations’). You can select one or more files.

WHONET allows you to select where you would like the analysis output to go to (Figure 3.1 label 8). The default is to the screen, but using the dropdown menu you could also choose to send the output to Excel, text or to Dbase, i.e. if you are creating a new file (the latter is the same as creating a new WHONET data file as these are created using Dbase).

If you select to create a new file, you must give the file a name (remember that the nomenclature you use is important for identifying the data contained within and for filing, i.e. it must make sense).

The output data file will automatically go to the default ‘Output files’ folder (if previously selected under ‘File locations’).

Once you run the analysis, the pathway to the new file will appear in the ‘File name’ field (Note: this field appears only after selecting the output to another file format other than to the screen).



Study = Isolate listing

efm Enterococcus faecium

Sex: m
Age: 16-150
AMP_ED10: R

W315WHO.065
W415WHO.065

Output to: dBASE

File name C:\WHONET\Output\EFM study_2

Figure 3.8: Screenshot of output to dBASE (WHONET format) with location pathway in ‘File name’ field (i.e., C:\WHONET\OUTPUT\EFM study_20190904.065).

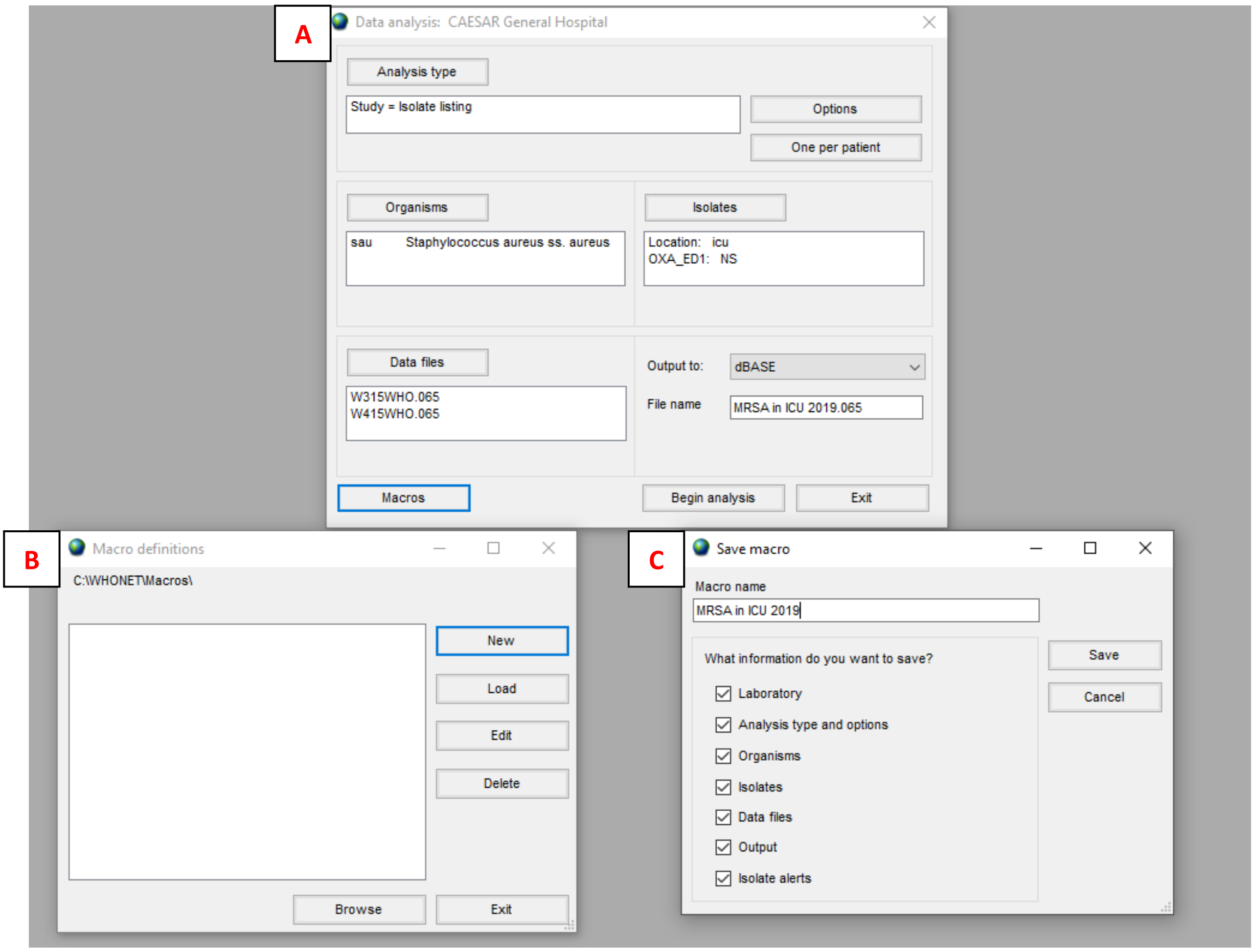
The buttons for ‘Begin analysis’ (Figure 3.1 label 9) and ‘Exit’ (Figure 3.1 label 10) are self-explanatory.

3.1 Macros

The ‘Macro’ button is used so that you can save the selection criteria mentioned above so the same analysis can be repeated either on different data files or in different time periods e.g. for quarterly reports etc.

3.1.1 Creating a new macro

- Make the selections for the analysis you want to perform (see Figure 3.9 label A): only include data files if these are the same files you are going to use every time, i.e. if you have a file with the data for the year to date that is continuously updated as the year goes on; and similarly only use an output file name if you are going to replace the same file at a later date to include the latest data. You can also select the output to go to the screen (default) or to Excel
- Click on the ‘Macros’ button as indicated in the bottom left of panel A
- This brings up the next panel, Figure 3.9 label B: select ‘New’ as indicated
- This brings up the next panel, Figure 3.9 label C: give the macro a meaningful name and then click on ‘Save’



Study = Isolate listing

sau Staphylococcus aureus ss. aureus

Location: icu
OXA_ED1: NS

W315WHO.065
W415WHO.065

Output to: dBASE
File name MRSA in ICU 2019.065

C:\WHONET\Macros\

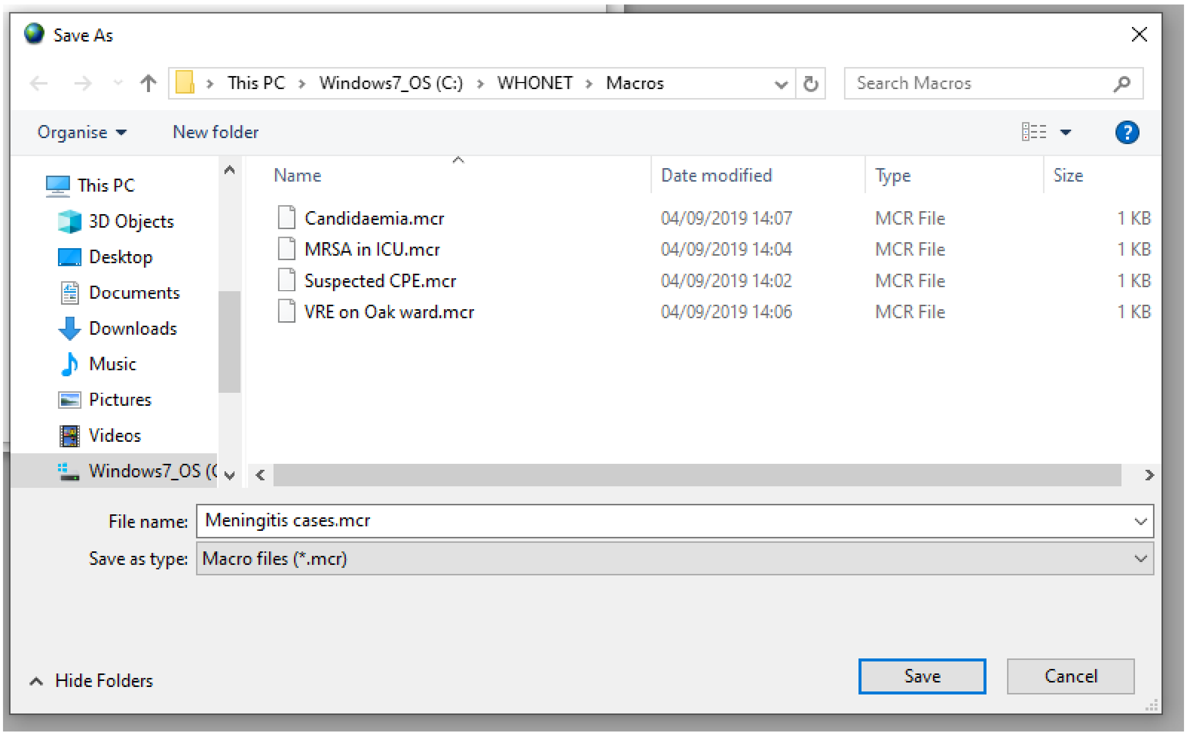
Macro name
MRSA in ICU 2019

What information do you want to save?
☑ Laboratory
☑ Analysis type and options
☑ Organisms
☑ Isolates
☑ Data files
☑ Output
☑ Isolate alerts

Figure 3.9: Create macro.

Make sure to save the macro in a safe place where you will be able to find it and where WHONET will ‘look’ for its macros.

By default macro files are stored in C:\WHONET\macros (see Figure 3.10). It is probably a good idea to change the location of these to a network drive (in case the local hard drive crashes resulting in loss of all files/data stored locally) (see section 2.4.6).



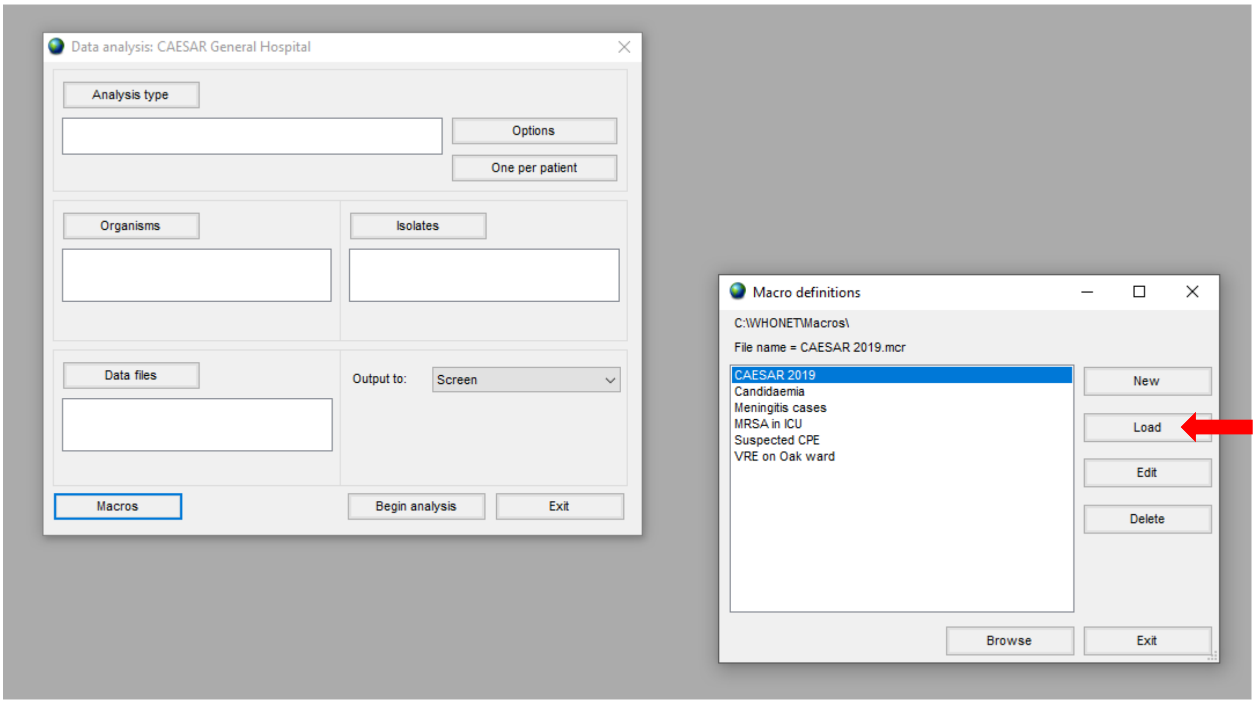
Name	Date modified	Type	Size
Candidaemia.mcr	04/09/2019 14:07	MCR File	1 KB
MRSA in ICU.mcr	04/09/2019 14:04	MCR File	1 KB
Suspected CPE.mcr	04/09/2019 14:02	MCR File	1 KB
VRE on Oak ward.mcr	04/09/2019 14:06	MCR File	1 KB

File name: Meningitis cases.mcr
Save as type: Macro files (*.mcr)

Figure 3.10: Save macro.

3.1.2 Using macros that have already been created

When you click on ‘Macros’ in the main Data analysis screen, the Macro definitions window below will appear (see Figure 3.11). This gives you the list of macros already saved. If you want to use a macro already saved, select the required macro from the list and click ‘Load’. Macros can also be changed (edited) if required.



Output to: Screen

C:\WHONET\Macros\

File name = CAESAR 2019.mcr

CAESAR 2019
Candidaemia
Meningitis cases
MRSA in ICU
Suspected CPE
VRE on Oak ward

Figure 3.11: Execute macro.

These macros can be shared from one user to the other, so that each user provides the same results when doing the analysis. Make sure to save any macros received from others in the folder where WHONET will search for macros, that is in C:\WHONET5\macros or on the hospital's server or network, which is more secure, as described above. In case a network server is not available make sure to have a backup copy of all your macros saved somewhere else as well. Macros are small text files that do not take much space/memory.

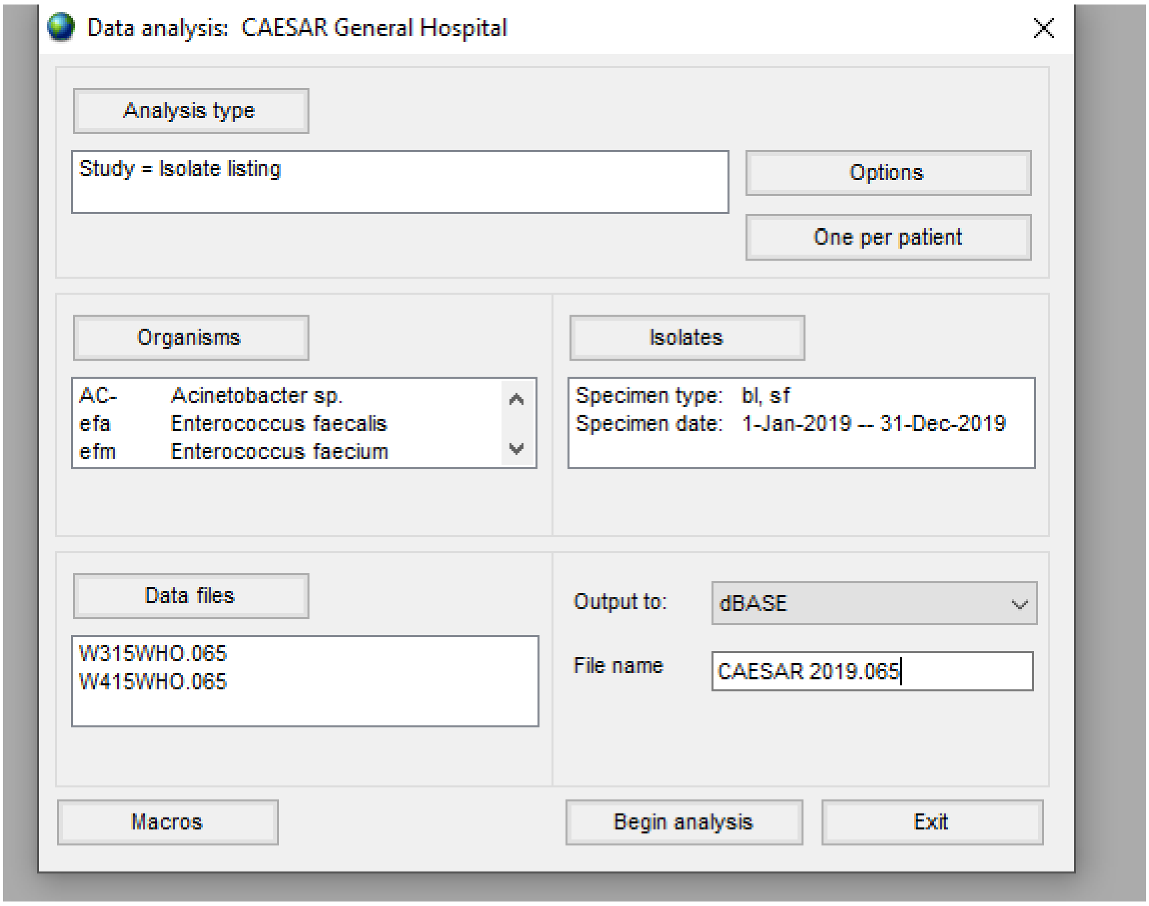
TIP: Macros make routine data analysis easier!

3.2 Useful analyses for CAESAR

3.2.1 Isolate listing and summary

This analysis type results in a simple line-listing of isolates.

Using the CAESAR General Hospital (LabCode WHO065) example, select the analysis type to 'Isolate listing and summary' and the Report Format to 'Listing'. Next select 'Organisms' entering the following codes AC-, efa, efm, eco, kpn, pae, sau, spn (which are all of the CAESAR pathogens) and the 'Data files' as W315WHO.065. In 'Isolates', restrict the analysis so that the only specimen types are bl (blood) and sf (CSF) and that the specimen dates cover the period you are interested in. In 'One per patient', restrict the analysis to the first isolate by patient. Leave the output to the screen (which is the default) and then click on 'Begin analysis' (see Figure 3.12). The output on the screen appears as in Figure 3.13.



