BayesLatentClassModels: A program for estimating diagnostic test properties and disease prevalence

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1. Introduction

BayesLatentClassModels (BLCM) is a software package that uses latent class models to estimate the properties of diagnostic tests (e.g. sensitivity and specificity), along with disease prevalence. It is particularly useful when there is no gold standard test (i.e. one with 100% sensitivity and specificity), and when there may be dependence between pairs of diagnostic tests due to a latent variable besides the disease e.g. a shared biological mechanism. BLCM can handle results from up to eight dichotomous diagnostic tests.

It uses a Bayesian approach that allows substantive prior information on the prevalence, sensitivities or specificities to be incorporated in the analysis. This can be important when the problem is non-identifiable.

The statistical methods implemented by BLCM are described in detail in the following articles:

1) *Bayesian estimation of disease prevalence and the parameters of diagnostic tests in the absence of a gold standard* Joseph L, Gyorkos T, Coupal L. American Journal of Epidemiology 1995;141(3):263-272.
2) *Modeling conditional dependence between diagnostic tests: a multiple latent variable model* Dendukuri N, Hadgu A, Wang L.. Statistics in Medicine 2009;28(3):441-461

2. Installing BLCM

BLCM requires that the free software packages R, Perl and Microsoft Windows Script be installed.

BLCM can be downloaded for free as a zip file (BayesLatentClassModels.zip) from http://www.nandinidendukuri.com. Save the program to any directory of your choice and unzip it. Double click on the Setup.exe file to install BLCM.

Follow the instructions in doc\InstallInstructions.html, which will be found in the **BayesLatentClassModels** home directory[1].

3. Running BLCM

3.1 Program Input

The BLCM program requires the following inputs:

i) the joint results of the diagnostic tests
ii) the latent variable associated with each diagnostic test
iii) prior information on the prevalence of each latent variable (a uniform prior distribution may be used in the absence of any prior information)
iv) initial values for prevalence of each latent variable
v) 95% limits for each test's sensitivity and specificity based on prior information
vi) total number of Gibbs sampler iterations and monitored iterations desired
vii) initial values for each test's sensitivity and specificity

Each of these inputs is further explained below.

3.2 Starting the program

Start **BayesLatentClassModels** by browsing through the Start/Programs menu and select the shortcut labelled BayesLatentClassModels or by double-clicking the file called BayesLatentClassModels.pl (which will be found in the subdirectory bin\ in the **BayesLatentClassModels** home directory).

[1] The software home directory is the directory where you installed it: by default, it is C:\Users\user name\Documents\Bayesian Software\BayesLatentClassModels or C:\Documents and Settings\user name\My Documents\Bayesian Software\BayesLatentClassModels, depending on your platform.

3.3 Data preparation

The easiest way to enter data is through a plain text file, where the results of the individual tests appear in the first few columns (one column for each test used) and the last column gives the frequency for that combination of test results. The labels used to identify each test and the frequency should appear as column headings.

The example data set in examples\data\ VisceralLeishmaniasis.txt appears on the right. There are three tests used here (FGT, IFAT and Parasitology), and 8 possible combinations of test results. Zeros (0) represent negative test results while ones (1) represent positive test results.

Data need not be aligned, but you can use tabulations in your data file to align columns, as it may make it more reader-friendly. BLCM data input is tab-insensitive.

FGT	IFAT	Parasitology	count
0	0	0	116
0	0	1	95
0	1	0	4
0	1	1	15
1	0	0	3
1	0	1	36
1	1	0	3
1	1	1	37

It is also possible to enter the data through the BLCM graphical user interface. Interactive data entry instructions are relegated to Appendix A.

3.4 Examples

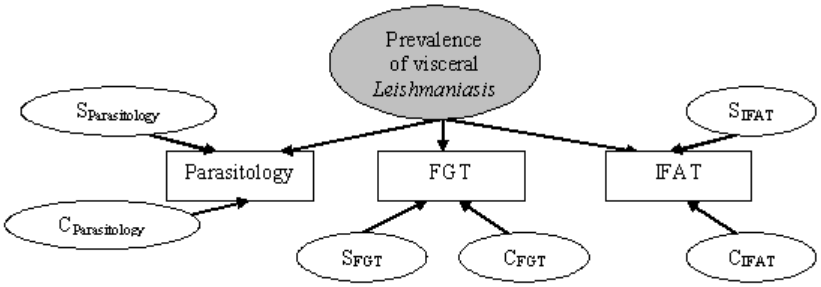
We now illustrate the use of BLCM via three examples of different latent class models. These examples are only for the purpose of illustrating BLCM**;** the models described are not necessarily the best fitting models.

The data set we use comprises the results of three non-gold standard diagnostic tests for *visceral leishmaniasis*. The complete data set with results from six different tests is described in Boelaert et al, 2004[2]. The combinations of results obtained on the three tests are given in the file examples\data\VisceralLeishmaniasis.txt in the BLCM home directory[2], provided with the software distribution.

3.4.1 Example 1: Latent Class Model assuming conditional independence

We will start with the simplest example, where the three tests are conditionally independent (this may happen, for example, if all tests measure the same latent variable, e.g. true disease status).

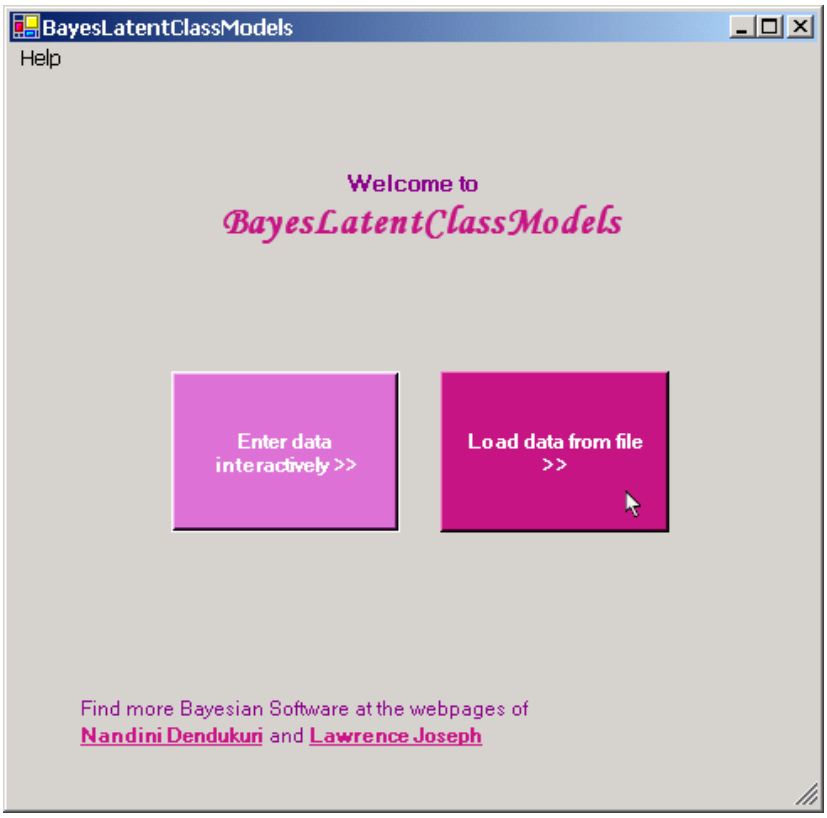
This model is depicted using the diagram on the right. The oval shapes represent the parameters to be estimated, while the rectangular shapes represent observed diagnostic test results. Sensitivitity and specificity are abbreviated as S and C.



[2] Boelaert M et al.*A comparative study of the effectiveness of diagnostic tests for visceral leishmaniasis.* Am J Trop Med Hyg. 2004 Jan;70(1):72-7

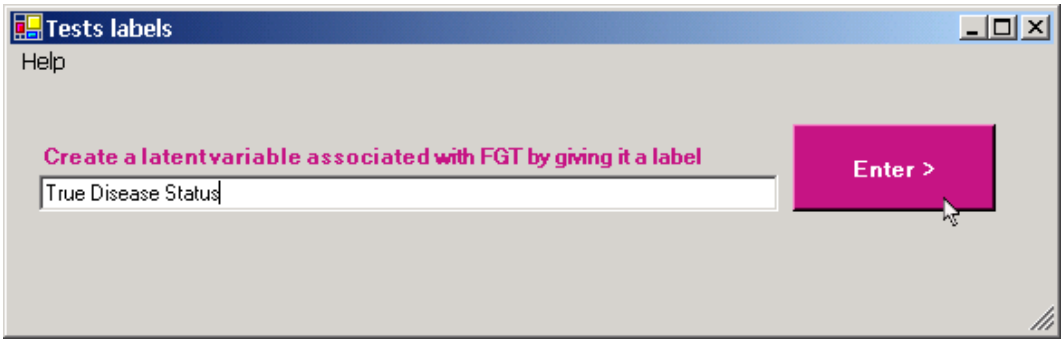
Starting BLCM opens the form on the right. It allows you to choose between entering data manually or through a plain text data file as described above.

Click *Load data from file>>*, which will open an **Open file** dialog box where you can browse to this example data file (examples\data\VisceralLeishmaniasis.txt).



The next series of forms will prompt you for a label for the latent variable associated with each diagnostic test.

The first form invites you to enter a label for the latent variable associated with FGT.



Type 'True Disease Status' (or any other label of your choice) in the text box and click *Enter* to proceed to other tests.