Study = Isolate listing

AC- Acinetobacter sp.
efa Enterococcus faecalis
efm Enterococcus faecium

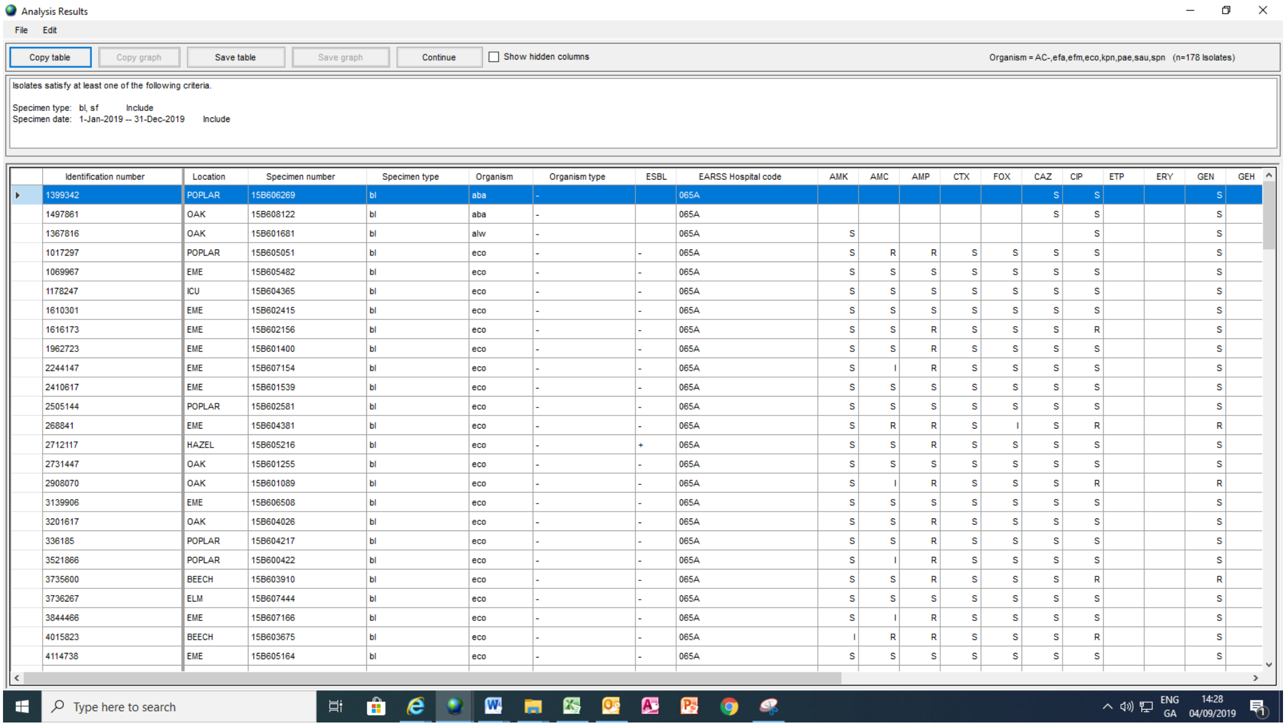
Specimen type: bl, sf
Specimen date: 1-Jan-2019 -- 31-Dec-2019

W315WHO.065
W415WHO.065

Output to: dBASE

File name CAESAR 2019.065

Figure 3.12: Data analysis, isolate listing.



Organism = AC-,efa,efm,eco,kpn,pae,sau,spn (n=178 Isolates)

Isolates satisfy at least one of the following criteria.

Specimen type: bl, sf Include
Specimen date: 1-Jan-2019 -- 31-Dec-2019 Include

Identification number	Location	Specimen number	Specimen type	Organism	Organism type	ESBL	EARSS Hospital code	AMK	AMC	AMP	CTX	FOX	CAZ	CIP	ETP	ERY	GEN	GEH
1399342	POPLAR	15B606269	bl	aba	-		065A						S	S			S	
1497861	OAK	15B608122	bl	aba	-		065A						S	S			S	
1367816	OAK	15B601681	bl	alw	-		065A	S						S			S	
1017297	POPLAR	15B605051	bl	eco	-	-	065A	S	R	R	S	S	S	S			S	
1069967	EME	15B605482	bl	eco	-	-	065A	S	S	S	S	S	S	S			S	
1178247	ICU	15B604365	bl	eco	-	-	065A	S	S	S	S	S	S	S			S	
1610301	EME	15B602415	bl	eco	-	-	065A	S	S	S	S	S	S	S			S	
1616173	EME	15B602156	bl	eco	-	-	065A	S	S	R	S	S	S	R			S	
1962723	EME	15B601400	bl	eco	-	-	065A	S	S	R	S	S	S	S			S	
2244147	EME	15B607154	bl	eco	-	-	065A	S	I	R	S	S	S	S			S	
2410617	EME	15B601539	bl	eco	-	-	065A	S	S	S	S	S	S	S			S	
2505144	POPLAR	15B602581	bl	eco	-	-	065A	S	S	S	S	S	S	S			S	
268841	EME	15B604381	bl	eco	-	-	065A	S	R	R	S	I	S	R			R	
2712117	HAZEL	15B605216	bl	eco	-	+	065A	S	S	R	S	S	S	S			S	
2731447	OAK	15B601255	bl	eco	-	-	065A	S	S	S	S	S	S	S			S	
2908070	OAK	15B601089	bl	eco	-	-	065A	S	I	R	S	S	S	R			R	
3139906	EME	15B606508	bl	eco	-	-	065A	S	S	S	S	S	S	S			S	
3201617	OAK	15B604026	bl	eco	-	-	065A	S	S	R	S	S	S	S			S	
336185	POPLAR	15B604217	bl	eco	-	-	065A	S	S	R	S	S	S	S			S	
3521866	POPLAR	15B600422	bl	eco	-	-	065A	S	I	R	S	S	S	S			S	
3735600	BEECH	15B603910	bl	eco	-	-	065A	S	S	R	S	S	S	R			R	
3736267	ELM	15B607444	bl	eco	-	-	065A	S	S	S	S	S	S	S			S	
3844466	EME	15B607166	bl	eco	-	-	065A	S	I	R	S	S	S	S			S	
4015823	BEECH	15B603675	bl	eco	-	-	065A	I	R	R	S	S	S	R			S	
4114738	EME	15B605164	bl	eco	-	-	065A	S	S	S	S	S	S	S			S	

Figure 3.13: Output from line-listing.

The data in columns can be sorted by clicking on the field name above the column: a single click will sort A-Z and a subsequent click will reverse the sort order.

The listing produced does not include the complete list of fields present in the laboratory configuration. Above the table, there is a tick box 'Show hidden columns' that can be selected to reveal the full data set.

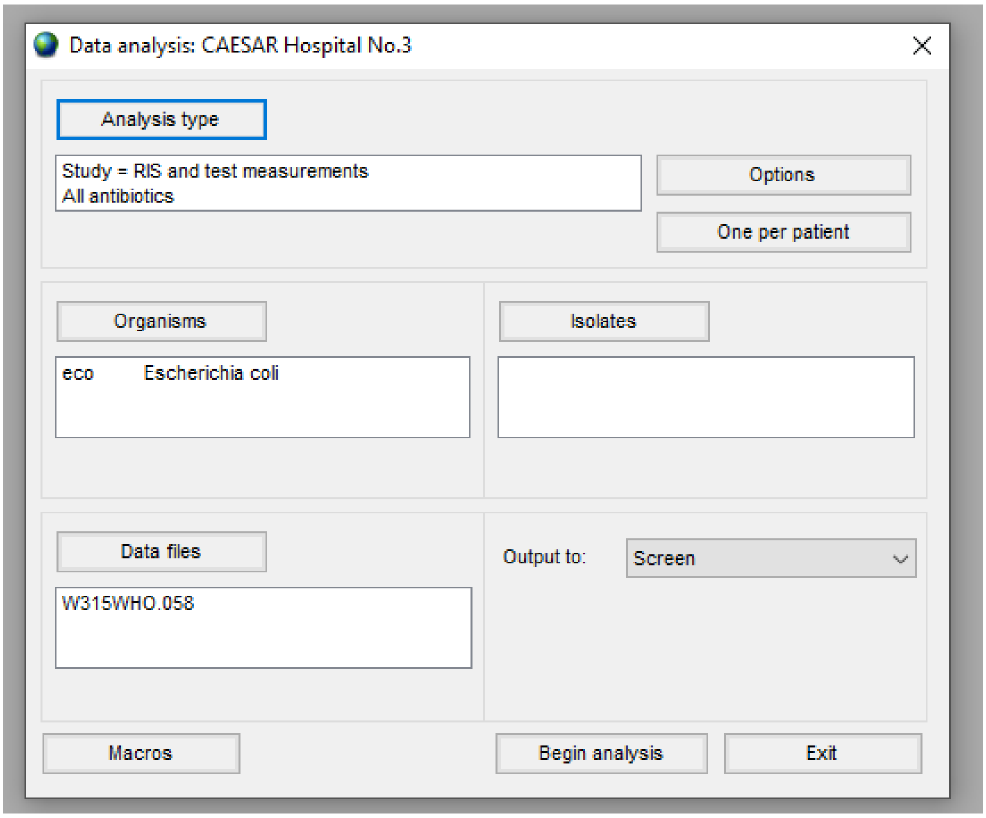
The table can be copied or printed by clicking on Copy table or Print table at top of the screen (this applies to all analyses types).

The isolate (or line-) listing is particularly useful for doing quick validation checks of your data:

- Sort the main columns to ensure there are no unexpected blanks, e.g. patient id, DOB, sex, specimen number, specimen type, specimen date
- Sort the specimen dates to make sure they make sense, e.g. if the data are for 2015 only, then there should be no date from 2014 or 2016, or 1945 (if specimen date has been entered incorrectly!)

3.2.2 %RIS and test measurements

In this type of analysis, we want to look at the percentage of isolates that are resistant or intermediate or susceptible to the antibiotics they have been tested against (see Figure 3.14). This can be visualised in a simple table or on a graph.



Study = RIS and test measurements
All antibiotics

eco Escherichia coli

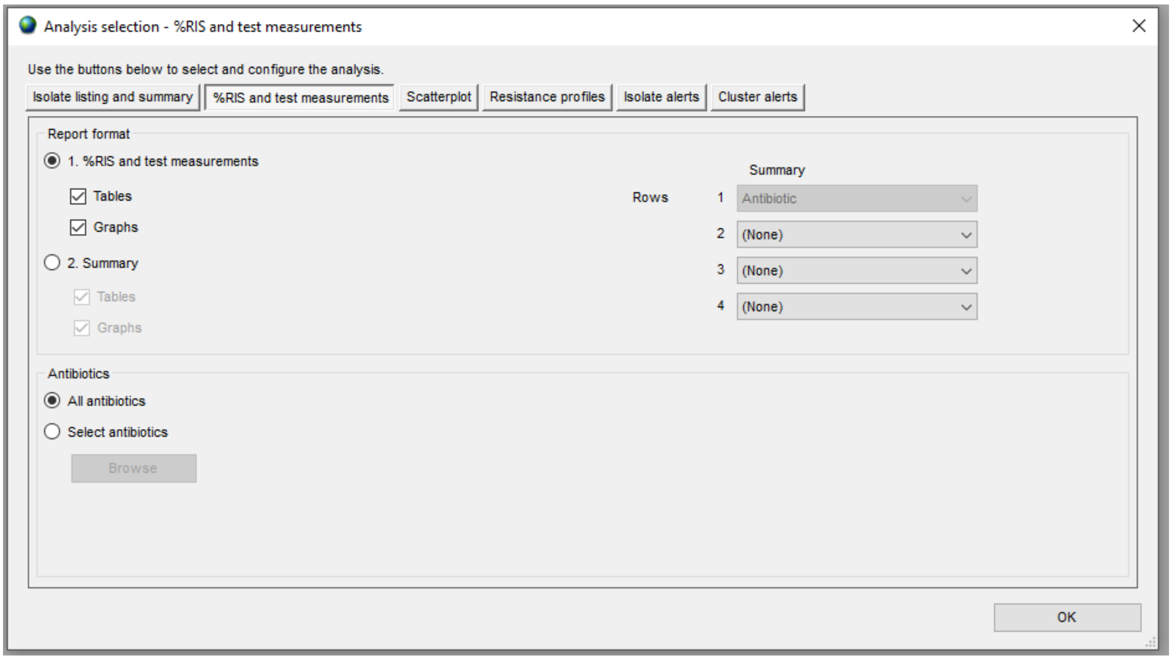
W315WHO.058

Output to: Screen

Figure 3.14: Data analysis, %RIS and measurements.

In this example, we are going to use the laboratory configuration and sample data file from CAESAR Hospital No. 3.

Figure 3.15 shows the selections made on the 'Analysis Selection' screen:



Use the buttons below to select and configure the analysis.

Report format

● 1. %RIS and test measurements

☑ Tables

☑ Graphs

○ 2. Summary

☑ Tables

☑ Graphs

Summary

Rows
1 Antibiotic
2 (None)
3 (None)
4 (None)

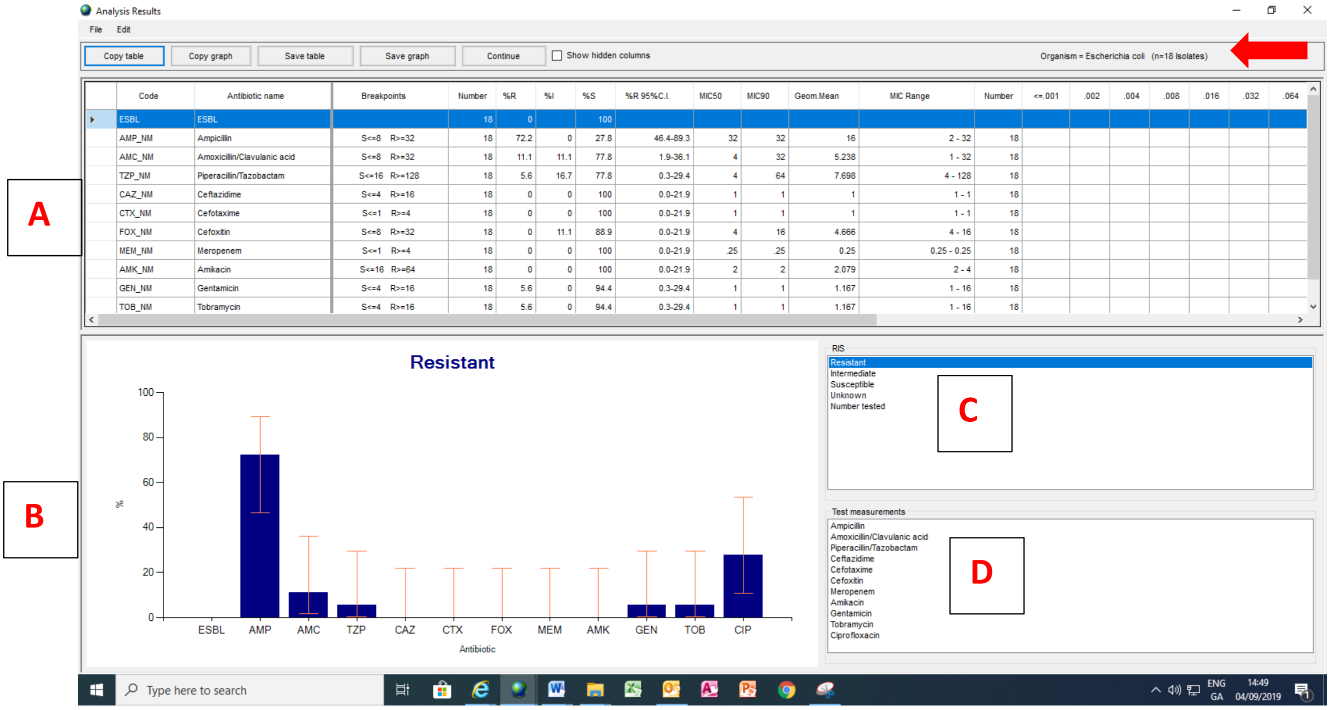
Antibiotics

● All antibiotics

○ Select antibiotics

Figure 3.15: Data analysis, %RIS and measurements, analysis selection.

We then select the organisms (=eco) and the data files (=w315who.058), leave the output to the screen and click on 'Begin analysis'. The following output is obtained (Figure 3.16):



Code	Antibiotic name	Breakpoints	Number	%R	%I	%S	%R 95%C.I.	MIC50	MIC90	Geom.Mean	MIC Range	Number	<=.001	.002	.004	.008	.016	.032	.064
ESBL	ESBL		18	0		100													
AMP_NM	Ampicillin	S<=8 R>=32	18	72.2	0	27.8	46.4-89.3	32	32	16	2 - 32	18							
AMC_NM	Amoxicillin/Clavulanic acid	S<=8 R>=32	18	11.1	11.1	77.8	1.9-36.1	4	32	5.238	1 - 32	18							
TZP_NM	Piperacillin/Tazobactam	S<=16 R>=128	18	5.6	16.7	77.8	0.3-29.4	4	64	7.698	4 - 128	18							
CAZ_NM	Ceftazidime	S<=4 R>=16	18	0	0	100	0.0-21.9	1	1	1	1 - 1	18							
CTX_NM	Cefotaxime	S<=1 R>=4	18	0	0	100	0.0-21.9	1	1	1	1 - 1	18							
FOX_NM	Cefoxitin	S<=8 R>=32	18	0	11.1	88.9	0.0-21.9	4	16	4.666	4 - 16	18							
MEM_NM	Meropenem	S<=1 R>=4	18	0	0	100	0.0-21.9	.25	.25	0.25	0.25 - 0.25	18							
AMK_NM	Amikacin	S<=16 R>=64	18	0	0	100	0.0-21.9	2	2	2.079	2 - 4	18							
GEN_NM	Gentamicin	S<=4 R>=16	18	5.6	0	94.4	0.3-29.4	1	1	1.167	1 - 16	18							
TOB_NM	Tobramycin	S<=4 R>=16	18	5.6	0	94.4	0.3-29.4	1	1	1.167	1 - 16	18							

Figure 3.16: Analysis Results screen with output from RIS analysis.