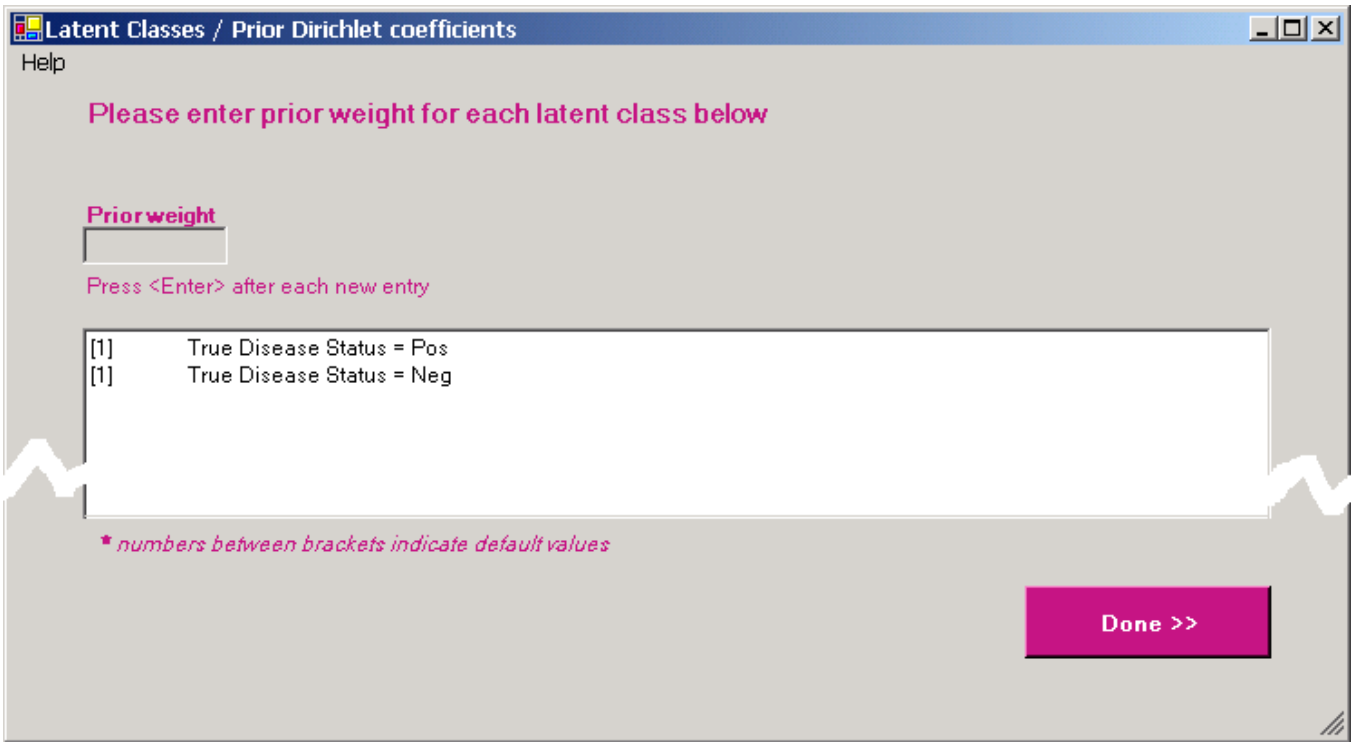
For subsequent test(s), it will be possible to choose from former test(s)' latent variable(s) or to enter a new one if the test is associated with a different latent variable. Note that latent variable labels are not case sensitive.

In this example, we assume that all three tests are conditionally independent, that is, that they are all associated with the same latent variable (labelled True Disease Status here). Therefore, we select this latent variable for each test.

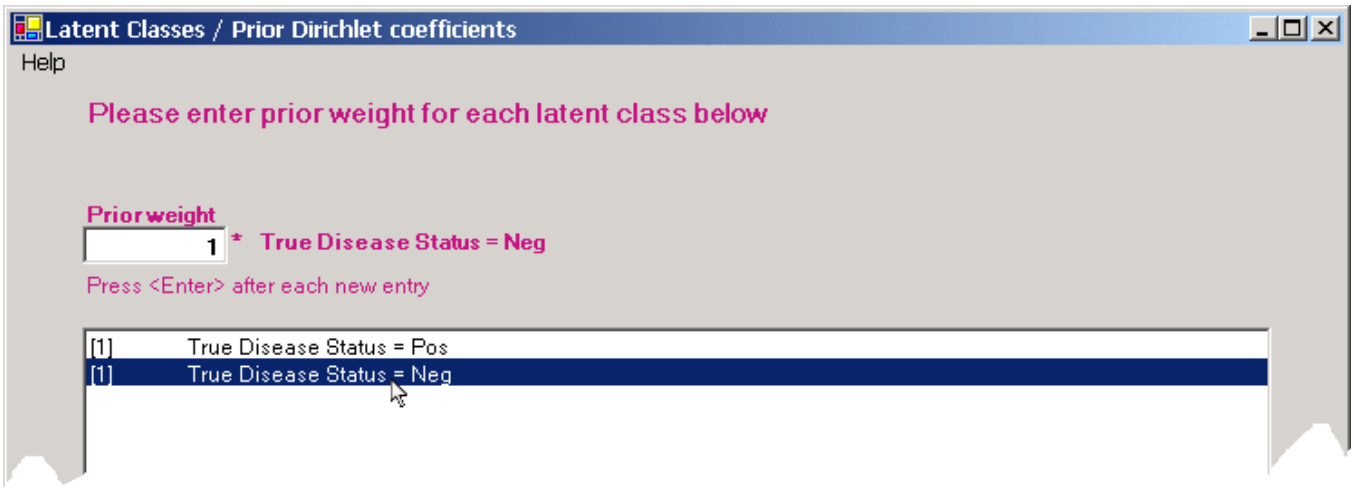
The data entered up to this point will be used by BLCM to determine if the model is identifiable. If not, prior information must be provided on a minimum number of parameters in order to obtain a meaningful solution. The model is not identifiable when the number of parameters to be estimated exceeds the number of degrees of freedom or the rank of the Jacobian.

At this point the BLCM window will disappear from the screen for a few seconds before returning with a message to tell the reader if any prior information is necessary. The model in Example 1 is identifiable and no prior information is necessary. Prior information can also be used when a problem is identifiable as we shall see in Example 2 below.

The next form (below) allows you to enter prior information about the prevalence of each latent variable. This is done by assigning a weight (technically, a coefficient from the Dirichlet distribution) for each latent class. In this example, we have a single dichotomous latent variable, and therefore two latent classes. By default, each latent class is *a priori* assigned a weight = 1, meaning in practice that both classes have equal weight prior to data collection. This is equivalent to saying we use a low information (sometimes called non-informative) prior distribution for the prevalence.

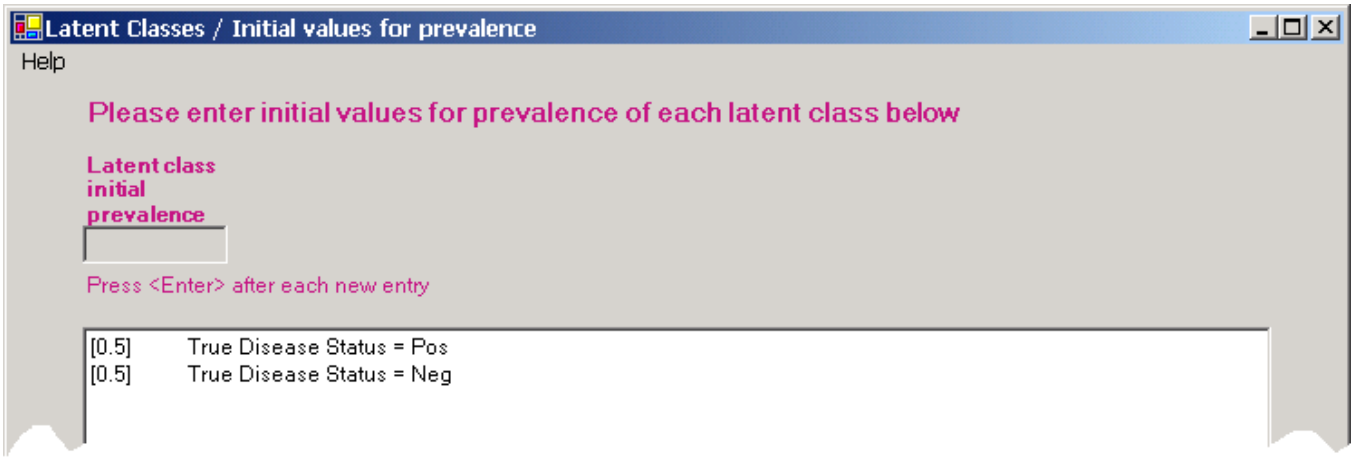


To change the prior weight assigned to each latent class, click on its label in the list and enter the weight in the **Prior weight** text box; type *Enter* after each entry.



In the current example, we retain the default values of 1 for each prior weight. Just click the **Done** button to proceed to the next form.

The next form (below) is used to enter initial values for the probability of each latent class. In our example, that would be equivalent to entering values for the probability of presence of True Disease and for the probability of absence of True Disease. Choose values that are reasonably close to the expected value of each prevalence. Values allowing equal probability to the latent classes are provided as a default. In theory, the results should be the same regardless of which initial values are used, these are used only to start the algorithm used and are eventually discarded. However, in practice, it is important to run BLCM with different starting values to ensure convergence to the same (or very similar) results from all starting values. Because of the stochastic nature of the Gibbs sampler algorithm, each run will result in slightly different values. For this reason, if you repeat the examples given in this manual, your results may not match exactly (but they should be very similar).



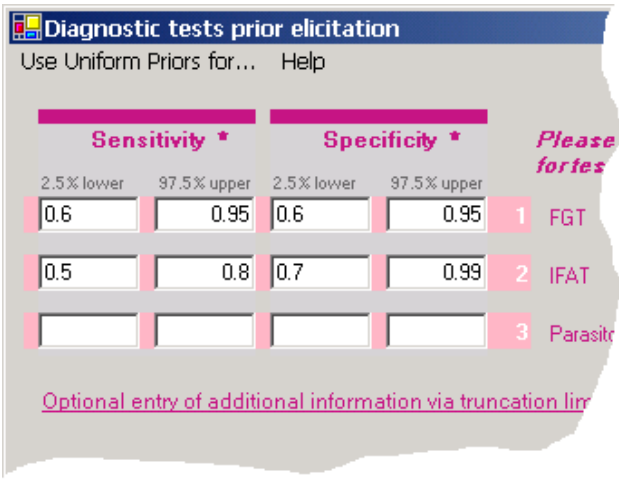
As in the previous form, you can change the initial value for a latent class by clicking its label and entering the value in the **Latent class initial prevalence** text box. Note that the default initial prevalences (values between brackets) will adjust to each new entry so that the sum always equals one.

Click **Done** to accept the default equal initial prevalence values for this example.

The next form is used to specify the prior distributions for the sensitivity and specificity for each test. This information can be entered in two ways: i) values can be provided for the 2.5% and 97.5% credible limits when prior information is available, or ii) a uniform (non-informative) prior distribution can be used.

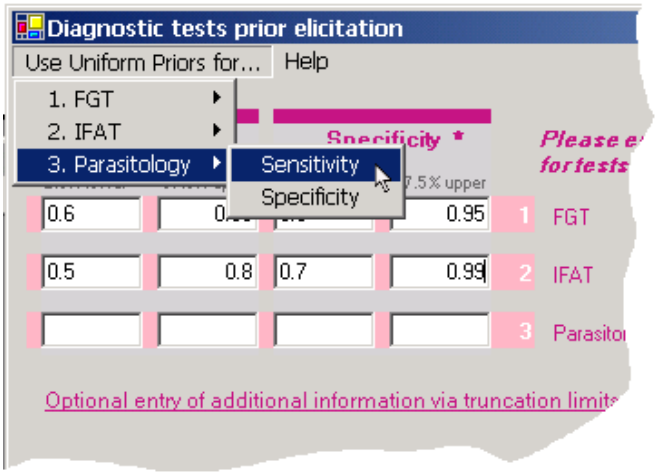
In either case, the information entered is converted into a Beta prior distribution for each parameter. Providing credible limits allows for greater weight in the center of the range defined by them, while the non-informative uniform distribution option assumes an equal weight for all values between 0 and 1.

On the right we have an example of a situation where the credible limits were based on prior information.

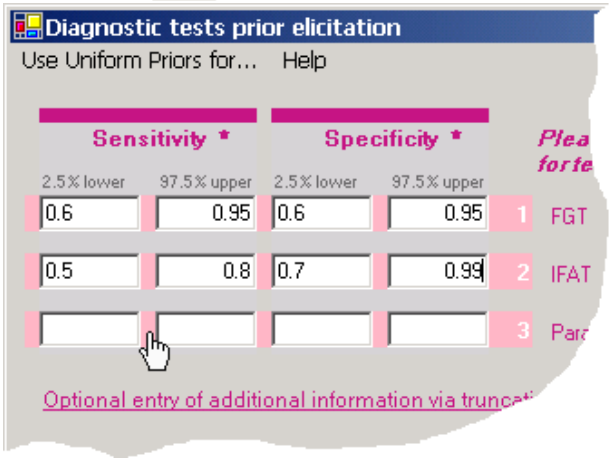


Those using a comma rather than a period as a decimal symbol should continue to use this style, assuming this concords with the setting under **Decimal symbol** in the **Customized Regional Options** form of the **Regional and Language Options** in the **Control Panel**. In this example, one would enter values 0,6, 0,95, and so on rather than 0.6, 0.95, etc.

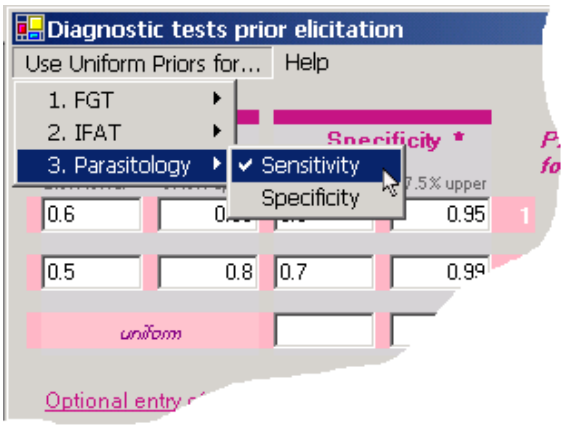
You can choose to use the alternate uniform prior distribution for a test parameter by selecting the parameter in question in the top-left menu **Use Uniform Priors for...**

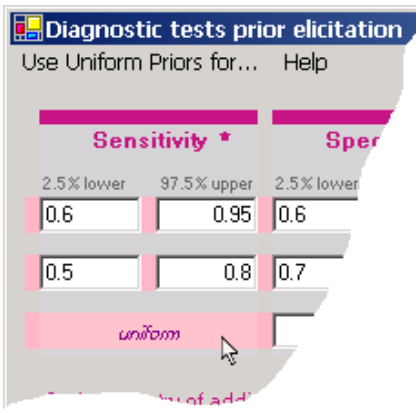


Alternatively, clicking the area between the "2.5% lower" and "97.5% upper" cells of a given parameter serves as a shortcut to selecting a non-informative prior (the mouse pointer will turn into a hand when hovering this region).

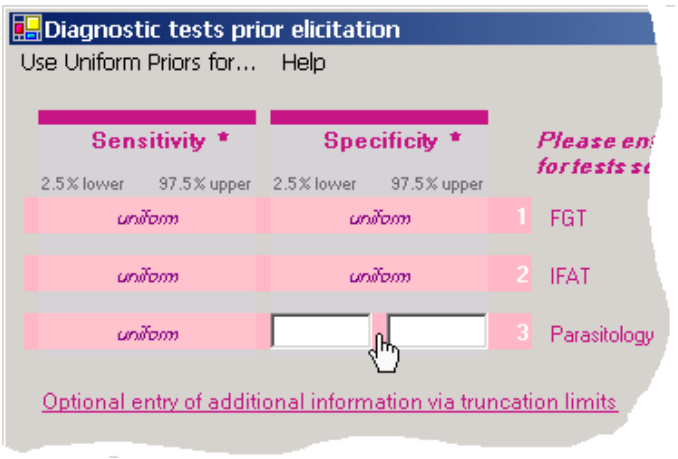


One can easily move back to the default Beta distribution for a test sensitivity or specificity by either unselecting the marked item through the top-left menu (1st image on the right) or by clicking the *uniform* light-pink rectangle (2nd image on the right) covering the parameter.





In the current example, we will use the non-informative uniform prior distributions on the sensitivities and specificities for each test. Click **Done** when done.

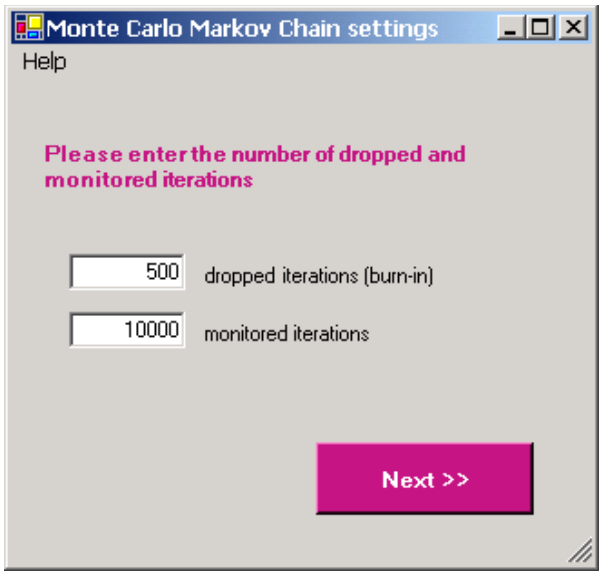


In general it is assumed that the possible range of values for the sensitivities and specificities is from 0 to 1. However, the **Optional entry of additional information via truncation limits** link in the lower part of the form allows you to truncate the prior distribution for some (or all) of the sensitivities and specificities.

BLCM uses an iterative sampling method called the Gibbs Sampler to obtain the posterior distributions of all parameters. The user has the option of specifying the number of burn-in iterations and the number of monitored iterations of the Gibbs Sampler.

The default values are 500 and 10000, respectively. This means the first 500 values sampled are discarded before final inferences are calculated, while the next 10000 values sampled are used for the analysis.

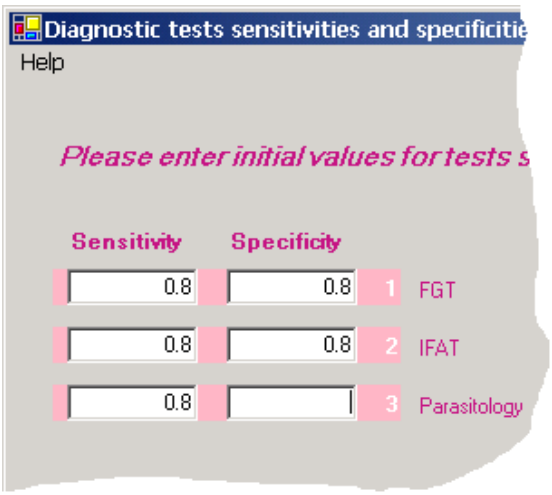
Click **Next** to accept the default values.



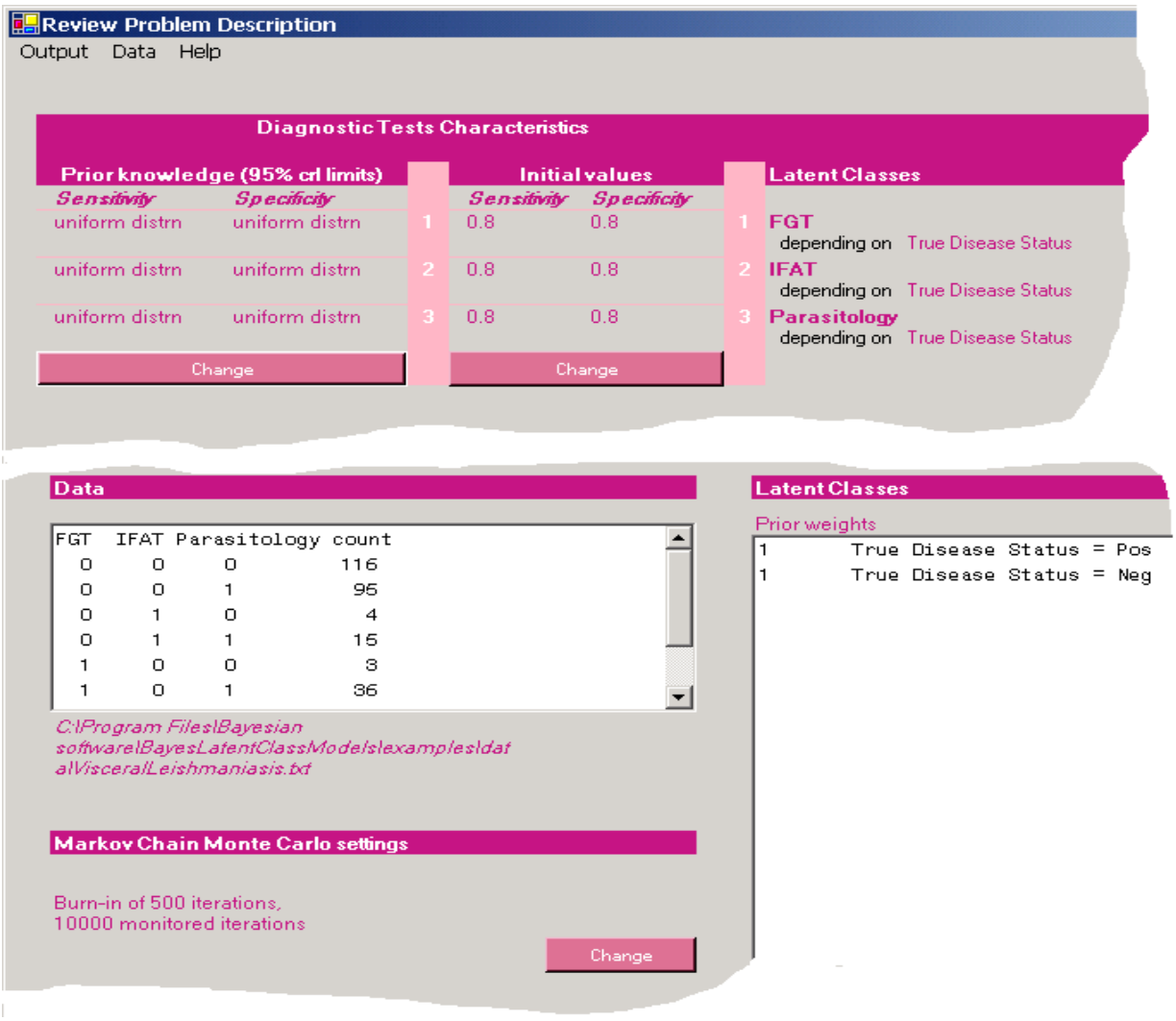
The last entry form is used to specify initial values for test sensitivities and specificities. As explained above, these are only used to begin the algorithm, and are not used for final inferences. Nevertheless, choosing good values can aid the convergence of the algorithm.