The upper panel in Figure 3.16 (label A) contains a table with the antimicrobial susceptibility results for each of the antibiotics tested. The output in this table includes the total number of isolates tested and the proportions that are resistant, intermediate and susceptible. In the example here, all 18 isolates in the file (indicated by the arrow) were tested against all of the antibiotics (note: the 2nd column labelled 'Number' is a count of test measurements (or quantitative data, such as zone diameter sizes and MICs) in the data set. Of the 18 *E. coli* isolates, 72.2% were resistant to ampicillin, while 27.8% were resistant to ciprofloxacin.

The lower left panel in Figure 3.16 (label B) shows this data in a graphical format.

In the bottom right panel in Figure 3.16 (label C), we can change what is being visualised in the graph. Resistant is highlighted in blue, hence we are looking at %Resistant. It is possible to change this to Susceptible (or Intermediate or Unknown or Number tested).

In the bottommost right panel in Figure 3.16 (label D), there is a list of antibiotics for which test measurements were available in the data file. By clicking on one of the antibiotics, (e.g. amoxicillin/clavulanic acid), we can now see the distribution (a histogram) of the test measurements for that particular antibiotic in our data file (see Figure 3.17). The red lines indicate the breakpoints.

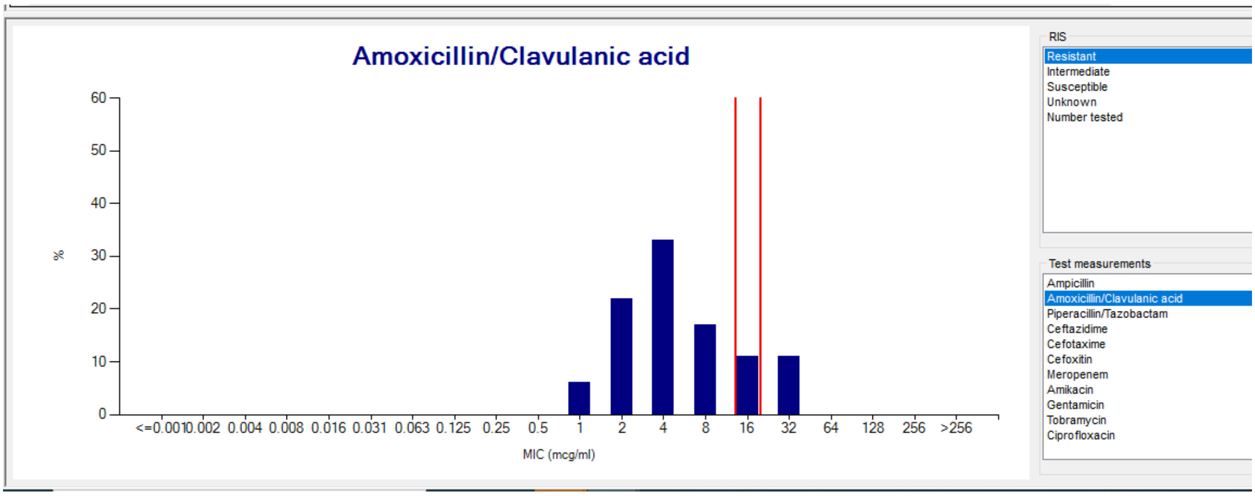


Figure 3.17: Histogram with breakpoints.

Tables and charts can easily be copied and pasted into Word or Excel files.

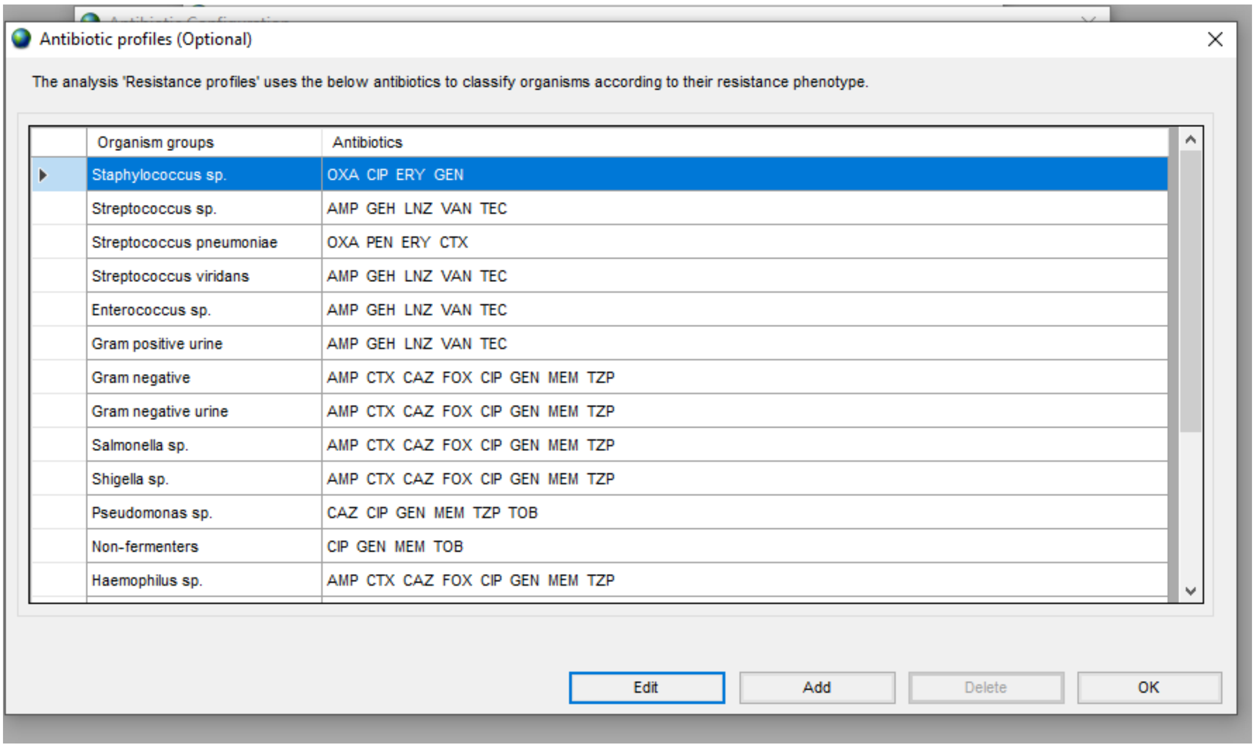
For more information on the RIS analysis type, please refer to the main manual.

3.2.3 Resistance profile

In this type of analysis, we want to look at the resistance profiles of all isolates in our data set. For this, it is important to set up profiles for various pathogens under surveillance. Resistance profiles can be visualised in a simple table or on a graph.

A resistance profile is basically a list of antibiotics to which the organism is resistant: the antibiotics included in the resistance profile should be those that are tested against all isolates of the organism. Resistance profiles can be set up in one of two ways:

1. In the ‘Laboratory configuration’ – go to the main WHONET screen, select ‘Modify laboratory’, then click on ‘Antibiotics’, followed by ‘Profiles’. Highlight the organism group for which you want to create a profile, then click on ‘Edit’. See Figure 3.18.

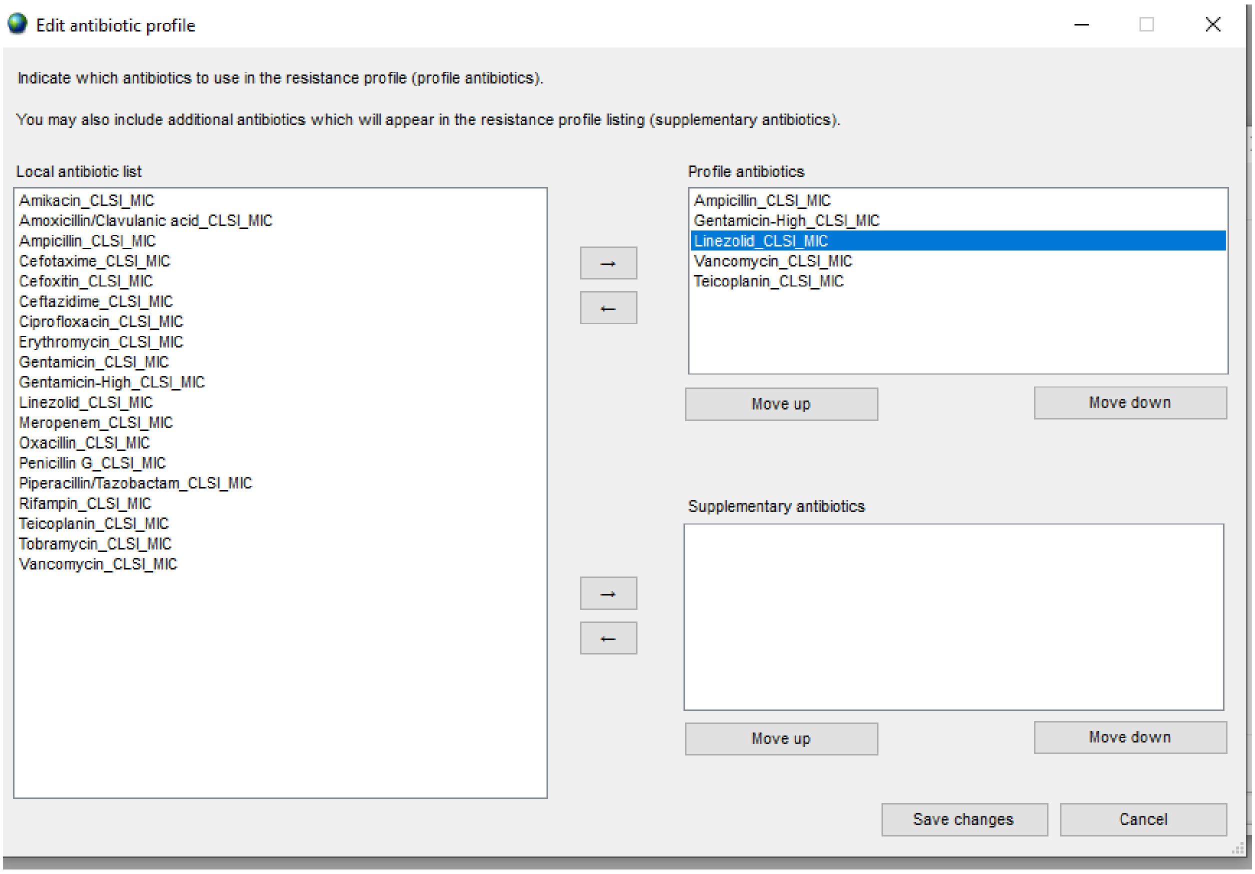


The analysis 'Resistance profiles' uses the below antibiotics to classify organisms according to their resistance phenotype.

Organism groups	Antibiotics
Staphylococcus sp.	OXA CIP ERY GEN
Streptococcus sp.	AMP GEH LNZ VAN TEC
Streptococcus pneumoniae	OXA PEN ERY CTX
Streptococcus viridans	AMP GEH LNZ VAN TEC
Enterococcus sp.	AMP GEH LNZ VAN TEC
Gram positive urine	AMP GEH LNZ VAN TEC
Gram negative	AMP CTX CAZ FOX CIP GEN MEM TZP
Gram negative urine	AMP CTX CAZ FOX CIP GEN MEM TZP
Salmonella sp.	AMP CTX CAZ FOX CIP GEN MEM TZP
Shigella sp.	AMP CTX CAZ FOX CIP GEN MEM TZP
Pseudomonas sp.	CAZ CIP GEN MEM TZP TOB
Non-fermenters	CIP GEN MEM TOB
Haemophilus sp.	AMP CTX CAZ FOX CIP GEN MEM TZP

Figure 3.18: Antibiotic profiles.

Select key antibiotics (from the ‘Local antibiotic list’ on the right; these are antibiotics that you have configured for your laboratory) to appear in the ‘Profile antibiotics’ panel on the upper right and any additional ones to appear in the ‘Supplementary antibiotics’ panel on the lower right (these will not appear in the profile, but will be included in the line-listing). See Figure 3.19.



Indicate which antibiotics to use in the resistance profile (profile antibiotics).

You may also include additional antibiotics which will appear in the resistance profile listing (supplementary antibiotics).

Local antibiotic list

- Amikacin_CLSI_MIC
- Amoxicillin/Clavulanic acid_CLSI_MIC
- Ampicillin_CLSI_MIC
- Cefotaxime_CLSI_MIC
- Cefoxitin_CLSI_MIC
- Ceftazidime_CLSI_MIC
- Ciprofloxacin_CLSI_MIC
- Erythromycin_CLSI_MIC
- Gentamicin_CLSI_MIC
- Gentamicin-High_CLSI_MIC
- Linezolid_CLSI_MIC
- Meropenem_CLSI_MIC
- Oxacillin_CLSI_MIC
- Penicillin G_CLSI_MIC
- Piperacillin/Tazobactam_CLSI_MIC
- Rifampin_CLSI_MIC
- Teicoplanin_CLSI_MIC
- Tobramycin_CLSI_MIC
- Vancomycin_CLSI_MIC

Profile antibiotics

- Ampicillin_CLSI_MIC
- Gentamicin-High_CLSI_MIC
- Linezolid_CLSI_MIC
- Vancomycin_CLSI_MIC
- Teicoplanin_CLSI_MIC

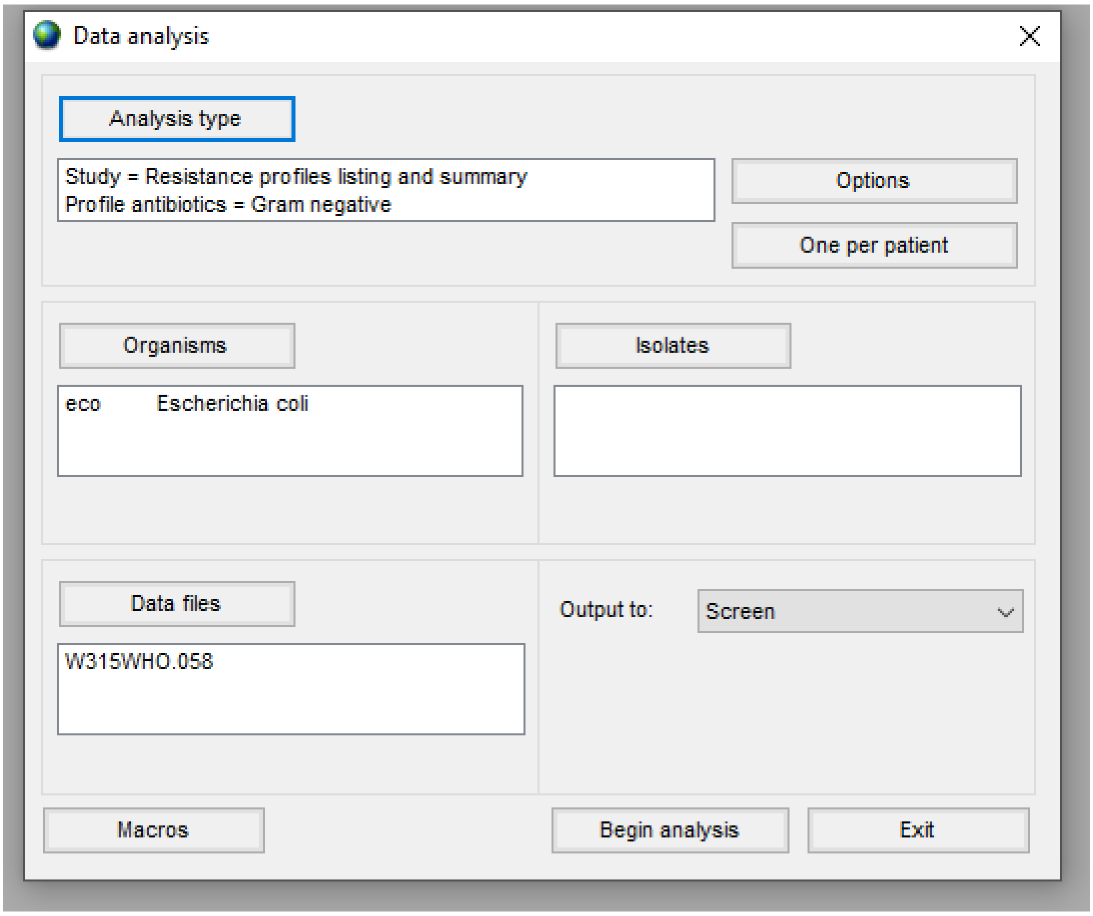
Supplementary antibiotics

Figure 3.19: Edit antibiotic profiles.

Once you are finished, click ‘Save changes’, then ‘Ok’, ‘Ok’ and ‘Save’.

2. In the ‘Analysis selection’ screen – once you have selected ‘Resistance profiles’ as the Analysis type, an option appears in the lower part of the screen to ‘Edit profiles’. Proceed as outlined in 1. above but note that resistance profiles created here are only temporary. Update the laboratory configuration for permanent resistance profiles.

To perform this analysis on *E. coli* isolates in our test lab 058 (CAESAR Hospital No.3), make the selections as indicated in the ‘Data analysis’ and the ‘Analysis Selection’ screens below (Figure 3.20 and Figure 3.21). Click on ‘Begin analysis’.



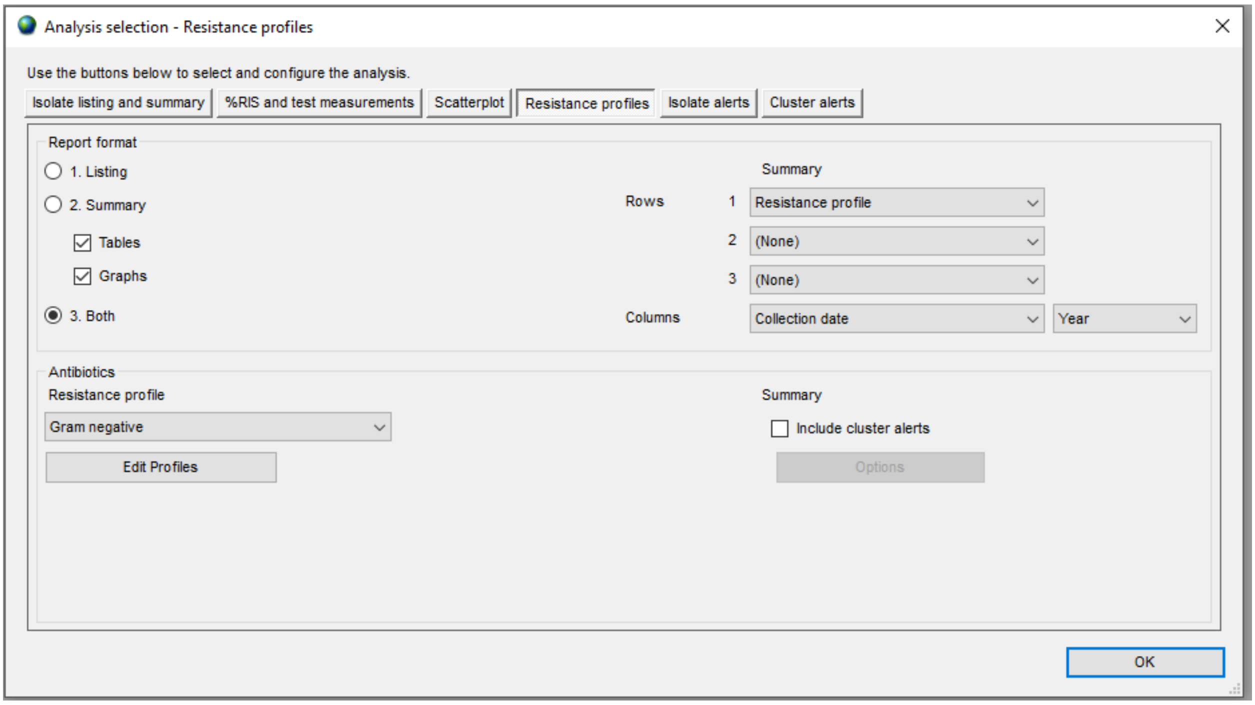
Study = Resistance profiles listing and summary
Profile antibiotics = Gram negative

eco Escherichia coli

W315WHO.058

Output to: Screen

Figure 3.20: Data analysis.



Use the buttons below to select and configure the analysis.

Report format
○ 1. Listing
○ 2. Summary
☑ Tables
☑ Graphs
● 3. Both

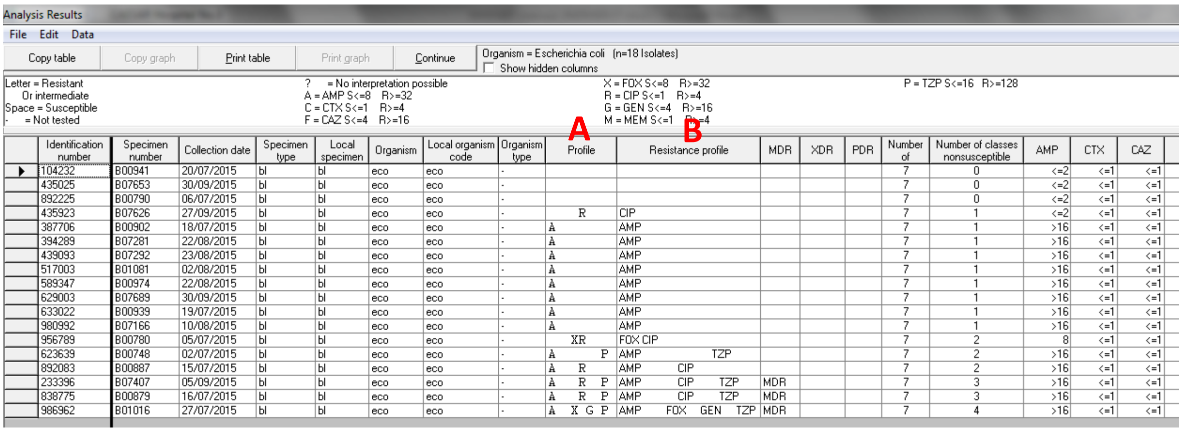
Summary
Rows 1 Resistance profile
2 (None)
3 (None)
Columns Collection date Year

Antibiotics
Resistance profile
Gram negative

Summary
☐ Include cluster alerts

Figure 3.21: Analysis selection.

The first part of the analysis will return a line-listing (as the ‘Report format’ selected was for both a listing and a summary). This includes two additional columns with the resistance profile: ‘Profile’ uses one-letter antibiotic codes (see Figure 3.22 label A), while ‘Resistance profile’ uses the standard three-letter antibiotic codes used in WHONET (see Figure 3.22 label B). The isolates in the line-listing are sorted from least to most resistant.



Organism = Escherichia coli (n=18 Isolates)

Letter = Resistant
Or intermediate
Space = Susceptible
- = Not tested

? = No interpretation possible
A = AMP S<=8 R>=32
C = CTX S<=1 R>=4
F = CAZ S<=4 R>=16

X = FOX S<=8 R>=32
R = CIP S<=1 R>=4
G = GEN S<=4 R>=16
M = MEM S<=1 R>=4

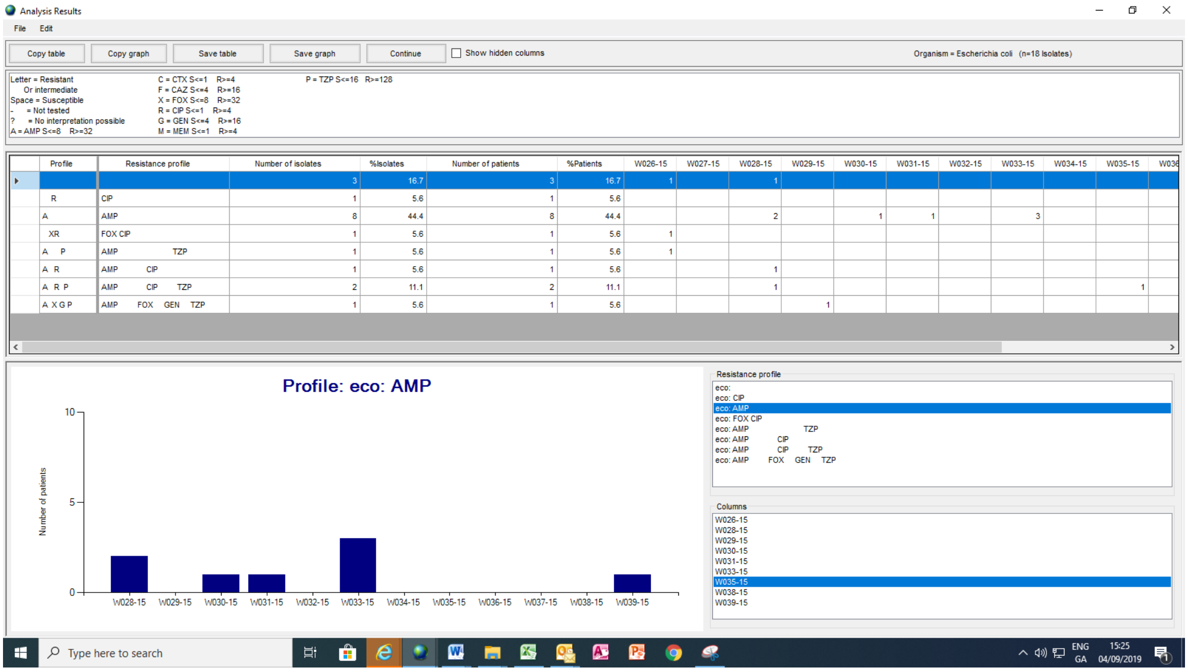
P = TZP S<=16 R>=128

Identification number	Specimen number	Collection date	Specimen type	Local specimen	Organism	Local organism code	Organism type	Profile	Resistance profile	MDR	XDR	PDR	Number of	Number of classes nonsusceptible	AMP	CTX	CAZ
104232	B00941	20/07/2015	bl	bl	eco	eco	-						7	0	<=2	<=1	<=1
435025	B07653	30/09/2015	bl	bl	eco	eco	-						7	0	<=2	<=1	<=1
892225	B00790	06/07/2015	bl	bl	eco	eco	-						7	0	<=2	<=1	<=1
435923	B07626	27/09/2015	bl	bl	eco	eco	-	R	CIP				7	1	<=2	<=1	<=1
387706	B00902	18/07/2015	bl	bl	eco	eco	-	A	AMP				7	1	>16	<=1	<=1
394289	B07281	22/08/2015	bl	bl	eco	eco	-	A	AMP				7	1	>16	<=1	<=1
439093	B07292	23/08/2015	bl	bl	eco	eco	-	A	AMP				7	1	>16	<=1	<=1
517003	B01081	02/08/2015	bl	bl	eco	eco	-	A	AMP				7	1	>16	<=1	<=1
589347	B00974	22/08/2015	bl	bl	eco	eco	-	A	AMP				7	1	>16	<=1	<=1
629003	B07689	30/09/2015	bl	bl	eco	eco	-	A	AMP				7	1	>16	<=1	<=1
633022	B00939	19/07/2015	bl	bl	eco	eco	-	A	AMP				7	1	>16	<=1	<=1
980992	B07166	10/08/2015	bl	bl	eco	eco	-	A	AMP				7	1	>16	<=1	<=1
956789	B00780	05/07/2015	bl	bl	eco	eco	-	XR	FOX CIP				7	2	8	<=1	<=1
623639	B00748	02/07/2015	bl	bl	eco	eco	-	A P	AMP TZP				7	2	>16	<=1	<=1
892083	B00887	15/07/2015	bl	bl	eco	eco	-	A R	AMP CIP				7	2	>16	<=1	<=1
233396	B07407	05/09/2015	bl	bl	eco	eco	-	A R P	AMP CIP TZP	MDR			7	3	>16	<=1	<=1
838775	B00879	16/07/2015	bl	bl	eco	eco	-	A R P	AMP CIP TZP	MDR			7	3	>16	<=1	<=1
986962	B01016	27/07/2015	bl	bl	eco	eco	-	A X G P	AMP FOX GEN TZP	MDR			7	4	>16	<=1	<=1

Figure 3.22: Line listing with resistance profiles.

The second part of the analysis will return the summary data with the isolates aggregated in a table according to their resistance profile, again from least to most resistant. The aggregate data are presented graphically in Figure 3.23 and Figure 3.24.

- Highlight a particular Resistance profile (AMP FOX GEN TZP in Figure 3.23) to see graphically the distribution of all isolates with this profile over the whole time frame in the dataset being analysed
- Highlight a particular month to see graphically all profiles identified in the dataset being analysed during this time period

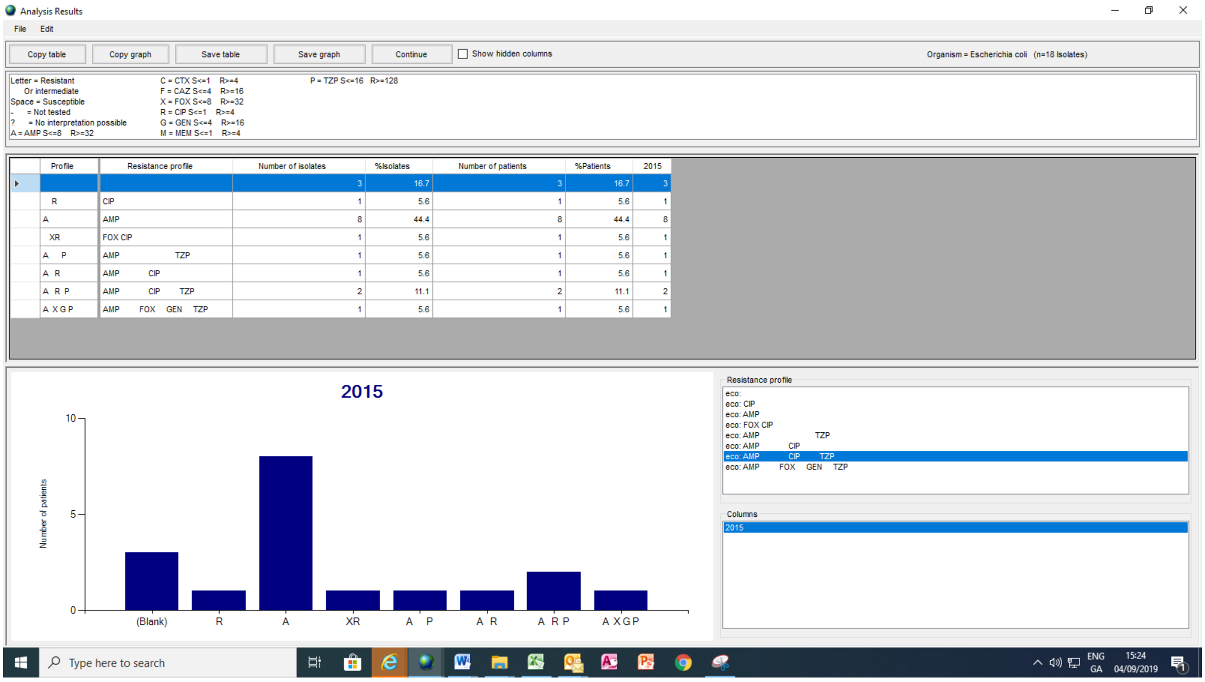


Organism = Escherichia coli (n=18 Isolates)

Letter = Resistant
Or intermediate
Space = Susceptible
\- = Not tested
? = No interpretation possible
A = AMP S<=8 R>=32
C = CTX S<=1 R>=4
F = CAZ S<=4 R>=16
X = FOX S<=8 R>=32
R = CIP S<=1 R>=4
G = GEN S<=4 R>=16
M = MEM S<=1 R>=4
P = TZP S<=16 R>=128

Profile	Resistance profile	Number of isolates	%Isolates	Number of patients	%Patients	W026-15	W027-15	W028-15	W029-15	W030-15	W031-15	W032-15	W033-15	W034-15	W035-15	W036
		3	16.7	3	16.7	1		1								
R	CIP	1	5.6	1	5.6											
A	AMP	8	44.4	8	44.4			2		1	1		3			
XR	FOX CIP	1	5.6	1	5.6	1										
A P	AMP TZP	1	5.6	1	5.6	1										
A R	AMP CIP	1	5.6	1	5.6			1								
A R P	AMP CIP TZP	2	11.1	2	11.1			1							1	
A X G P	AMP FOX GEN TZP	1	5.6	1	5.6				1							

Figure 3.23: Resistance profiles for E. coli isolates by week in 2015.



Organism = Escherichia coli (n=18 Isolates)

Letter = Resistant
Or intermediate
Space = Susceptible
\- = Not tested
? = No interpretation possible
A = AMP S<=8 R>=32
C = CTX S<=1 R>=4
F = CAZ S<=4 R>=16
X = FOX S<=8 R>=32
R = CIP S<=1 R>=4
G = GEN S<=4 R>=16
M = MEM S<=1 R>=4
P = TZP S<=16 R>=128

Profile	Resistance profile	Number of isolates	%Isolates	Number of patients	%Patients	2015
		3	16.7	3	16.7	3
R	CIP	1	5.6	1	5.6	1
A	AMP	8	44.4	8	44.4	8
XR	FOX CIP	1	5.6	1	5.6	1
A P	AMP TZP	1	5.6	1	5.6	1
A R	AMP CIP	1	5.6	1	5.6	1
A R P	AMP CIP TZP	2	11.1	2	11.1	2
A X G P	AMP FOX GEN TZP	1	5.6	1	5.6	1

Figure 3.24: Resistance profiles for E. coli isolates in 2015.

All tables and charts can be copied out of WHONET into Word (for reports), Excel (for further analysis) and PowerPoint (for presentations).

4 Exporting WHONET files to the CAESAR format

4.1 Preparing CAESAR data that is already in WHONET to send to the national data manager

This section applies to local data managers. For national data managers refer to section 4.2.

If your data file only contains CAESAR data for one quarter/year (i.e. there is no other data, including data associated with other pathogens, specimen types, quarters) then:

- Go to the location on your network drive where your WHONET data files are stored
- Make a copy of the correct file. For example, a file labelled 'W415WHO.065' will be 'W415WHO – Copy.065'
- You may need to open up this file using WHONET to remove patient names (First names and Last names), to add in any additional information that has become available, such as MIC or serotype results or an important comment regarding an isolate
- When you are happy that the file is ready to send to your National Data Manager:
- Encrypt a copy of the file using a software such as Axcrypt, Winzip, etc. (Optional, but recommended from a data security perspective: if in doubt, consult with your local IT department and your national data manager)
- Attach the (encrypted) file to an email and send

If your data file contains AMR data for your whole laboratory (i.e. there is data other than that for CAESAR, i.e. including other pathogens and specimen types) and for a time period exceeding that which you are interested in (e.g. data relates to five-years but you only want the last year's data) then:

- Open WHONET and go to 'Data analysis' from the main WHONET screen
- From the 'Analysis type', select 'Isolate listing'
- Click on 'One per patient?', select 'By patient' and 'First isolate with antibiotic results' and then click on 'OK'
- Click on 'Organisms' and select the eight pathogens under surveillance (3-letter codes: sau, spn, eco, efa, efm, kpn, pae and AC-, the latter in capitals captures all species of Acinetobacter)
- Click on 'Isolates' and highlight specimen type. Double-click to bring up the 'Isolates' selection screen. Enter the codes for blood (bl) and CSF (sf). By default, the button for 'Include' is selected so only these specimen types will be returned in this analysis. Click 'OK' and then 'OK' again Click on 'Data files' to select the data file or files containing the data of interest (you can go to the default or navigate to the file location)
- The 'Output to' is to the screen by default
- Click on 'Begin analysis' and check the output on the screen to make sure it is showing the required data
- Change 'Output to' to WHONET 5 (Dbase) and give the new file that you are about to create a meaningful name, e.g. CAESAR2015Q3-4.065 (remember to include the suffix with the lab's code: in this example, '.065')
- Click on 'Begin analysis'

- The new file will be created. The location of this new file will be in default location for output files from WHONET (either in C:\WHONET5\output OR on a network location that you have previously chosen – see section 2.4.6).