For our example we entered 0.8 as the initial value for all parameters.

Click **Done** when done.



The last form (below) is the Problem Description Review form, from which you can view each piece of information entered previously. Clicking the appropriate **Change** button allows you to change some of the values entered.



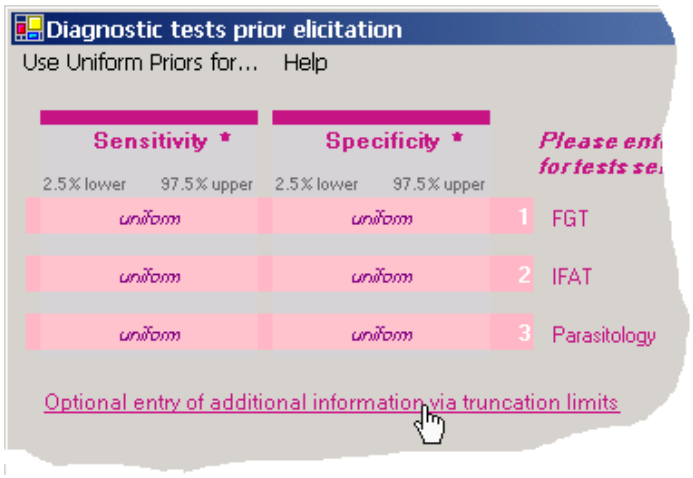
Select output file location through the top-left **Output/Save as...** menu.

Click the **Proceed to Gibbs sampling** button to start the actual Gibbs sampling and wait for the **Program completed** form, which will give you the links to the two output files created (one rtf file with all the relevant summary statistics and a pdf file with the trace plots of the prevalences, sensitivities and specificities). Note that the running times of the program can vary from as little as a few minutes to several hours, depending on the inputs used. A copy of the output file for Example 1 can be found in Appendix B, section B.1. The output itself is discussed in Section 4 below.

3.4.2 Example 2: Using truncated prior distributions for sensitivity and specificity

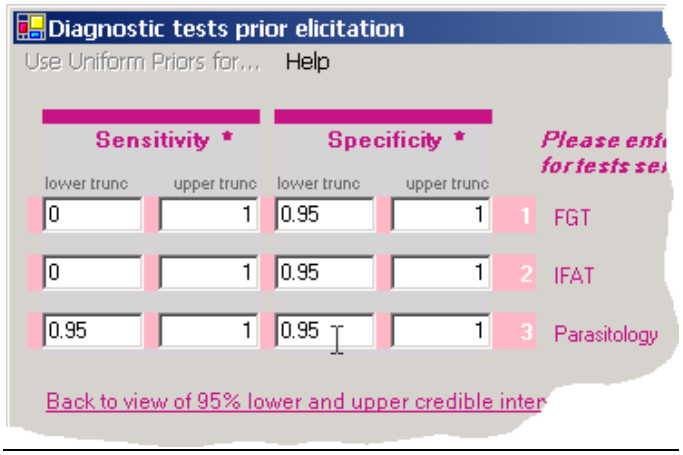
In this example, we repeat the analysis done in Example 1 but in the context of a close-to-gold-standard test. Indeed, suppose the clinicians involved in the study strongly believe that Test no 3 (Parasitology) is close to being perfect, and that there is a consensus to model the prior information by a uniform distribution on 0.95-1 for both its sensitivity and specificity. Suppose also that there is some prior information suggesting that the specificities of the FGT and IFAT tests are very high and lie between 0.95-1.

Repeat the steps in Example 1 till the form where prior distributions for the sensitivities and specificities are entered. Click the **Optional entry of additional information via truncation limits** link on this form.



Enter 0.95 in the **lower 11runk** text boxes for Parasitology sensitivity and specificity, as well as for the specificity of FGT and IFAT tests.

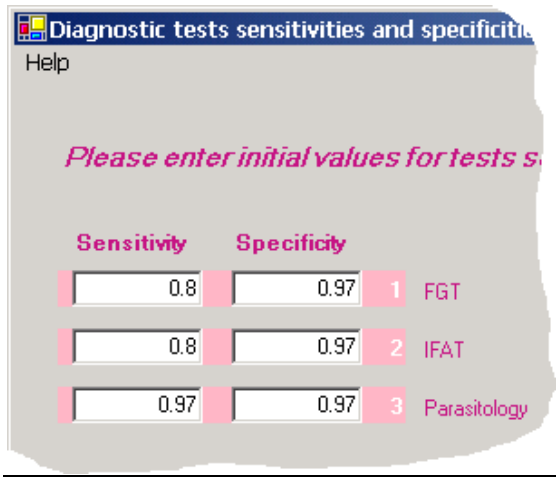
Click the **Back to view of 95% lower and upper credible interval limits** link on the lower part of the form to get back to the previous form.



Fill the remaining forms exactly as in example 1, except that the initial values for the sensitivities' and specificities' which now must be greater than 0.95, to be consistent with the truncated domain as discussed above.

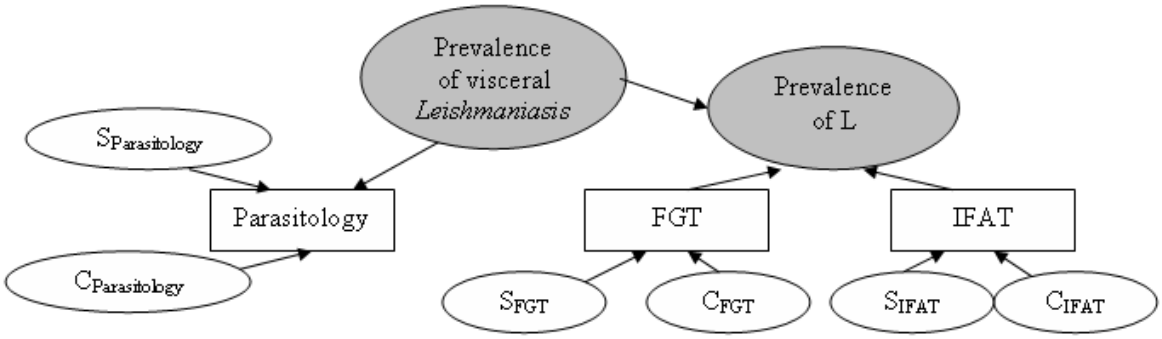
We chose the value 0.97 for Parasitology sensitivity and specificity, as well as for the specificity of the FGT and IFAT tests.

A copy of the output file for Example 2 can be found in Appendix B, section B.2. The output is discussed in Section 4 below.

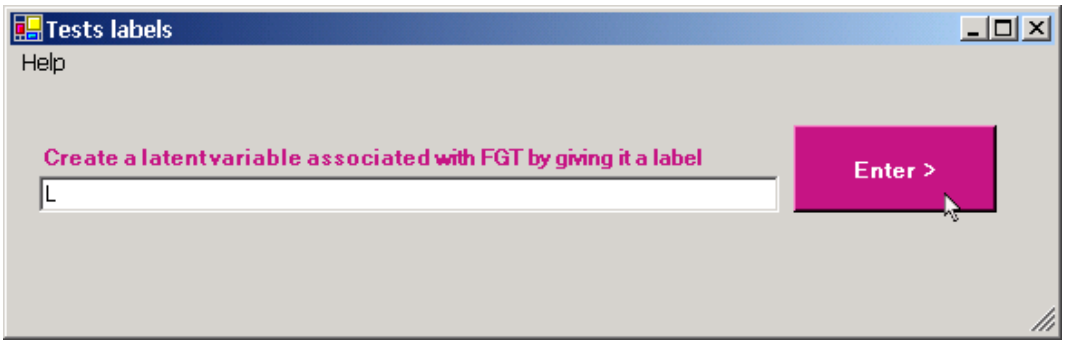


3.4.3 Example 3: Modeling conditional dependence

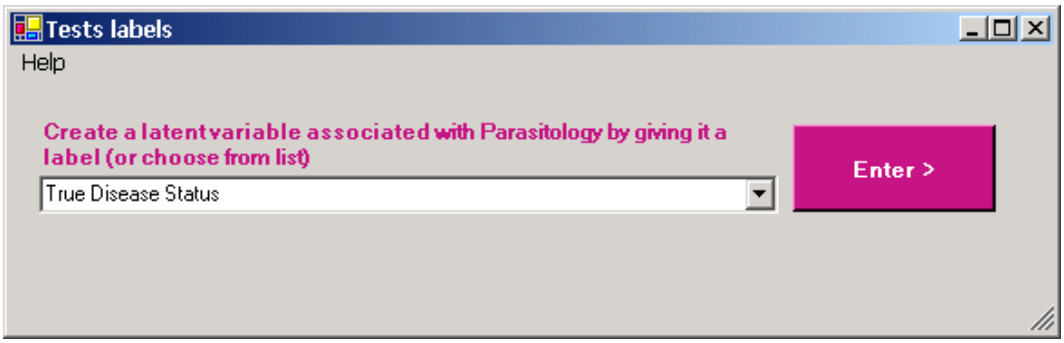
We now extend the model in Example 1 to demonstrate how BLCM can be used to model dependence between diagnostic tests conditional on a latent class other than true disease status. The FGT and IFAT tests are assumed to be associated with a common latent variable L instead of True Disease Status. This variable could represent, for example, "antibody status" as both these tests are designed to detect antibodies for visceral *leishmaniasis*. This structure sets up a conditional dependence between these two tests within the latent classes True Disease Status positive and True Disease Status negative. The model is depicted in the diagram below:



After loading the data file, enter *L* as a label for latent variable associated with both tests FGT and IFAT.