4.2 Preparing data in WHONET to send to the international CAESAR data manager

This section applies to national data managers.

Create a National Configuration 'laboratory' in WHONET, giving this a Laboratory Code distinct from any of the Laboratory Codes used nationally in your CAESAR surveillance network. In the example below, there are two laboratories in the national network CAESAR General Hospital (lab code 065) and CAESAR Hospital No.3 (lab code 058). The national configuration is given the laboratory name 'CAESAR National Configuration' with the lab code 'WH1'.

Depending on the volume of data a country has, it might be preferable to create different CAESAR national configuration files for each of the pathogen groups:

e.g.

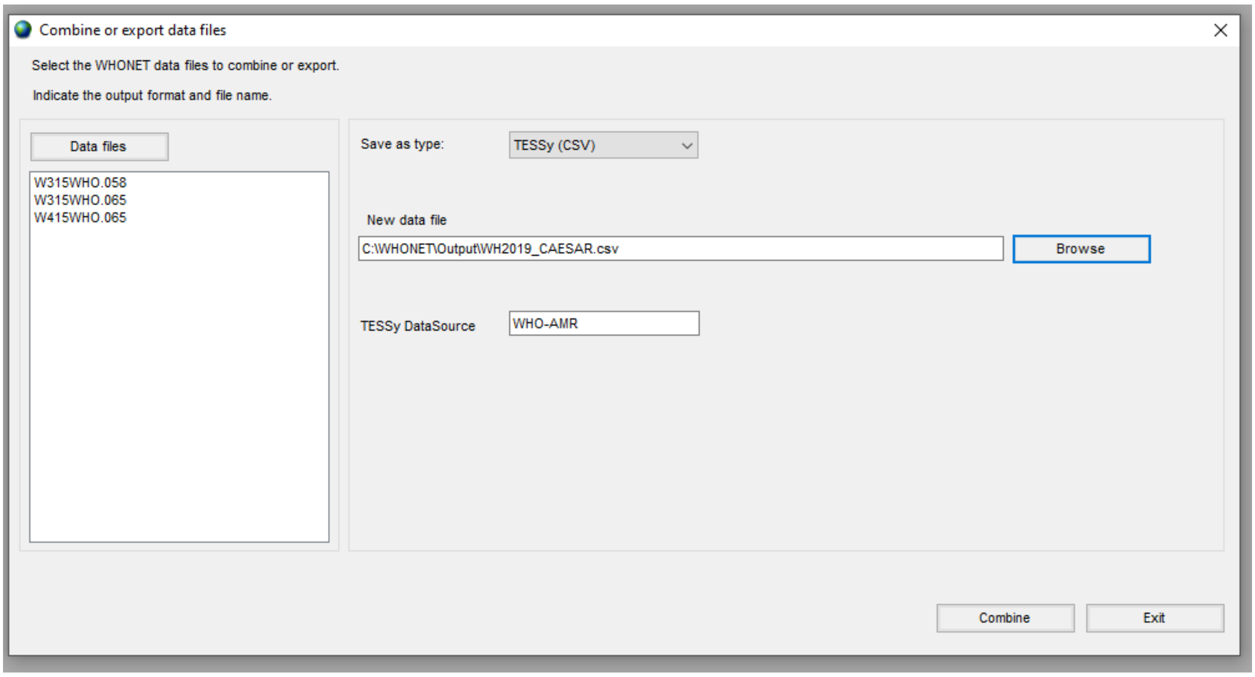
LAB NAME	LAB CODE
CC-CAESAR-SAU	CC1
CC-CAESAR-ECO-KPN	CC2
CC-CAESAR-EFA-EFM	CC3, etc.

Each of the above configurations will only contain the specific antibiotics required for that particular pathogen/group of pathogens. Note: CC above refers to Country code, e.g. UZ = Uzbekistan.

It is important that the national configuration file includes all of the relevant antibiotic combinations from each of the laboratories. For example, one laboratory might test for MRSA in *S. aureus* using a cefoxitin disk while another might test for MRSA using an oxacillin Etest or MIC; therefore, both cefoxitin and oxacillin will need to be included in the national configuration.

Steps for combining data files at the national level for sending to CAESAR:

- In WHONET, open the laboratory with your national configuration, in our example this is the 'CAESAR National Configuration' (lab code = WH1)
- From the WHONET main screen, go to 'Data entry', then 'Combine or export files' to bring up the 'Combine or export data files' screen (see Figure 4.1):



Select the WHONET data files to combine or export.

Indicate the output format and file name.

W315WHO.058
W315WHO.065
W415WHO.065

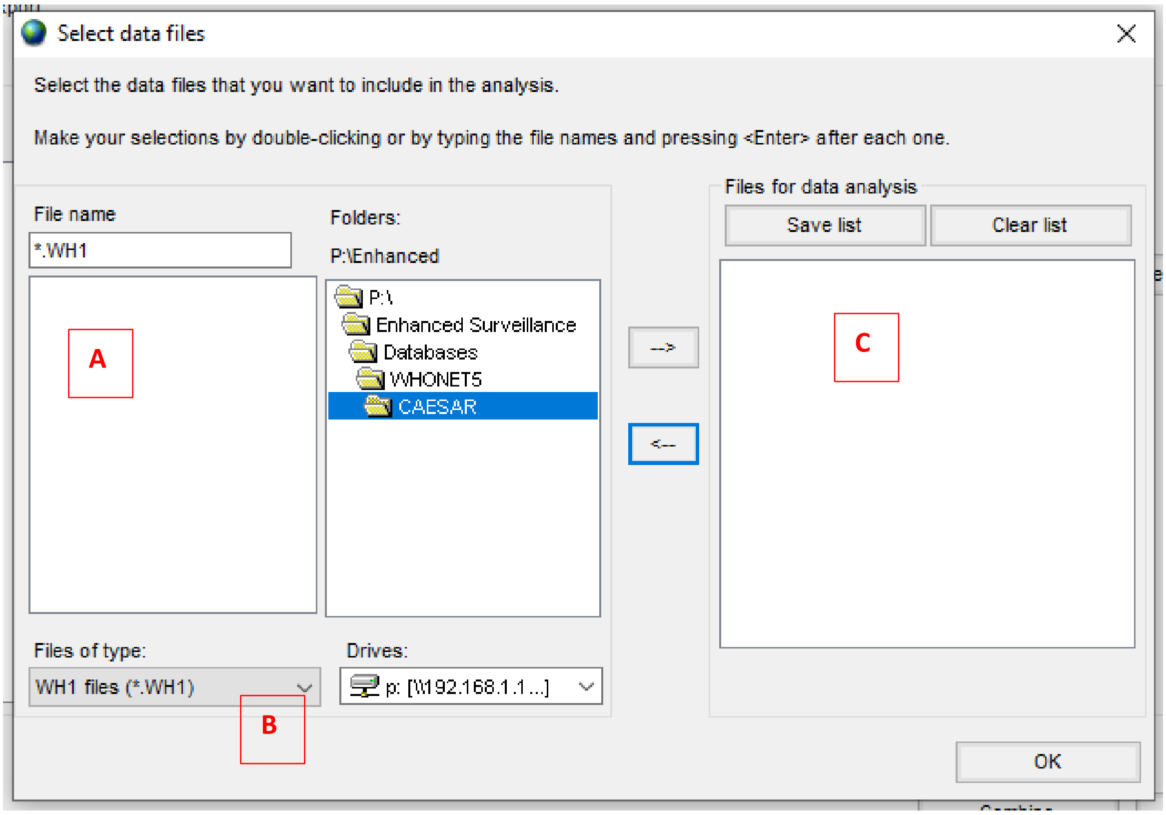
Save as type: TESSy (CSV)

New data file
C:\WHONET\Output\WH2019_CAESAR.csv

TESSy DataSource WHO-AMR

Figure 4.1: Combining datasets.

- Select the files you want to combine: clicking on ‘Data files’ will take you to the C:\WHONET\data folder by default unless you have set different File locations (see Figure 4.1). By default, WHONET will look for files with the same extension as the laboratory code, WH1. As this is national configuration, we want to be able to select all files from all laboratories in our national network. Click on the dropdown menu for ‘Files of type’ (Figure 4.2 label B) and select ‘All files (*.*)’. All file types present will be returned in the panel on the left (Figure 4.2 label A). Select all of these and double-click to bring them across to the panel on the right, ‘Files for data analysis’ (Figure 4.2 label C). Click ‘OK’.



Select data files

Select the data files that you want to include in the analysis.

Make your selections by double-clicking or by typing the file names and pressing <Enter> after each one.

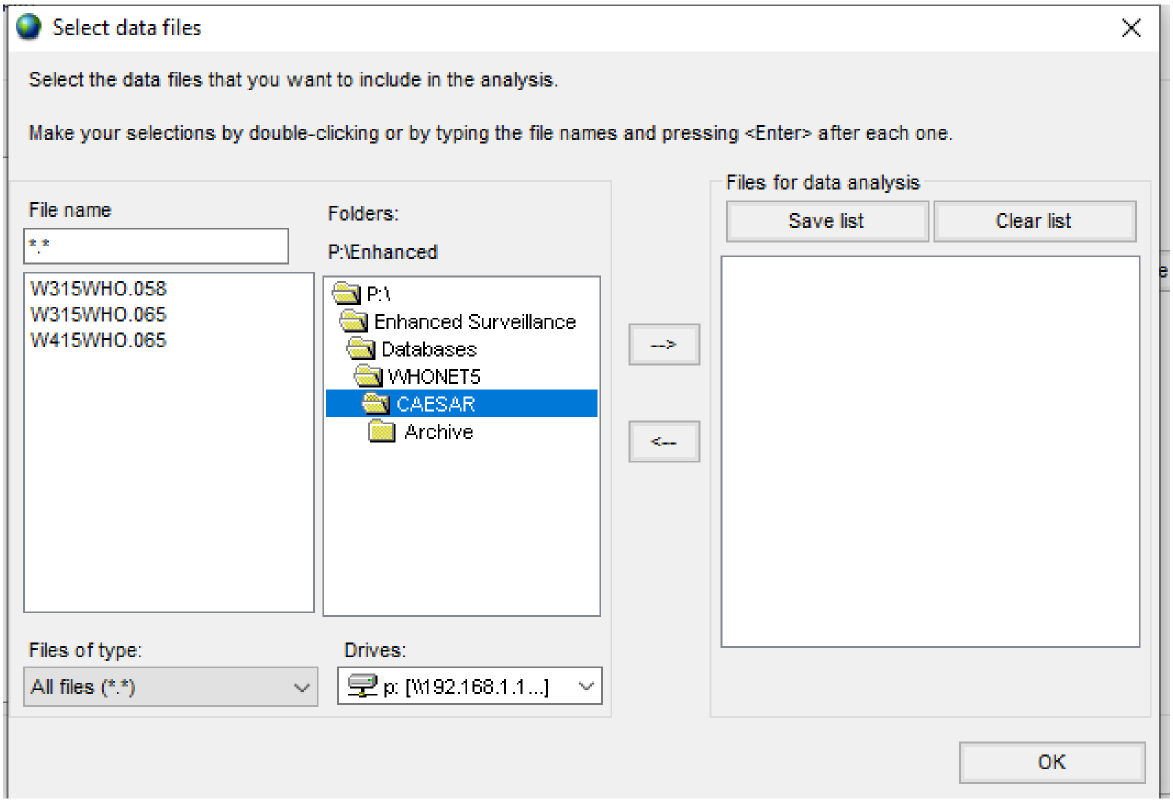
File name: *.WH1

Folders: P:\Enhanced

Files of type: WH1 files (*.WH1)

Drives: p: [\\192.168.1.1...]

Figure 4.2: Selecting files.



Select the data files that you want to include in the analysis.

Make your selections by double-clicking or by typing the file names and pressing <Enter> after each one.

File name: *.*

W315WHO.058
W315WHO.065
W415WHO.065

Folders: P:\Enhanced

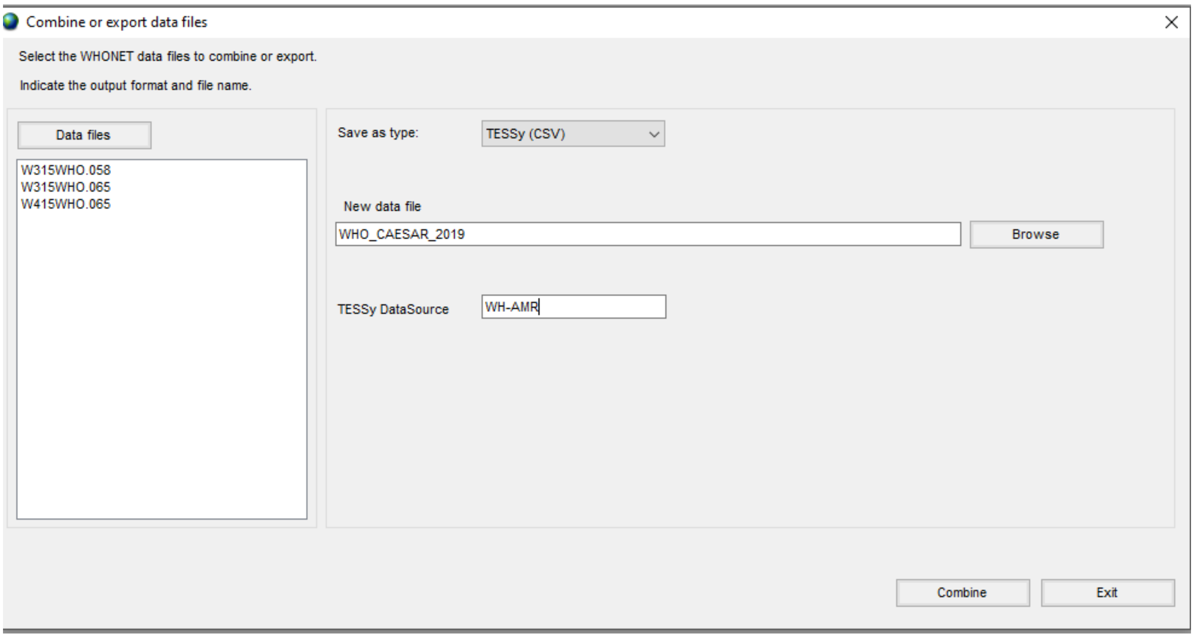
P:\
Enhanced Surveillance
Databases
WHONET5
CAESAR
Archive

Files of type: All files (*.*)

Drives: p: [\\192.168.1.1...]

Figure 4.3: Selecting files (all types).

- Give the new file you are creating a name (see notes on naming files and file locations). You can browse to the location where you want the new file to be saved, otherwise the new file will go to the default location for Output files from WHONET.
- For ‘Save as type’, use the dropdown menu and select ‘TESSy (CSV)’ (Figure 4.4)
- Then enter TESSy DataSource as agreed with the international CAESAR data manager, for example WHO-AMR (or UZ-AMR)



Select the WHONET data files to combine or export.

Indicate the output format and file name.

W315WHO.058
W315WHO.065
W415WHO.065

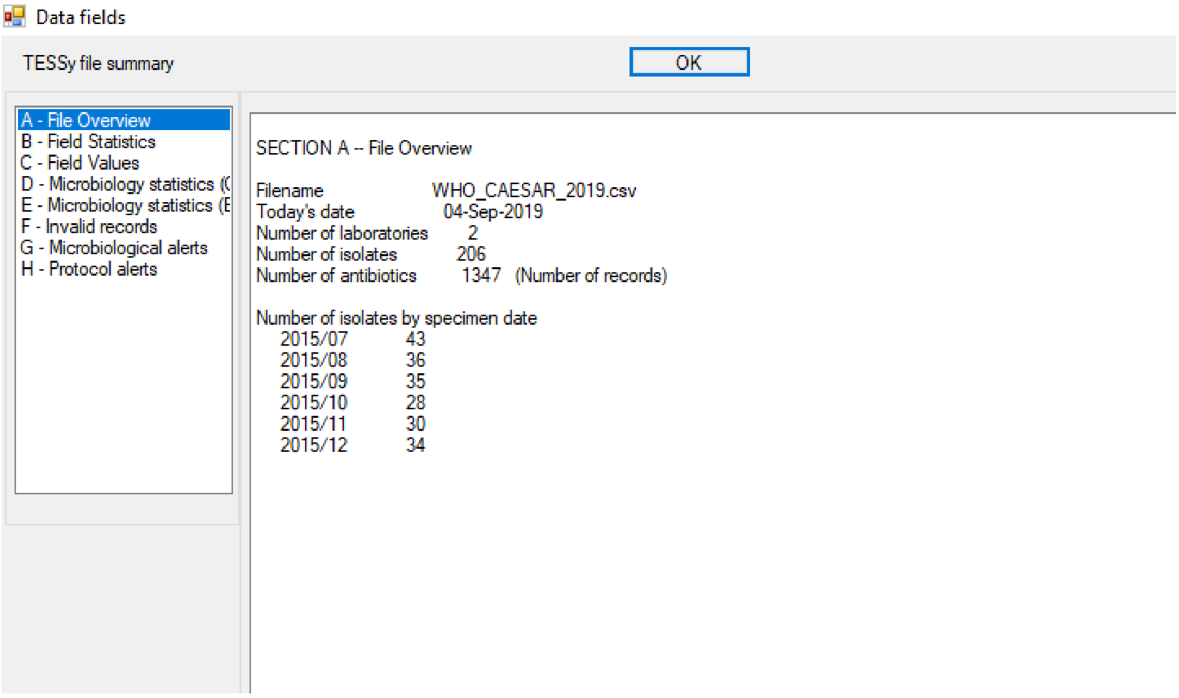
Save as type: TESSy (CSV)

New data file: WHO_CAESAR_2019

TESSy DataSource: WH-AMR

Figure 4.4: Selecting output type.