Define *True Disease Status* as the latent variable associated with Parasitology.



This model is not identifiable and informative prior distributions are needed on a minimum of two parameters. We use the truncated priors for the sensitivity and specificity of Parasitology and the specificity of the FGT and IFAT tests as described in Example 2.

Fill the remaining forms exactly as in Example 2. A copy of the output file for Example 3 can be found in Appendix B, section B.3. A discussion of the output appears in Section 4 below.

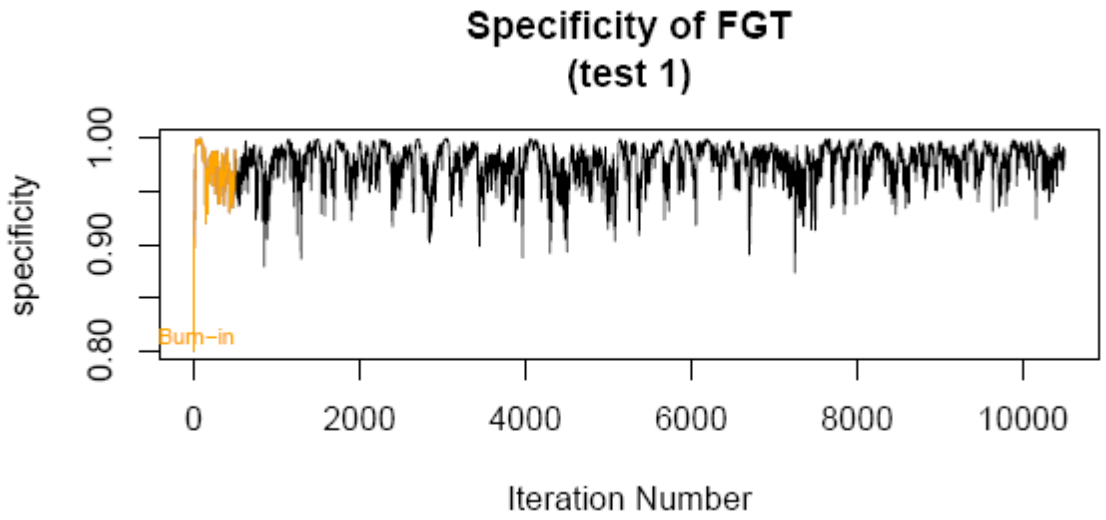
4. Interpreting the BLCM output file

In this section we discuss how to interpret the output provided by BLCM. Two output files are generated by BLCM: i) a pdf file with trace plots from the Gibbs iterations for each estimated parameter, and ii) a rtf file with descriptive statistics from the posterior distributions. The trace plots are useful for assessing convergence of the algorithm, while the posterior distribution summaries provide the statistical inferences for each parameter.

4.1 The graphical summary

BLCM produces a trace plot for each parameter, i.e. a plot of each parameter vs. the iteration number of the Gibbs sampler, to help evaluate whether the Gibbs sampler has converged. The Gibbs sampler needs to have converged in order for the statistics given in the rtf file to be valid. If it has converged, the trace plots taper to a fixed range of values. The BLCM program should be run repeatedly with different starting values (say 5 different values) in order to determine if the Gibbs sampler converges to the same range of values each time for each parameter. If not, either the model needs to be altered, for example, by adding more informative prior distributions or the Gibbs sampler needs to be run for more iterations.

For the example discussed in section 3.4.1, the following trace plot (top of next page) for the Specificity of the FGT test indicates that the Gibbs sampler converged fairly quickly (within the first 100 iterations) to a range of values between 0.95 and 1. Observing this same pattern from starting values other than 0.8 suggests that the Gibbs sampler has converged for this parameter. Convergence for all parameters indicates that the results are likely to be valid.



.

4.2 Descriptive statistics

This file is divided into three sections. The first section lists a summary of the problem: the data set, the prior distributions on the prevalence of each latent variable and the sensitivities and specificities, the initial values and the result of the identifiability check. The second section provides the mean, median and 95% credible limits of the posterior distributions of the prevalence of each latent variable, the sensitivities and specificities of each test, and the predictive values of the joint results of the tests. The third section provides diagnostic statistics to evaluate the appropriateness of the latent class model. We next discuss how to interpret this output, focusing mainly on the second and third sections for each of the examples in Section 3.4.

4.2.1 Descriptive statistics for Example 1:

For brevity, the latent classes are labelled as Class1 and Class2, where Class1 corresponds to True Disease Status = Pos and Class 2 to True Disease Status = Neg.

At the end of the first section of the output is a summary of the identifiability of the model. The number of parameters, degrees of freedom and rank of the Jacobian are presented along with a note concerning identifiability.

```
Number of parameters:  7
Degrees of freedom: 7
Rank of the Jacobian:  7
The model is identifiable.
```

The Gibbs sampler iterations used for the descriptive statistics are from 501-10500. The first 500 iterations (burn-in) were dropped to make sure we did not use values sampled before the Gibbs sampler had converged.

```
Iteration:  501 -- 10500
```

The prevalence of the True Disease Status variable was estimated to be 0.329 (or 0.33, depending on whether one prefers the median or mean as a point estimate) with a 95% credible interval of (0.253, 0.418). The prevalence of the complementary latent class – the absence of True Disease – also appears in the output.

```
Prevalence:

       2.5 %  50 % 97.5 % Mean
Class1 0.253 0.329  0.418 0.33
```

The probability that each test is positive within each latent class is listed next. For example, the probability that the FGT test is positive in Class1 is estimated as 0.747 (0.590, 0.902) while in Class2 it is much lower 0.017 (0.001, 0.057).

These probabilities are eventually used to estimate the sensitivities and specificities. For this example, Sensitivity of FGT = P(FGT+|Class1) and Specificity of FGT=P(FGT-|Class2)=1-P(FGT+|Class2).
The final summary statistic is the predictive value for each latent class corresponding to each combination of test results. For example, the probability that a patient who is positive on the FGT test alone belongs to Class1 was estimated as 0.57 (0.14, 0.96).

```
Pr(Test+|Class):


Class 1 (True Disease Status = Pos)

                  2.5 %  50 % 97.5 %  Mean
P(FGT+|Class1)    0.590 0.747  0.902 0.746

P(FGT+|Class2)    0.001 0.017  0.057 0.020



Pr(Class|Pattern):


Class 1 (True Disease Status = Pos)

               2.5 % 50 % 97.5 % Mean
P(Class 1|100)  0.14 0.57   0.96 0.56
```

The third portion of the rtf output file lists diagnostic statistics that can be used to evaluate how well the latent class model fits the data. This portion of the output is useful for models where the number of degrees of freedom + the number of informative prior distributions exceeds the number of parameters.

Such a situation is described in the next two examples.

In the current example, the number of degrees of freedom equals the number of parameters, so that the model fits the data nearly perfectly (assuming that the model is correct).

This is reflected in the close agreement between the median predicted and observed number of patients with each combination of diagnostic test results. For example, based on the model the predicted median number of patients with negative results on all three tests is 114, which is very close to the observed value of 116.

```
Expected frequency of each test profile (compared to
observed frequency):


    2.5 % 50 % 97.5 % Mean Observed
000    98  114    131  114      116
```

The near-perfect fit of the model is also reflected in the similarity between expected and observed probabilities of agreement. For example, the expected probability of agreement between FGT and IFAT tests in Class1 is 0.510 according to the model. This was very close to the observed probability of agreement between the two tests of 0.518 within this latent class.

The final statistic tells us that the probability that the expected agreement exceeds the observed agreement is 0.423. Since this value is close to 0.5 it does not indicate a problem. Very large values (>0.95) or small values (<0.05) would suggest that the model does not fit the data well.

```
Expected agreement between each pair of tests (E):

Class 1 (True Disease Status = Pos)
                   2.5 %  50 % 97.5 %  Mean
FGT & IFAT         0.402 0.510  0.631 0.513


Observed agreement between each pair of tests (O):

Class 1 (True Disease Status = Pos)
                   2.5 %  50 % 97.5 %  Mean
FGT & IFAT         0.470 0.518  0.582 0.520

P(Expected>Observed):

       FGT & IFAT
Class1      0.423
```

4.2.2 Descriptive statistics for Example 2:

In the second example, we continued to assume that the tests were conditionally independent but that there was some informative prior information we assumed that the sensitivity and specificity of Parasitology were very high, in the range from 0.95 to 1, and also that the specificity of the FGT and IFAT tests were between 0.95 to 1. The graphical summary indicated that the Gibbs sampler converged. Below we discuss the parameters that have now changed compared to the previous example.

The prevalence of the True Disease Status variable has now changed considerably to 0.604 with a 95% credible interval of (0.543, 0.664). This is because the specificity of Parasitology is much higher than in example 1.

```
Prevalence:

       2.5 %  50 % 97.5 %  Mean
Class1 0.543 0.604  0.664 0.604
```

The sensitivities of FGT and IFAT are much lower under this model. The specificities of FGT and IFAT have not changed much, except that their lower credible interval limits are now above 0.95. The sensitivity and specificity of Parasitology are limited to the range 0.95-1 because of their prior distributions.

```
Sensitivities for True.Disease.Status:

             2.5 %  50 % 97.5 %  Mean
FGT          0.345 0.415  0.490 0.416
IFAT         0.238 0.301  0.372 0.302
Parasitology 0.950 0.962  0.987 0.964

Specificities for True.Disease.Status:

             2.5 %  50 % 97.5 %  Mean
FGT          0.953 0.982  0.999 0.980
IFAT         0.952 0.973  0.995 0.973
Parasitology 0.951 0.967  0.999 0.970
```

The higher specificity of Parasitology translates into a higher positive predictive value for combinations of test results where Parasitology is positive.

```
Pr(Class|Pattern):

Class 1 (True Disease Status = Pos)

               2.5 % 50 % 97.5 % Mean
P(Class 1|001)  0.91 0.95   1.00 0.95
```

Because informative prior distributions were used in this example, it is especially important to check the diagnostic statistics.

We find that there is poor agreement between the expected and observed values for several combinations of test results. In particular the model seems to overestimate

```
Expected frequency of each test profile (compared to
observed frequency):

    2.5 % 50 % 97.5 % Mean Observed
001    64   77     91   77       95
011    24   32     41   32       15
101    42   52     64   52       36
111    16   22     30   23       37
```

the number of patients with disagreement on IFAT and FGT (tests 1 and 2) results and underestimate the number of patients for which these tests are in agreement.

The agreement statistics suggest that the expected agreement between FGT and IFAT under this model is much lower than the observed agreement.

```
Expected agreement between each pair of tests (E):

Class 1 (True Disease Status = Pos)
                   2.5 %  50 % 97.5 %  Mean
FGT & IFAT         0.455 0.534  0.611 0.534


Observed agreement between each pair of tests (O):

Class 1 (True Disease Status = Pos)
                   2.5 %  50 % 97.5 %  Mean
FGT & IFAT         0.697 0.713  0.727 0.713

P(Expected>Observed):

       FGT & IFAT
Class1      0.000
```

4.2.3 Descriptive statistics for Example 3:

For the final example we used the same set of prior distributions as previously. However, we allowed for conditional dependence between the IFAT and FGT tests by allowing them to depend on a different latent variable, labelled L. Once again, we ensured that the Gibbs sampler had converged by examining the graphical summary before examining the following descriptive statistics.

The addition of the latent variable L increases the total number of latent classes to 4. Under the "Problem Description" section these are labelled Class1-Class4 for brevity.

```
Class1: L = Pos, True Disease Status = Pos
Class2: L = Pos, True Disease Status = Neg
Class3: L = Neg, True Disease Status = Pos
Class4: L = Neg, True Disease Status = Neg
```

We now have a prevalence for each of the four latent classes. We find that the second latent class is very small suggesting that effectively there are only three latent classes. The class that was previously classified as TD=pos in Example 2 is divided into those that are L=Pos, TD=Pos (0.319) and L=Neg, TD=Pos (0.274).

```
Prevalence:

       2.5 %  50 % 97.5 %  Mean
Class1 0.251 0.319  0.398 0.321
Class2 0.001 0.018  0.048 0.019
Class3 0.200 0.274  0.345 0.274
Class4 0.328 0.386  0.447 0.386
```

This model estimates the sensitivity and specificity with respect to L and with respect to the True Disease Status separately.

We find that the sensitivity and specificity of FGT and IFAT are higher with respect to L than with respect to True Disease Status. The reverse is true for Parasitology.

```
Sensitivities for L:

             2.5 %  50 % 97.5 %  Mean
FGT          0.594 0.732  0.863 0.732
IFAT         0.399 0.517  0.633 0.515
Parasitology 0.852 0.926  0.971 0.922

Specificities for L:

             2.5 %  50 % 97.5 %  Mean
FGT          0.956 0.987  0.999 0.984
IFAT         0.952 0.972  0.996 0.972
Parasitology 0.503 0.581  0.664 0.582
```

```
Sensitivities for True.Disease.Status:

             2.5 %  50 % 97.5 %  Mean
FGT          0.329 0.399  0.473 0.400
IFAT         0.227 0.289  0.359 0.290
Parasitology 0.951 0.977  0.999 0.976

Specificities for True.Disease.Status:

             2.5 %  50 % 97.5 %  Mean
FGT          0.903 0.952  0.987 0.950
IFAT         0.916 0.950  0.978 0.949
Parasitology 0.951 0.975  0.999 0.975

Pr(Class|Pattern):

Class 1 (L = Pos, True Disease Status = Pos)

               2.5 % 50 % 97.5 % Mean
P(Class 1|100)  0.01 0.17   0.59 0.20
```

The final summary statistic is the predictive value for each latent class corresponding to each combination of test results. For example, the probability that a patient who is positive on the FGT test alone belongs to Class1 was estimated as 0.17 (0.01, 0.59).

The close agreement between the expected and observed number of patients for each combination of test results suggests that the model is of good fit. This is also reflected in the values of P(Expected>Observed) agreement that are close to 0.5.

5. Change log

Version 1.1 (April 2008). In earlier version, default path to R may not have been defined properly on Windows x64 platforms. This has now been corrected.

Version 1.2 (June 2008). Earlier versions accepted commas in numeric inputs, which, depending on their placement, could have led to unintended inputs being used. If a comma is found, a pop-up box now asks you to remove it, eliminating all ambiguity.

Version 1.3 (January 2009). The program now accepts either commas or periods as decimal symbols, depending on Regional Settings. Both commas and periods cannot be used at the same time, you must use the option chosen for your computer. See section 3.4.1 (p. 7) for full details.

Version 1.4 (October 2010). The R package was recompiled under R2.10.1.

Version 1.4.1 (May 2011). A minor update that may help in correctly identifying the path to R in the initial run (especially for Windows 7 and Windows Vista users).

Versions 1.5 and 1.5.1 (December 2011). The previous default application folder (c:\Program Files) caused write permission problems for some Windows 7 and Vista users. Default application folder now changed to C:\Users\user name\Documents.

Versions 1.6 and 1.6.1 (February 2012). Minor technical problem solved from previous version.

Version 1.7 (July 2012). Minor update: cmd.exe now closes automatically when program terminates.

Version 1.8 (August 2012). The path to the sub-directory where temporary files are stored was added to the Help menu of the initial form. While you can usually ignore these files, they can sometimes be helpful in troubleshooting when there are problems.

Versions 1.9, 1.9.1 and 1.9.2 (June 2013). Minor update: A few minor esthetical changes were made. A new feature now prevents program failure if no system-defined temporary directory exists.

Version 1.10 (September 2014). R code was recompiled to be compliant with R-3.1.1.

Version 1.11 (January 2015). Minor update.

Version 1.11.1 (April 2015). Minor bug fix update: a potential installation problem was solved.

Version 1.11.2 (April 2015). Update to hyperlinks and contact email address in manual and package. Reference to R package lcmr dropped.

Versions 1.12, 1.12.1 and 1.12.2 (December 2015). Minor update. The sensitivity & specificity prior distribution entry form did not show correctly in previous version.

Version 1.13 (December 2015). In previous versions, it was not possible to save output to Desktop: this is now fixed.

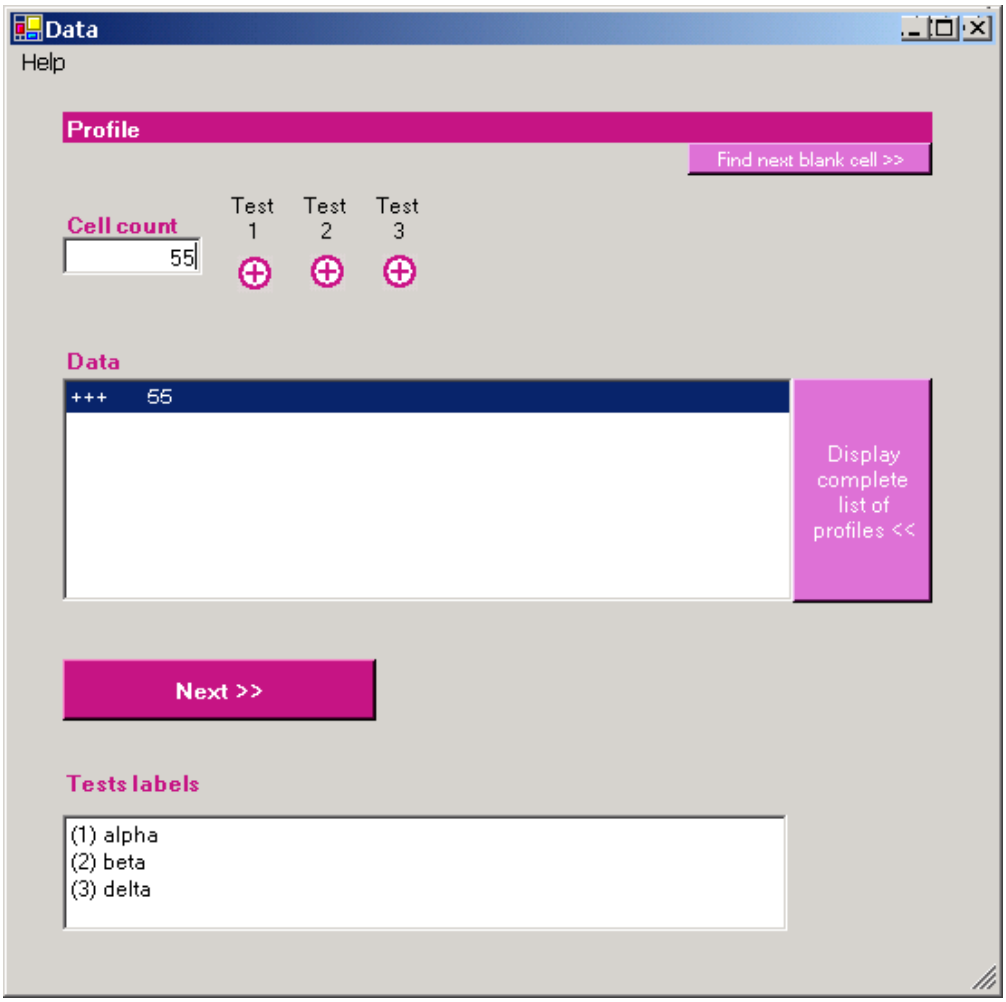
Version 1.14 (September 2017). **BayesLatentClassModels** now works on Windows 8 & 10. Windows 7 users do not need to reinstall or upgrade.

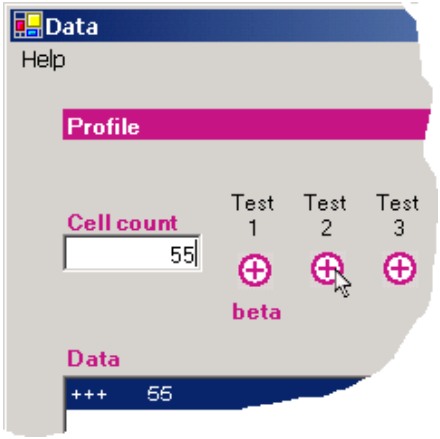
Questions? Please send email to: Nandini.Dendukuri@McGill.ca
Other Bayesian software packages are available at
http://www.medicine.mcgill.ca/epidemiology/Joseph

Appendix A: Interactive data entry

The interactive Data entry form opens with all tests positive, as shown here. If no patient had a positive result for every test, the cell count can be left empty; otherwise, enter the number of patients showing positive results on each test and type *Enter*. The tests results and the cell count will appear in the **Data** list box in the middle of the form.