- Click ‘Combine’
- You could get a message saying that the files were successfully combined. Click ‘OK’ to continue
- The EARS-Net/CAESAR Data Check and Feedback Report will load automatically (Figure 4.5):



```
SECTION A -- File Overview

Filename                WHO_CAESAR_2019.csv
Today's date              04-Sep-2019
Number of laboratories       2
Number of isolates          206
Number of antibiotics        1347   (Number of records)

Number of isolates by specimen date
    2015/07         43
    2015/08         36
    2015/09         35
    2015/10         28
    2015/11         30
    2015/12         34
```

Figure 4.5: Selecting file summary.

- Click on each of the different sections indicated on the left panel (marked A to H) and check that the following are as expected:
    - Number of laboratories

    - Number of isolates
    - Date range
    - No missing data fields that are mandatory
    - Microbiology statistics (Overall)
    - Microbiology statistics (By laboratory)
    - Invalid fields
    - Microbiological alerts
    - EARS-Net/CAESAR protocol alerts
- Make corrections to the original data files if required and then re-combine as above and review the Data Check and Feedback Report again until you are happy the data are ready to send to the international CAESAR data manager.

4.3 Dealing with problems with WHONET/BacLink

Local users in a country: Any general problems with WHONET, i.e. you are not sure how to do something: contact your national data manager.

Encountering potential bugs in the software: contact the developers of WHONET, but check with your national data manager first as there may not be a bug or they may already be aware of the issue and the developers have already been contacted.

National data managers: Any general problems with WHONET, i.e. you are not sure how to do something: contact your CAESAR colleagues with known expertise or the developers of WHONET.

Encountering bugs in the software: contact the developers of WHONET (they will get back to you but they may need a reminder if no response).

5 Data validation

After you have analysed your data in WHONET there are a few things you can look at to catch errors or missing data.

Species

- ☐ Does your data file contain all the species you expect?
  - Make sure that any missing species were in the original file and that they were translated correctly if BacLink was used, or if the species was selected when exporting from the original file into CAESER data file.

Antibiotics

- ☐ **D**oes your data file contain all the antibiotics you expect?
  - Make sure that the missing antibiotics were in the original file.
  - Check that the antibiotic codes are translated correctly in BacLink and make sure that they have been added to the laboratory configuration in WHONET.

Number of tested isolates

- ☐ Does the number of isolates match what you would expect for this period of time?
  - If you have a lot less isolates maybe some isolates are missing?
  - If you have a lot more isolates compared to a similar time period maybe you were missing some isolates in the previous time period?

  In both cases it could also be due to a change in sampling so ask the laboratory if they can explain any big differences. Also see ‘Sample dates’ below.

Duplicates

- ☐ Does your file contain duplicate isolates of a particular organism from a single patient?
  - If so, you will need to re-do your analysis (see section 3) to include one isolate (of a species) per patient (first isolate only).

Sample dates

- ☐ Does your data file contain isolates with a sample date not included in the time period under surveillance?
  - If so, remove the isolates or disregard them during analysis.
  - Make sure that you have isolates from the whole time period under surveillance. If you had 75 isolates in January and 92 in February it is unlikely (but not impossible) that you only had 3 in March.
  - If for some reason the laboratory adds a new code for a certain antibiotic during the year, make sure that both the original and the new code is exported from the laboratory information system. If only the original code is exported you will miss the test results for this drug after the date of change. If only the new code is exported you will miss results prior to the date of change.

Resistance levels

☐ Do the levels of resistance for all drug/bug combinations match what you have previously seen in your country or laboratory?
  - If not, does it seem likely that the difference reflects a true change in antibiotic resistance levels or could it be due to an error?

Since the resistance level is the percentage of resistant isolates of all tested isolates, an error in either the number of resistant isolates or the total number of isolates will influence the reported level of resistance. An unusually high level of resistance could therefore be due too many resistant isolates or a too low total number of isolates.

If a certain resistance level is unusually high, consider what you are using as a denominator. Normally you would use the number of tested isolates as the denominator. Ideally all isolates are susceptibility tested for all relevant drugs and if this is the case your number of tested isolates will be identical to the total number of isolates. But in reality this is not always the case. If all isolates are not susceptibility tested you need to consider whether or not the tested isolates are representative for the population you are trying to describe in your analysis. If 90% of all isolates are susceptibility tested they are most likely representative. Fifty or even 10% may be representative, but it depends on how the isolates are selected for susceptibility testing. If only a few isolates are susceptibility tested based on a suspicion of a certain resistance you may risk overestimating the resistance level dramatically.

Example: The laboratory has isolated 100 *Streptococcus pneumoniae*. As a screening for penicillin resistance all of the isolates are tested with an oxacillin disk. Ten of the isolates are resistant to oxacillin. These 10 isolates are then tested for penicillin resistance using the MIC method. Of the 10 ten isolates tested for penicillin resistance only one turns out to be resistant. If you were to report the penicillin resistance in *S. pneumoniae* it would make sense to look in your database and say 'Of the 10 isolates tested for penicillin one isolate was resistant therefore the resistance level is 1/10 = 10%'. But in reality it is one of the total 100 isolates that is resistant so the result should be 1/100 = 1%. So be careful if only a limited number of isolates are selected for susceptibility testing for a particular drug.

6 Submitting your data to CAESAR

When you have validated your data and exported them to a csv file in the CAESAR format you are ready to submit your data to CAESAR. This is done by sending your csv file by email to CAESAR's international data manager: **caesar@rivm.nl**. If your data file is very big you may encounter problems with the maximum attachment size in some email systems. Even if the file is within the limit it may take a while to send it by email depending on your internet connection speed. In this case consider compressing the file using a file compression program. In Windows you can easily compress your data file by right-clicking the file, clicking 'Send to' and then 'Compressed (zipped) Folder'. This should reduce the size of the file by about 90%.

When the international CAESAR data manager has received your data file, the data will be checked by a program that generates a small report that summarizes the findings in your data. This feedback report will be send to you for approval. You should go through this feedback report and check if the numbers look credible. If everything looks OK you should reply to the international CAESAR data manager that everything appears to be in order and that you approve the data. If you find errors or something just doesn't look right, you can try to find the error in your data yourself or you can ask the international CAESAR data manager if he can find any errors. When you have approved your data the international CAESAR data manager will add them to the CAESAR database and your data will be ready for publication. You have now finished the submission of your CAESAR data.

7 Data security

This section is concerned with anonymization of patient information, backing up your data, keeping data on network drives instead of PC desktop, encryption etc.

It is of utmost importance to safeguard a patient's privacy and in this regard security measures must be taken to protect the confidentiality of laboratory data. Laboratories are responsible for putting policies and procedures in place to assure confidentiality of patient information. The personal information of patients is not needed for CAESAR such as name, surname, citizenship number, address, phone number, etc. However, unique identifiers in addition to some basic demographic data (e.g. age and sex for epidemiological purposes) are required, but this is anonymized before submission to CAESAR.

Also it is important to establish a means to protect against loss of data. It is a good idea to keep the CAESAR data on a network drive which is backed up regularly and is authorized just for the national surveillance team instead of keeping the data on your local hard drive. This way you won't lose your data if your hard drive breaks down. You can ask to your IT department for assistance.

It is important to establish a means to protect against loss of data. As a national data manager always keep the original data you received for an agreed period after data collection (e.g. 5 years).

If you need to send data that contains identifiable patient information e.g. to your national data manager you should consider encrypting your data. You can either encrypt the data file or send it in an encrypted email. Talk to your local IT department and national data manager about this.

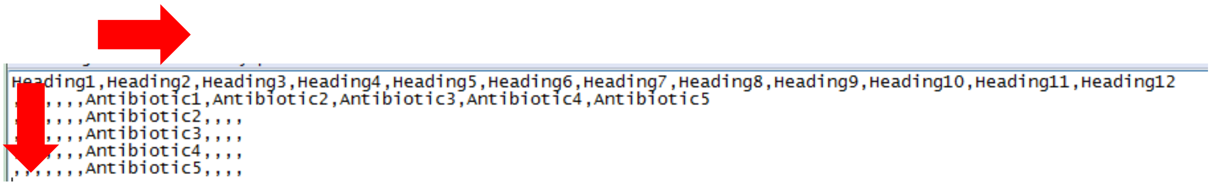
Annex 1 BacLink

A1.1 Setting up BacLink

A1.1.1 Formats and structures

Before conversion it is important to get familiar with the structure and contents of your data file. BacLink accepts different formats e.g. Tab-separated text files, .mdb, fixed text files or other text files with different delimiters. To be able to configure BacLink you need to know the following about your file:

1. File format
2. Does your file include antibiotic results, if yes go further
3. Test methods. e.g. Disk diffusion (categorized, zone diameters or both), MIC/Etests
4. Guidelines e.g. EUCAST, CLSI
   Note: it is best to select the correct guidelines, test methods including disk potencies for the pathogen and guidelines followed
5. Structure of antibiotic results. One row per antibiotic or one row per isolate (Figure A 1)



```
Heading1,Heading2,Heading3,Heading4,Heading5,Heading6,Heading7,Heading8,Heading9,Heading10,Heading11,Heading12
,,,,Antibiotic1,Antibiotic2,Antibiotic3,Antibiotic4,Antibiotic5
,,,,Antibiotic2,,,,
,,,,Antibiotic3,,,,
,,,,Antibiotic4,,,,
,,,,,,Antibiotic5,,,,
```

Figure A 1: File structure. Right arrow: one row per isolate. Down arrow: one line per antibiotic.

6. Antibiotic sequence, fixed or variable.

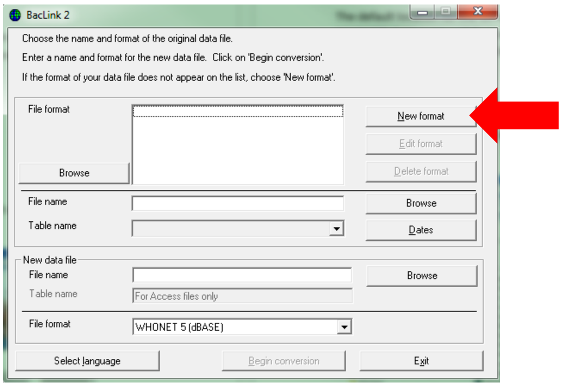
BacLink does not support direct import from an EXCEL file. If your data are stored in an Excel file export the data to a Tab-delimited text file from Excel and import this file in BacLink.

TIP: BacLink can only work with a structured file. If there are any redundant rows in your data file either before or after the rows containing the field names or the data itself then these should be deleted.

TIP: Format dates in your raw data file before proceeding to translate the file using BacLink to avoid problems with dates later.

A1.1.2 Configuring a new format

1. Select 'New format' (see Figure A 2)

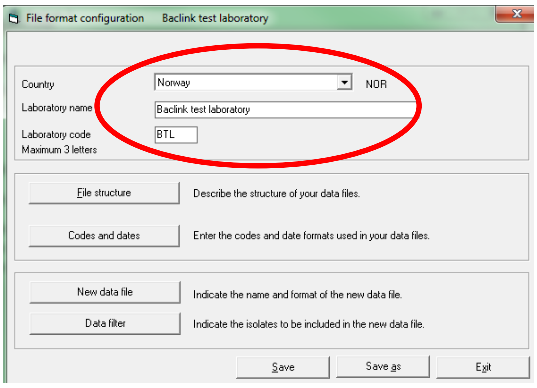


Choose the name and format of the original data file.
Enter a name and format for the new data file. Click on 'Begin conversion'.
If the format of your data file does not appear on the list, choose 'New format'.

New data file
File name:
Table name: For Access files only
File format: WHONET 5 (dBASE)

Figure A 2: Create new format.

2. Select Country from the drop down box, enter a laboratory name and enter up to 3 characters for the Laboratory code. The laboratory code (assigned by your national data manager; the format will be in accordance with that recommended by CAESAR, i.e.3-digits) will be used in BacLink and in WHONET as the default file extension for your WHONET data files. See Figure A 3.

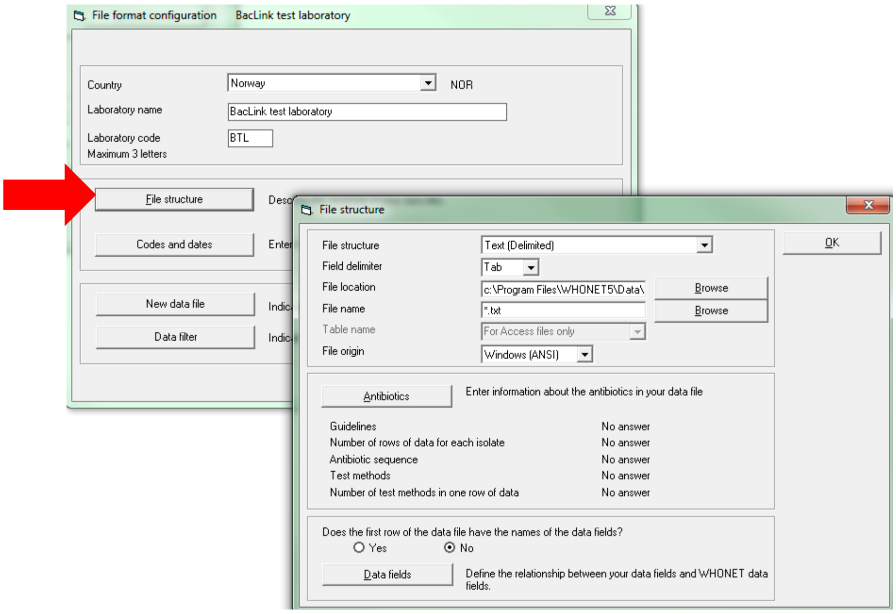


Country: Norway NOR
Laboratory name: Baclink test laboratory
Laboratory code
Maximum 3 letters: BTL

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.

Figure A 3: Select country and assign laboratory code.

3. Click on ‘File structure’, a new window labelled ‘File structure’ pops up. Select your File structure and delimiter from the dropdown menu. Enter File location and File name. In this example our file is a tab-separated text file. See Figure A 4.



File format configuration BacLink test laboratory

Country: Norway NOR

Laboratory name: BacLink test laboratory

Laboratory code (Maximum 3 letters): BTL

File structure

File structure: Text (Delimited)

Field delimiter: Tab

File location: c:\Program Files\WHONET5\Data\

File name: *.txt

Table name: For Access files only

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

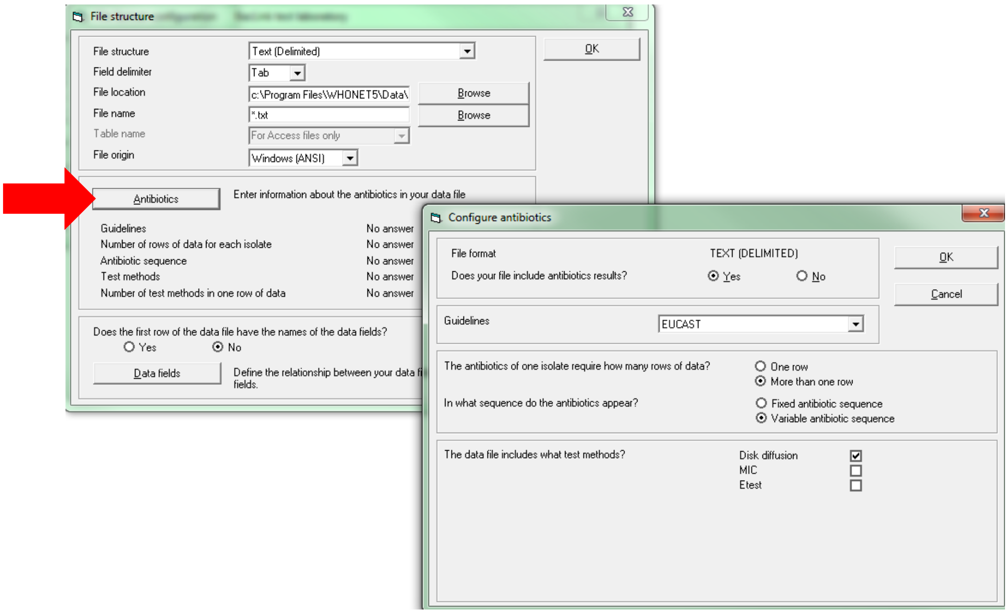
Number of test methods in one row of data: No answer

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.

Figure A 4: File structure.

4. Click on 'Antibiotics', a new window 'Configure antibiotics' pops up. If your data file does not contain antibiotic results, select 'No' and click 'OK'. If 'YES' select Guideline from the dropdown menu. It is important to know the structure of antibiotic results. Choose whether your data file has one row per isolate or more than one row per isolate, fixed or variable antibiotic sequence. See Figure A 5.



Configure antibiotics

File format: TEXT (DELIMITED)

Does your file include antibiotics results? ● Yes ○ No

Guidelines: EUCAST

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?