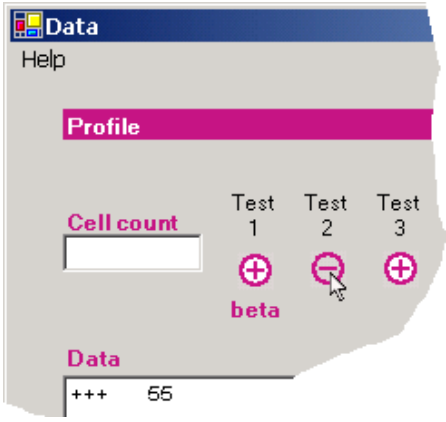
Note the list of test labels at the bottom of the form, which may be used as a reminder of the tests' order.





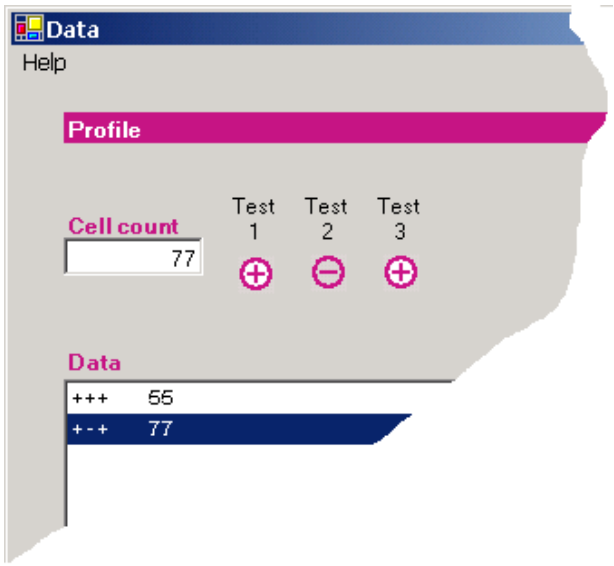
Note that when you cover a test result icon with the pointer, the corresponding test label is also displayed below the series of test result icons (left side caption).

Clicking on a circled plus sign (indicating a positive test result) will turn it (right-side caption) into a circled minus sign (indicating a negative test result) and vice-versa.

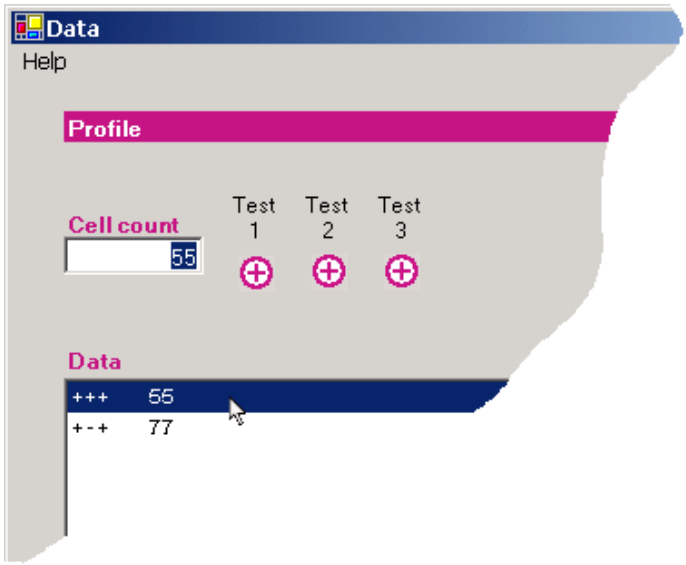


Enter the appropriate cell count (in this case, the number of patients with positive test results for both tests 1 and 3, and a negative result on test 2) and click *Enter*.

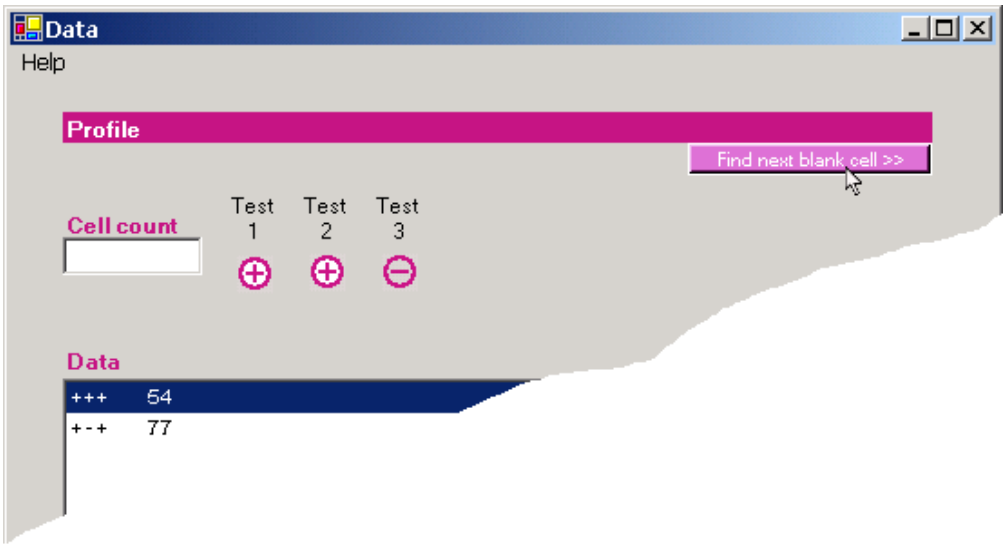
The new cell count is added to the **Data** list box.



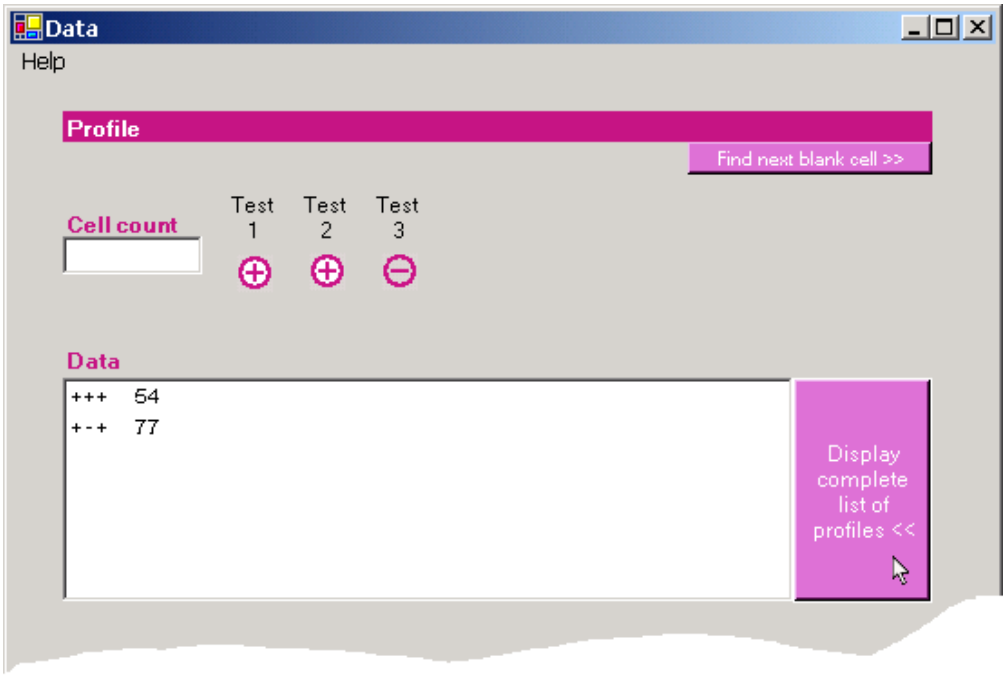
If a cell count was mistyped, you can correct it by either clicking the circled plus/minus signs at the right of **Cell count** to re-enter the tests results series in question, or simply click the incorrect cell count in the **Data** list box: the cell count will be reported in the **Cell count** text box and the series of test results plus/minus icons updated accordingly. Enter the correct number of patients in the cell count and type *Enter* to make the correction.



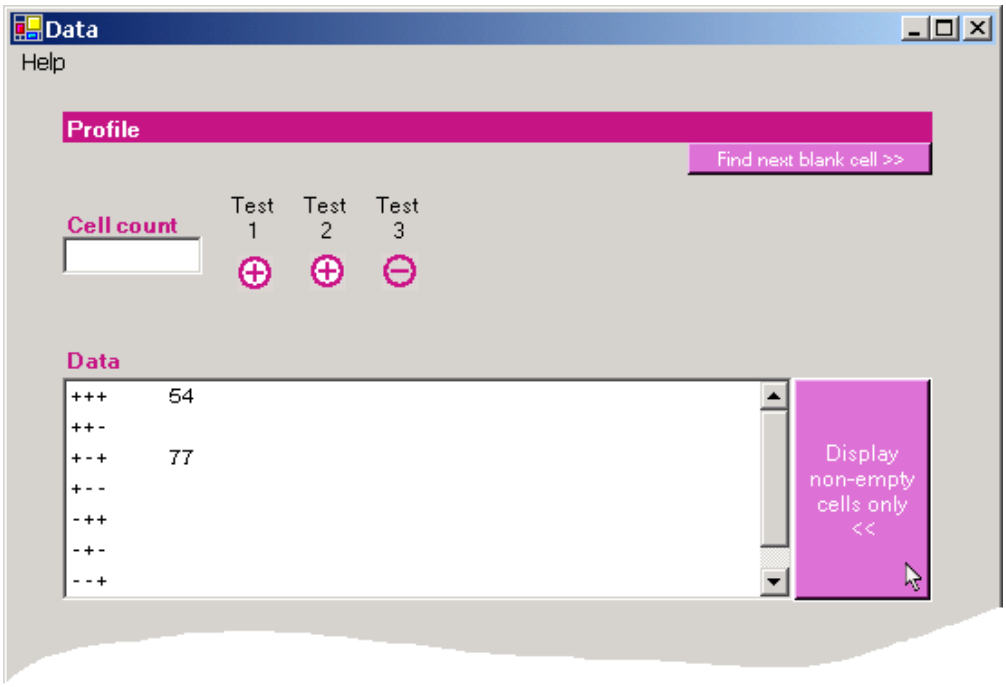
You can continue to enter the different cell counts by clicking the plus/minus signs to indicate each possible series of test results, or can click the top-right button labelled **Find next blank cell**, which will display the next series of test results for which the cell count has not been entered yet (++-, in this case).