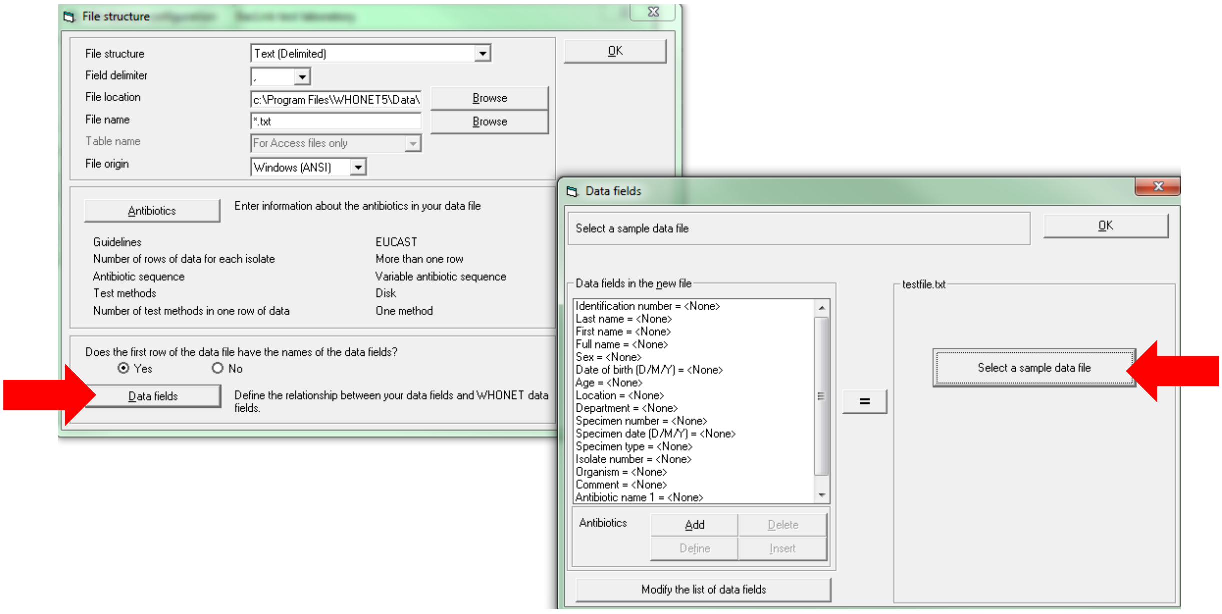
Disk diffusion ☑

MIC ☐

Etest ☐

Figure A 5: Antibiotics screen.

5. Click on 'Data fields'. Here you define which fields you would like to map into your WHONET file. Important, if you have headings in your file, make sure that the headings are the same in all the files you plan to map into a WHONET file. See Figure A 6.



File structure

File structure: Text (Delimited)
Field delimiter: ,
File location: c:\Program Files\WHONET5\Data\
File name: *.txt
Table name: For Access files only
File origin: Windows (ANSI)

Enter information about the antibiotics in your data file

Guidelines: EUCAST
Number of rows of data for each isolate: More than one row
Antibiotic sequence: Variable 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

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

Data fields

Select a sample data file

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 name 1 = <None>

testfile.txt

Figure A 6: Selecting data fields.

TIP: It is a good idea to check the mapping each time you want to convert a file using a BacLink file format already configured, especially important if you only rarely use BacLink. This is particularly useful for new users who are not fully familiar with their file formats. If the field names change even very slightly from one file to another then BacLink will not recognise the new field name, no mapping will take place and your newly created WHONET data file will be missing data.

6. For the CAESAR report the following variables are required and need to be in the file. Some of the variables will be created by WHONET. See Table A 1.

Table A 1: CAESAR variables.

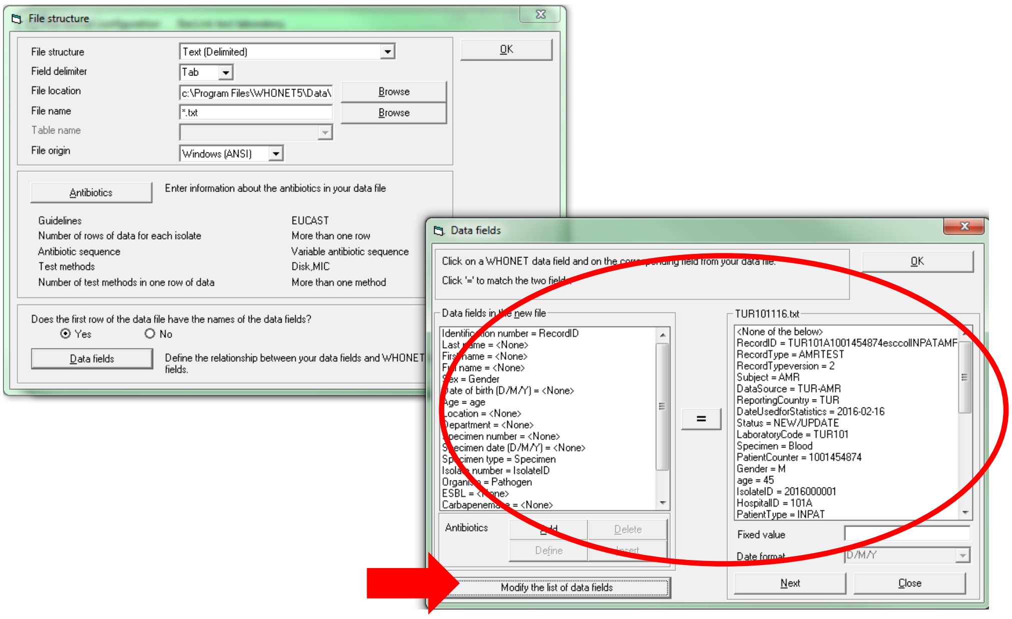
Table 1: Overview of the set of variables for AMR surveillance

Variables for AMR surveillance	**Required for CAESAR**	**Field in BacLink**	**Fieldnames**	**Comments**
RecordID	No	No		For EARS-Net/TESSy compatibility only.#
RecordType	No	No		For EARS-Net/TESSy compatibility only.#
RecordTypeversion	No	No		For EARS-Net/TESSy compatibility only.#
Subject	No	No		For EARS-Net/TESSy compatibility only.#
DataSource	No	No		For EARS-Net/TESSy compatibility only.#
ReportingCountry	**Yes**	Yes	Country	
DateUsedforStatistics	**Yes**	Yes	Specimen date	
Status	No	No		For EARS-Net/TESSy compatibility only.#
LaboratoryCode	**Yes**	Yes	Laboratory	
Specimen	**Yes**	Yes	Specimen type	
PatientCounter	**Yes**	Yes	Identification number	Encryption in WHONET
Gender	**Yes**	Yes	Sex	
age	**Yes**	Yes	Age	Birth-date is also an option
IsolateID	**Yes**	Yes	Specimen number	
HospitalID	**Yes**	Yes	EARSS Hospital code*	
PatientType	**Yes**	Yes	Defined by location field	
HospitalUnitType	**Yes**	Yes	Defined by location field	
Pathogen	**Yes**	Yes	Organism	
DateOfHospitalisation	No	Yes	Date of admission*	
ResultPCRmec	No	Yes	PCR for mecA*	
ResultPbp2aAggl	No	Yes	PBP2a latex agglutination*	
Serotype	No	Yes	Serotype*	
esbl	No	Yes	ESBL	
ResultCarbapenemases	No	Yes	Carbapenemase	
Antibiotic	**Yes**	Yes	Antibiotic name 1	Be aware of method when choosing antibiotic code
SIR	**Yes**	Yes	Antibiotic result 1	Categorized or numeric based on method
ResultZoneSign	No	Yes	Fieldname given by the ab-code and input-value	
ResultZoneValue	No	Yes	Fieldname given by the ab-code	
ResultZoneSIR	No	Yes	Fieldname given by the ab-code	
ResultMICSign	No	Yes	Fieldname given by the ab-code and input-value	
ResultMICvalue	No	Yes	Fieldname given by the ab-code	
ResultMICSIR	No	Yes	Fieldname given by the ab-code and input-value	
ResultEtestSign	No	Yes	Fieldname given by the ab-code and input-value	
ResultEtestValue	No	Yes	Fieldname given by the ab-code	
ResultEtestSIR	No	Yes	Fieldname given by the ab-code and input-value	
Diskload	No	Yes	Fieldname given by the ab-code	
ReferenceGuidelinesSIR	No	Yes	Fieldname given by the ab-code	

* Can be added from the "Modify the list of data fields"
# Not currently in use for CAESAR

7. After clicking ‘Select a sample data file’, the information in your file needs to be mapped to the WHONET fields. The list on the left contains the WHONET information fields. The list on the right contains the

information fields in your data file. Click the WHONET field name and the field in your file that you want to map to it. When the two fields are highlighted click the ‘=‘ button between the two lists to map the codes. Make sure that all of the required variables are included in the mapping. Be aware of the date formats before clicking ‘=‘ in order for the dates to be correct. See Figure A 7.



File structure: Text (Delimited)
Field delimiter: Tab
File location: c:\Program Files\WHONET5\Data\
File name: *.txt
Table name
File origin: Windows (ANSI)

Enter information about the antibiotics in your data file

Guidelines: EUCAST
Number of rows of data for each isolate: More than one row
Antibiotic sequence: Variable antibiotic sequence
Test methods: Disk,MIC
Number of test methods in one row of data: More than one method

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

Define the relationship between your data fields and WHONET fields.

Click on a WHONET data field and on the corresponding field from your data file.

Click '=' to match the two fields.

Data fields in the new file

Identification number = RecordID
Last name = <None>
First name = <None>
Full name = <None>
Sex = Gender
Date of birth (D/M/Y) = <None>
Age = age
Location = <None>
Department = <None>
Specimen number = <None>
Specimen date (D/M/Y) = <None>
Specimen type = Specimen
Isolate number = IsolateID
Organism = Pathogen
ESBL = <None>
Carbapenemase = <None>

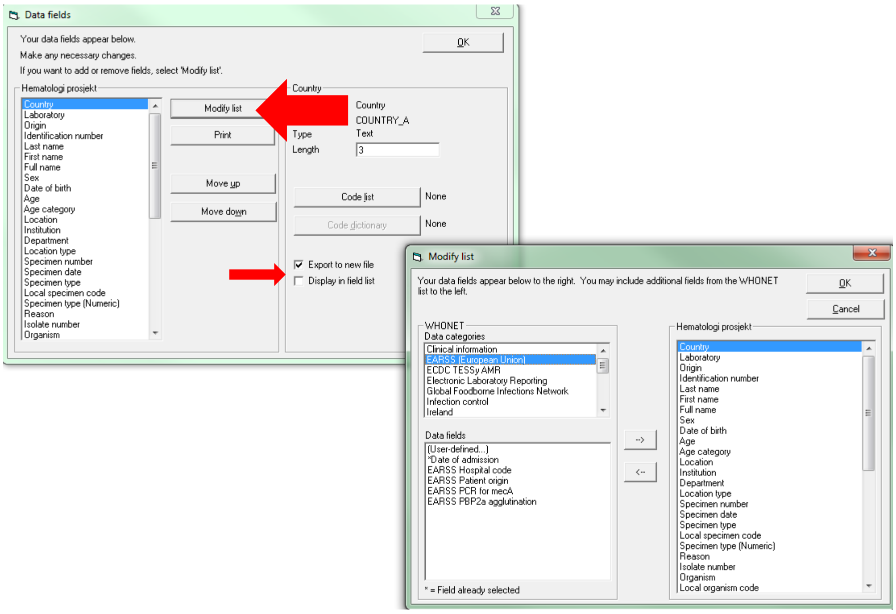
TUR101116.txt

<None of the below>
RecordID = TUR101A1001454874esccolINPATAMF
RecordType = AMRTEST
RecordTypeversion = 2
Subject = AMR
DataSource = TUR-AMR
ReportingCountry = TUR
DateUsedforStatistics = 2016-02-16
Status = NEW/UPDATE
LaboratoryCode = TUR101
Specimen = Blood
PatientCounter = 1001454874
Gender = M
age = 45
IsolateID = 2016000001
HospitalID = 101A
PatientType = INPAT

Fixed value
Date format: D/M/Y

Figure A 7: Mapping variables.

8. Some fields will not be available in the default list. Click ‘Modify list of data fields’(see Figure A 7 arrow). If the field you would like to include exist in the list but are not visible tick ‘Display in list’ for the one you would like to include. If the field doesn’t exist click ‘Modify list’ and choose the field based on your data you would like to include and click ‘Ok’. See Figure A 8.



Your data fields appear below.
Make any necessary changes.
If you want to add or remove fields, select 'Modify list'.

Hematologi prosjekt

Country
Laboratory
Origin
Identification number
Last name
First name
Full name
Sex
Date of birth
Age
Age category
Location
Institution
Department
Location type
Specimen number
Specimen date
Specimen type
Local specimen code
Specimen type (Numeric)
Reason
Isolate number
Organism

Country
Country
COUNTRY_A
Type: Text
Length: 3
Code list: None
Code dictionary: None
☑ Export to new file
☐ Display in field list

Your data fields appear below to the right. You may include additional fields from the WHONET list to the left.

WHONET

Data categories

Clinical information
EARSS (European Union)
ECDC TESSy AMR
Electronic Laboratory Reporting
Global Foodborne Infections Network
Infection control
Ireland

Data fields

(User-defined...)
*Date of admission
EARSS Hospital code
EARSS Patient origin
EARSS PCR for mecA
EARSS PBP2a agglutination

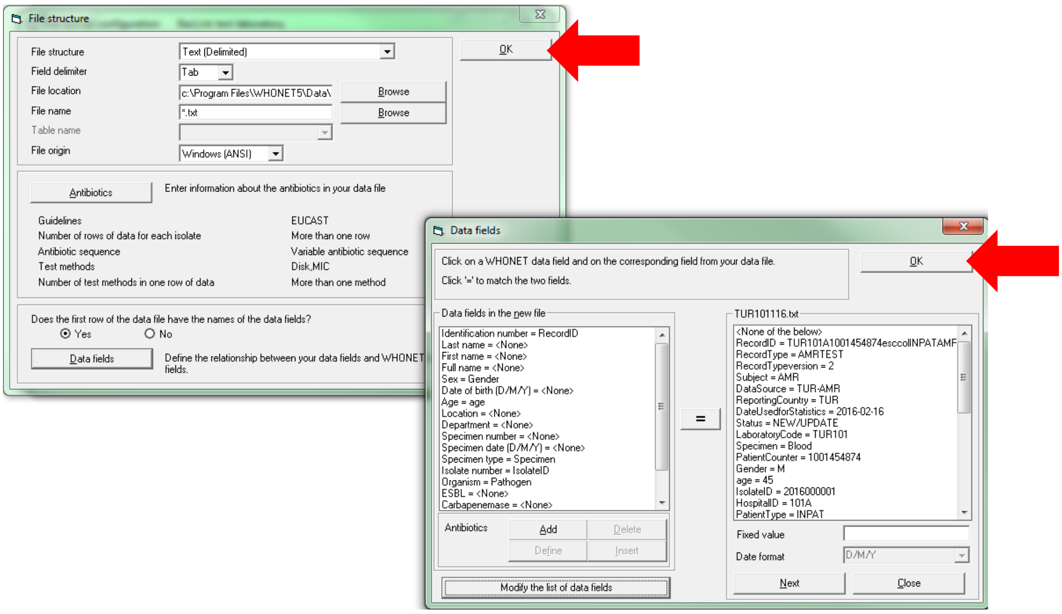
* = Field already selected

Hematologi prosjekt

Country
Laboratory
Origin
Identification number
Last name
First name
Full name
Sex
Date of birth
Age
Age category
Location
Institution
Department
Location type
Specimen number
Specimen date
Specimen type
Local specimen code
Specimen type (Numeric)
Reason
Isolate number
Organism
Local organism code

Figure A 8: Modify list of variables.

9. After finalizing all the mappings click ‘OK’ and ‘OK’ (see Figure A 9).



File structure
File structure: Text (Delimited)
Field delimiter: Tab
File location: c:\Program Files\WHONET5\Data\
File name: *.txt
Table name:
File origin: Windows (ANSI)

Enter information about the antibiotics in your data file

Guidelines: EUCAST
Number of rows of data for each isolate: More than one row
Antibiotic sequence: Variable antibiotic sequence
Test methods: Disk,MIC
Number of test methods in one row of data: More than one method

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

Define the relationship between your data fields and WHONET fields.

Data fields

Click on a WHONET data field and on the corresponding field from your data file.
Click '=' to match the two fields.

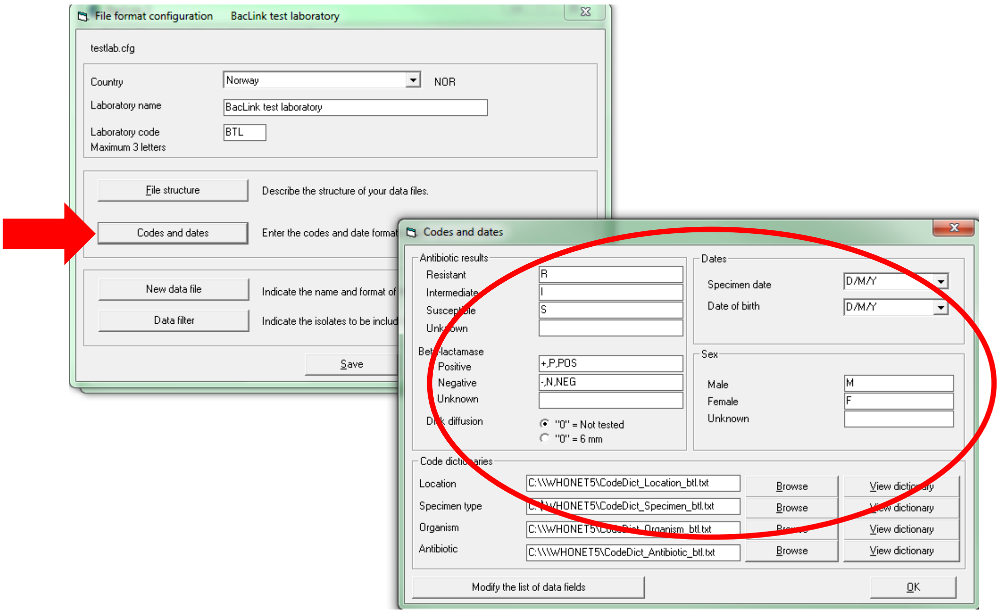
Data fields in the new file
Identification number = RecordID
Last name = <None>
First name = <None>
Full name = <None>
Sex = Gender
Date of birth (D/M/Y) = <None>
Age = age
Location = <None>
Department = <None>
Specimen number = <None>
Specimen date (D/M/Y) = <None>
Specimen type = Specimen
Isolate number = IsolateID
Organism = Pathogen
ESBL = <None>
Carbapenemase = <None>

TUR101116.txt
<None of the below>
RecordID = TUR101A1001454874esccolINPATAMF
RecordType = AMRTEST
RecordTypeversion = 2
Subject = AMR
DataSource = TUR-AMR
ReportingCountry = TUR
DateUsedforStatistics = 2016-02-16
Status = NEW/UPDATE
LaboratoryCode = TUR101
Specimen = Blood
PatientCounter = 1001454874
Gender = M
age = 45
IsolateID = 2016000001
HospitalID = 101A
PatientType = INPAT

Fixed value:
Date format: D/M/Y

Figure A 9: Finalize mapping.

10. Click on ‘Codes and Dates’. Select your date formats, abbreviations for RIS, Sex and change your locations for codes. After finalizing click ‘OK’. See Figure A 10.



testlab.cfg
Country: Norway NOR
Laboratory name: BacLink test laboratory
Laboratory code (Maximum 3 letters): BTL

Describe the structure of your data files.
Enter the codes and date format
Indicate the name and format of
Indicate the isolates to be includ

Antibiotic results
Resistant: R
Intermediate: I
Susceptible: S
Unknown:
Beta-lactamase
Positive: +,P,POS
Negative: -,N,NEG
Unknown:
Disk diffusion: ● "0" = Not tested ○ "0" = 6 mm

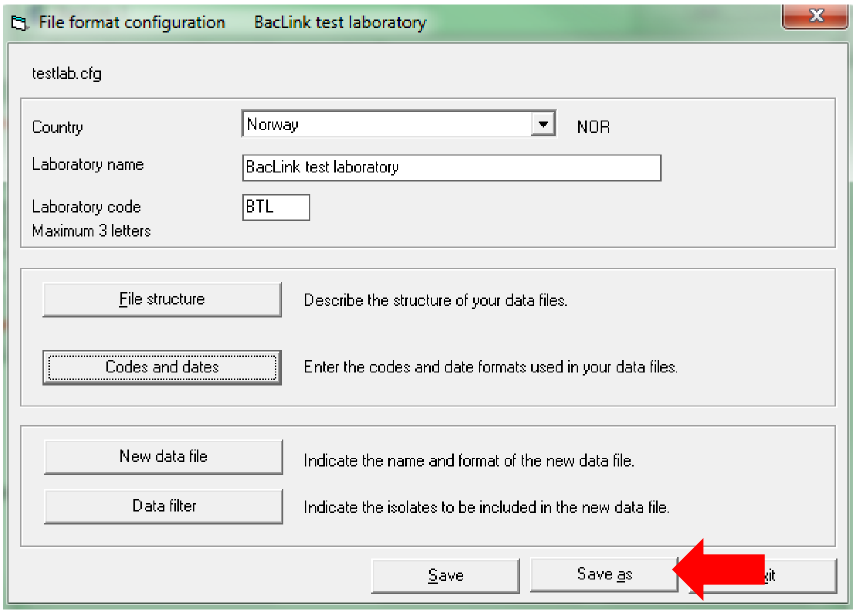
Dates
Specimen date: D/M/Y
Date of birth: D/M/Y

Sex
Male: M
Female: F
Unknown:

Code dictionaries
Location: C:\\WHONET5\CodeDict_Location_btl.txt
Specimen type: C:\\WHONET5\CodeDict_Specimen_btl.txt
Organism: C:\\WHONET5\CodeDict_Organism_btl.txt
Antibiotic: C:\\\WHONET5\CodeDict_Antibiotic_btl.txt

Figure A 10: Codes and dates screen.

11. Click on ‘Save as’ and give your configuration file a name. This file needs to be located in the same folder as the BacLink.exe file. After saving click ‘Exit’. See Figure A 11.



File format configuration   BacLink test laboratory

testlab.cfg

Country: Norway   NOR

Laboratory name: BacLink test laboratory

Laboratory code: BTL

Maximum 3 letters

Describe the structure of your data files.

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

Indicate the name and format of the new data file.

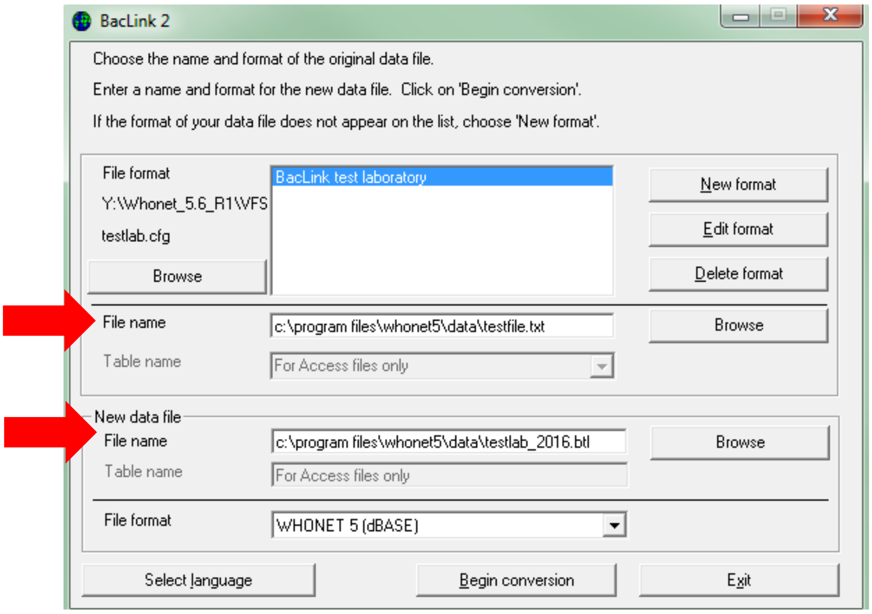
Indicate the isolates to be included in the new data file.

Figure A 11: Save configuration.

12. Now you have finalized the configuration for the mapping and are ready to convert your file to a WHONET file.

A1.2 Converting data files

1. Select a File name and location. This is your data file that you want to convert to a WHONET file. Select the name and the location of the new file (WHONET file), then click 'Begin conversion'. See Figure A 12.



BacLink 2

Choose the name and format of the original data file.

Enter a name and format for the new data file. Click on 'Begin conversion'.

If the format of your data file does not appear on the list, choose 'New format'.

File format: Y:\Whonet_5.6_R1\VFS testlab.cfg — BacLink test laboratory

File name: c:\program files\whonet5\data\testfile.txt

Table name: For Access files only

New data file

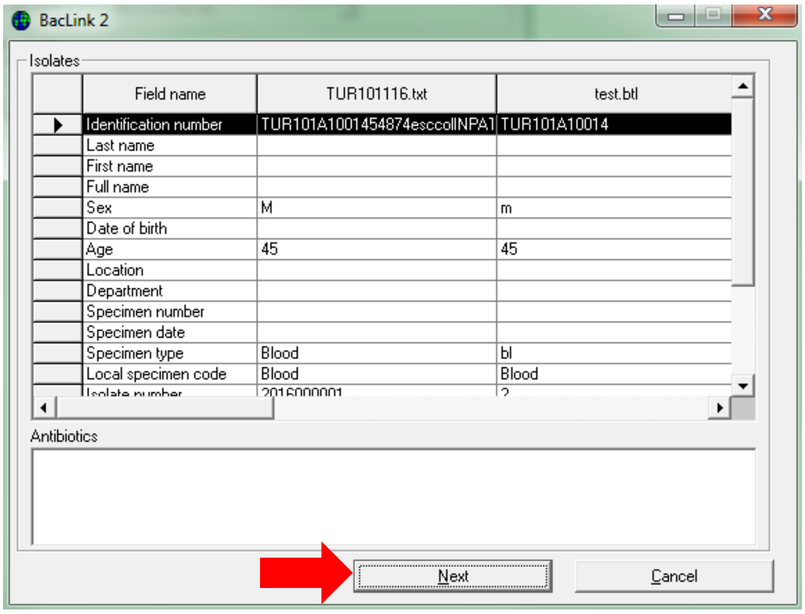
File name: c:\program files\whonet5\data\testlab_2016.btl

Table name: For Access files only

File format: WHONET 5 (dBASE)

Figure A 12: Convert file.

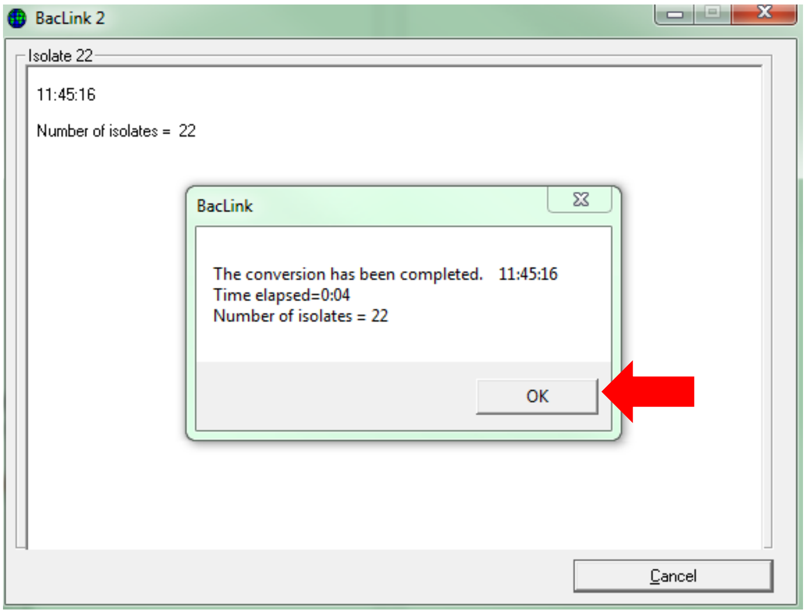
2. BacLink will step through the first 3 isolates before it runs through the rest of the file. You will see the Field name, the content of this field in your file and what BacLink will write in the new file. You can use this to check if BacLink translates your data correctly. Click 'Next' 3 times. See Figure A 13.



	Field name	TUR101116.txt	test.btl
▶	Identification number	TUR101A1001454874esccolINPA1	TUR101A10014
	Last name		
	First name		
	Full name		
	Sex	M	m
	Date of birth		
	Age	45	45
	Location		
	Department		
	Specimen number		
	Specimen date		
	Specimen type	Blood	bl
	Local specimen code	Blood	Blood
	Isolate number	2016000001	2

Figure A 13: First 3 lines: result of conversion.

3. BacLink will give information about time spent and number of isolates in the file. It is always a good idea to check whether this number is reasonable. If not you will need to go back to your configuration and reconfigure. Click ‘OK’. See Figure A 14.



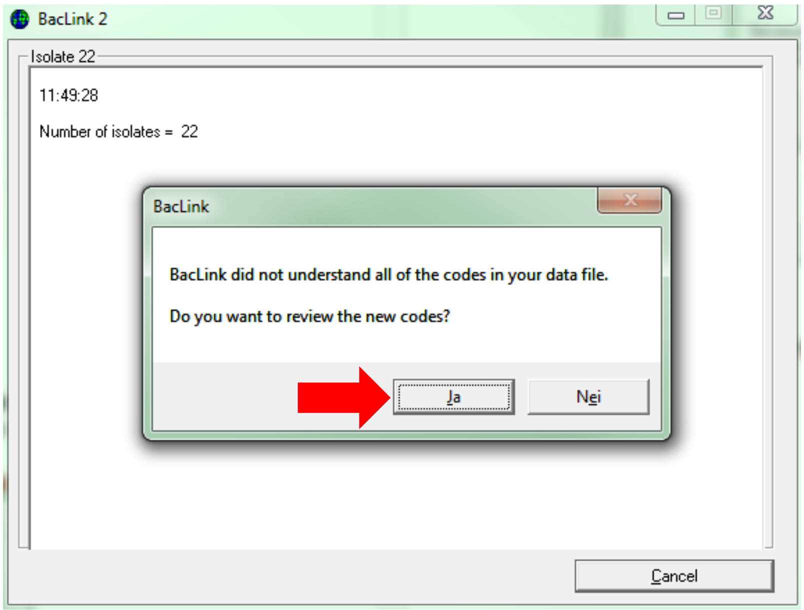
11:45:16

Number of isolates = 22

The conversion has been completed. 11:45:16
Time elapsed=0:04
Number of isolates = 22

Figure A 14: End of conversion.

4. A message will pop up whether you would like to review new codes, click ‘YES’. See Figure A 15.



Isolate 22

11:49:28

Number of isolates = 22

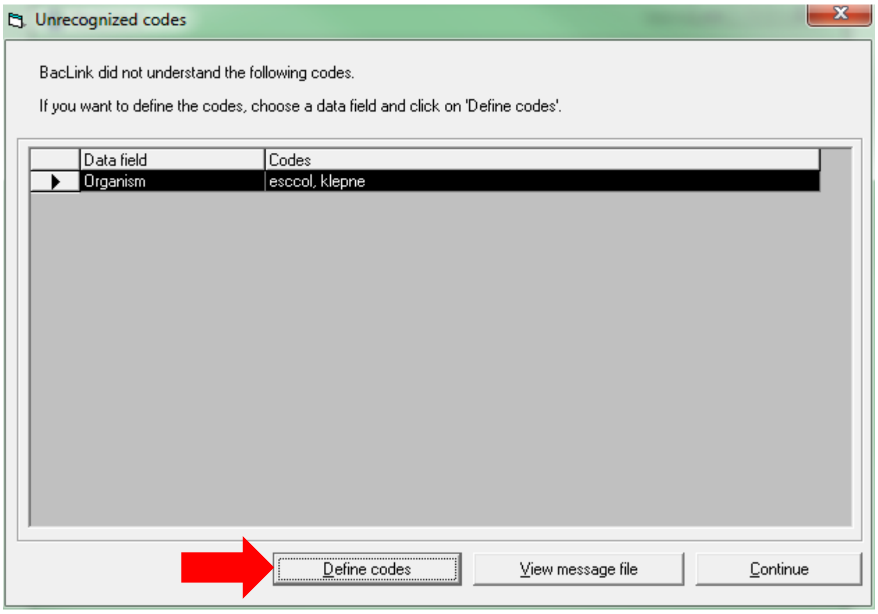
BacLink did not understand all of the codes in your data file.

Do you want to review the new codes?

Figure A 15: Choose to review new codes.

TIP: always click 'Yes' if you get this message as there may be codes that BacLink has not yet encountered from your data files. Even if the codes from your data files are exactly the same as those used in WHONET, BacLink will not understand any new codes until they have been mapped.

5. BacLink shows what data fields contain data codes BacLink doesn't understand. In this case 'Organism' with the codes 'esccol 'and 'klepne'. Click on 'Define codes'. See Figure A 16.



BacLink did not understand the following codes.

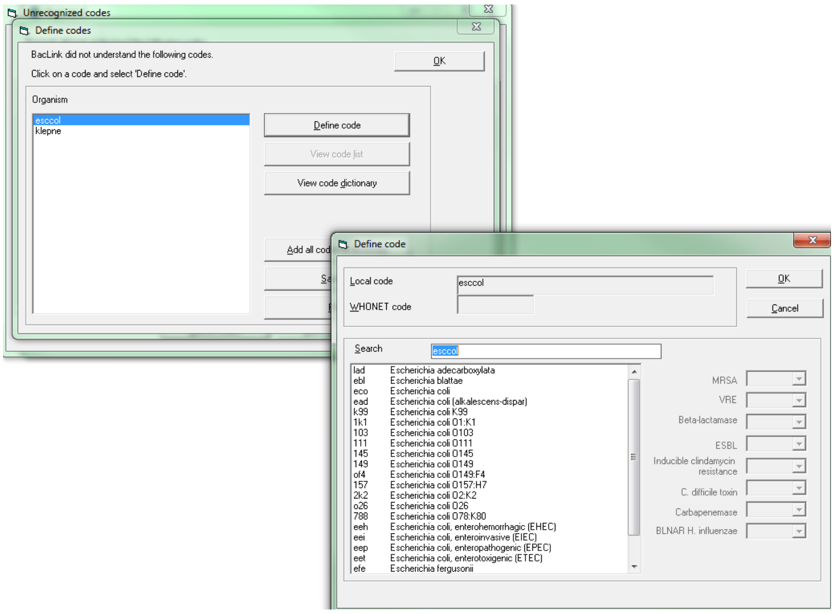
If you want to define the codes, choose a data field and click on 'Define codes'.

Data field	Codes
Organism	esccol, klepne

Figure A 16: Unknown codes.

6. Each new code will be listed and you have to go through the list in order to explain to BacLink what the codes mean. Select the code then click on 'Define code'. A list of possible codes will pop up. BacLink will narrow the search based on what you type in the 'Search' field. Choose one of these codes then select

‘OK’. Do the same with the next code until the ‘Define code’ list is empty. If more than one Data field contain unknown codes, repeat this operation. See Figure A 17.



BacLink did not understand the following codes.

Click on a code and select 'Define code'.

Organism

esccol
klepne

Local code: esccol

WHONET code:

Search: esccol

lad	Escherichia adecarboxylata
ebl	Escherichia blattae
eco	Escherichia coli
ead	Escherichia coli (alkalescens-dispar)
k99	Escherichia coli K99
1k1	Escherichia coli O1:K1
103	Escherichia coli O103
111	Escherichia coli O111
145	Escherichia coli O145
149	Escherichia coli O149
of4	Escherichia coli O149:F4
157	Escherichia coli O157:H7
2k2	Escherichia coli O2:K2
o26	Escherichia coli O26
788	Escherichia coli O78:K80
eeh	Escherichia coli, enterohemorrhagic (EHEC)
eei	Escherichia coli, enteroinvasive (EIEC)
eep	Escherichia coli, enteropathogenic (EPEC)
eet	Escherichia coli, enterotoxigenic (ETEC)
efe	Escherichia fergusonii

Figure A 17: Add codes.

7. After all the new codes are mapped and explained, redo the ‘Begin conversion’ in step 1 and the list of new codes will be empty. Always redo the conversion after you map new codes to make sure all the data are translated properly.

Congratulations, you are now ready to analyse your data in WHONET!