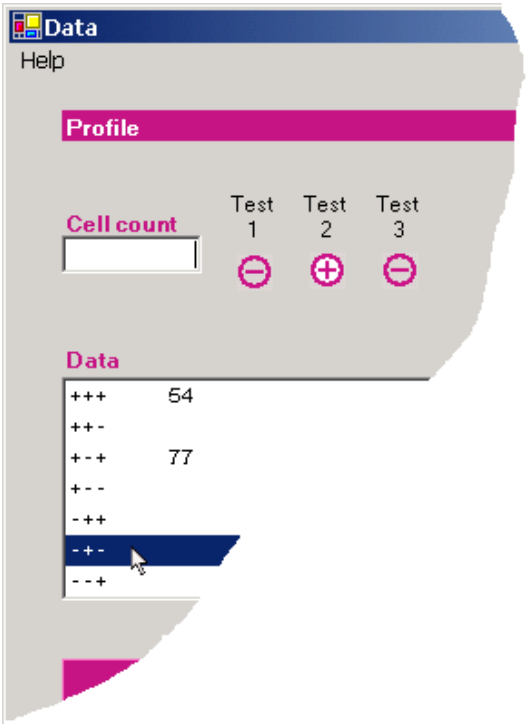
One can also display the complete list of test result combinations by clicking the appropriate button at the right end of the **Data** list box.



This will allow you to view at a glance all possible test result combinations in the **Data** list box and to identify cell counts not yet entered.



Clicking on a test results pattern in the **Data** list box will display the corresponding plus/minus test results icons to the right of **Cell count:** you can then enter the appropriate cell count in the **Cell count** text box and type *Enter*.



Click the **Next** button when all cell counts have been entered.

When data are entered manually, the last form (the Problem Review Form) allows the user to save the data in a text file, making it easier to reanalyze with **BLCM** in the future.

Appendix B: Descriptive statistics for each example

Output of Example 1:

```
Wed Oct 17 12:52:50 2007                              BayesLatentClassModels 1.0
================================================================================
                        Problem description / Prior input
================================================================================


Test 1 (FGT)
        95% prior credible interval for
        - sensitivity: uniform distribution
        - specificity: uniform distribution

        latent variable: True Disease Status

Test 2 (IFAT)
        95% prior credible interval for
        - sensitivity: uniform distribution
        - specificity: uniform distribution

        latent variable: True Disease Status

Test 3 (Parasitology)
        95% prior credible interval for
        - sensitivity: uniform distribution
        - specificity: uniform distribution

        latent variable: True Disease Status

--------------------------------------------------------------------------------
Data file: C:\Work\Software\Interface development\Manual\VL3.dat.txt
--------------------------------------------------------------------------------

Initial values for

        test 1  sensitivity: 0.8
                specificity: 0.8
        test 2  sensitivity: 0.8
                specificity: 0.8
        test 3  sensitivity: 0.8
                specificity: 0.8

--------------------------------------------------------------------------------

Dirichlet prior parameters and initial values for prevalences for each Latent Class:

        Latent  Dirichlet       Prevalence
        Class 1 parameter       initial value

        Pos     1               0.5
        Neg     1               0.5

where:
        Latent variable 1 is: True Disease Status

In the output below, Class<number> refer to the following classes combinations:

  Class1:      True Disease Status = Pos
  Class2:      True Disease Status = Neg



Number of parameters:  7
Degrees of freedom: 7
Rank of the Jacobian:  7
The model is identifiable
```

```
================================================================================
                    Summary of the posterior distributions
       of latent variable prevalence and diagnostic test characteristics
================================================================================

Iteration:  501 -- 10500
--------------------------------------------------------------------------------
Prevalence:

       2.5 %  50 % 97.5 % Mean
Class1 0.253 0.329  0.418 0.33
Class2 0.582 0.671  0.747 0.67

--------------------------------------------------------------------------------
Pr(Test+|Class):

Class 1 (True Disease Status = Pos)

                         2.5 %  50 % 97.5 %  Mean
P(FGT+|Class1)           0.590 0.747  0.902 0.746
P(IFAT+|Class1)          0.402 0.520  0.635 0.520
P(Parasitology+|Class1) 0.859 0.931  0.979 0.928

Class 2 (True Disease Status = Neg)

                         2.5 %  50 % 97.5 %  Mean
P(FGT+|Class2)           0.001 0.017  0.057 0.020
P(IFAT+|Class2)          0.005 0.032  0.078 0.034
P(Parasitology+|Class2) 0.337 0.424  0.500 0.422

--------------------------------------------------------------------------------
Sensitivities for True.Disease.Status:

             2.5 %  50 % 97.5 %  Mean
FGT          0.590 0.747  0.902 0.746
IFAT         0.402 0.520  0.635 0.520
Parasitology 0.859 0.931  0.979 0.928

Specificities for True.Disease.Status:

             2.5 %  50 % 97.5 %  Mean
FGT          0.943 0.983  0.999 0.980
IFAT         0.922 0.968  0.995 0.966
Parasitology 0.500 0.576  0.663 0.578

--------------------------------------------------------------------------------
Pr(Class|Pattern):

Class 1 (True Disease Status = Pos)

               2.5 % 50 % 97.5 % Mean
P(Class 1|000)  0.00 0.01   0.02 0.01
P(Class 1|001)  0.03 0.12   0.28 0.13
P(Class 1|010)  0.02 0.19   0.76 0.25
P(Class 1|011)  0.38 0.82   0.98 0.79
P(Class 1|100)  0.14 0.57   0.96 0.56
P(Class 1|101)  0.84 0.96   1.00 0.95
P(Class 1|110)  0.82 0.98   1.00 0.96
P(Class 1|111)  0.99 1.00   1.00 1.00

Class 2 (True Disease Status = Neg)

               2.5 % 50 % 97.5 % Mean
P(Class 2|000)  0.98 0.99   1.00 0.99
P(Class 2|001)  0.72 0.88   0.97 0.87
P(Class 2|010)  0.24 0.81   0.98 0.75
P(Class 2|011)  0.02 0.18   0.62 0.21
P(Class 2|100)  0.04 0.43   0.86 0.44
P(Class 2|101)  0.00 0.04   0.16 0.05
P(Class 2|110)  0.00 0.02   0.18 0.04
```

```
P(Class 2|111)  0.00 0.00   0.01 0.00
================================================================================
                              Model diagnostics

================================================================================

 Expected frequency of each test profile:

    2.5 % 50 % 97.5 % Mean Observed
000    98  114    131  114      116
001    80   95    111   95       95
010     2    5     10    5        4
011     9   15     24   16       15
100     2    5      9    5        3
101    26   35     46   35       36
110     1    3      6    3        3
111    26   36     48   36       37

 Expected agreement between each pair of tests (E):

Class 1 (True Disease Status = Pos)
                    2.5 %  50 % 97.5 %  Mean
FGT & IFAT          0.402 0.510  0.631 0.513
FGT & Parasitology  0.546 0.712  0.871 0.710
IFAT & Parasitology 0.381 0.518  0.660 0.518
Class 2 (True Disease Status = Neg)
                    2.5 %  50 % 97.5 %  Mean
FGT & IFAT          0.887 0.950  0.990 0.947
FGT & Parasitology  0.475 0.573  0.682 0.575
IFAT & Parasitology 0.474 0.571  0.679 0.573

 Observed agreement between each pair of tests (O):

Class 1 (True Disease Status = Pos)
                    2.5 %  50 % 97.5 %  Mean
FGT & IFAT          0.470 0.518  0.582 0.520
FGT & Parasitology  0.613 0.722  0.849 0.724
IFAT & Parasitology 0.441 0.510  0.565 0.508
Class 2 (True Disease Status = Neg)
                    2.5 %  50 % 97.5 %  Mean
FGT & IFAT          0.916 0.957  0.990 0.956
FGT & Parasitology  0.540 0.577  0.632 0.580
IFAT & Parasitology 0.549 0.574  0.628 0.578

--------------------------------------------------------------------------------
P(Expected>Observed):

       FGT & IFAT FGT & Parasitology IFAT & Parasitology
Class1      0.423              0.398               0.526
Class2      0.317              0.441               0.433

================================================================================
Run time: 9:36 min
```

Output of Example 2:

```
Wed Oct 17 13:06:00 2007                              BayesLatentClassModels 1.0
================================================================================
                        Problem description / Prior input

================================================================================


Test 1 (FGT)
        95% prior credible interval for
        - sensitivity: uniform distribution
        - specificity: uniform distribution  --- truncated on [0.95, 1]

        latent variable: True Disease Status

Test 2 (IFAT)
        95% prior credible interval for
        - sensitivity: uniform distribution
        - specificity: uniform distribution  --- truncated on [0.95, 1]

        latent variable: True Disease Status

Test 3 (Parasitology)
        95% prior credible interval for
        - sensitivity: uniform distribution  --- truncated on [0.95, 1]
        - specificity: uniform distribution  --- truncated on [0.95, 1]

        latent variable: True Disease Status

--------------------------------------------------------------------------------

Data file: E:\VL3.dat.txt

--------------------------------------------------------------------------------

Initial values for

        test 1  sensitivity: 0.8
                specificity: 0.97
        test 2  sensitivity: 0.8
                specificity: 0.97
        test 3  sensitivity: 0.97
                specificity: 0.97


--------------------------------------------------------------------------------

Dirichlet prior parameters and initial values for prevalences for each Latent Class:

        Latent  Dirichlet       Prevalence
        Class 1 parameter       initial value

        Pos     1               0.5
        Neg     1               0.5

where:
        Latent variable 1 is: True Disease Status

In the output below, Class<number> refer to the following classes combinations:

  Class1:      True Disease Status = Pos
  Class2:      True Disease Status = Neg


Number of parameters:  7
Degrees of freedom: 7
Rank of the Jacobian:  7
The model is identifiable.
```

```
================================================================================
                    Summary of the posterior distributions
       of latent variable prevalence and diagnostic test characteristics
================================================================================

Iteration:  501 -- 10500
--------------------------------------------------------------------------------
Prevalence:

       2.5 %  50 % 97.5 %  Mean
Class1 0.543 0.604  0.664 0.604
Class2 0.336 0.396  0.457 0.396

--------------------------------------------------------------------------------
Pr(Test+|Class):

Class 1 (True Disease Status = Pos)

                        2.5 %  50 % 97.5 %  Mean
P(FGT+|Class1)          0.345 0.415  0.490 0.416
P(IFAT+|Class1)         0.238 0.301  0.372 0.302
P(Parasitology+|Class1) 0.950 0.962  0.987 0.964

Class 2 (True Disease Status = Neg)

                        2.5 %  50 % 97.5 %  Mean
P(FGT+|Class2)          0.001 0.018  0.047 0.020
P(IFAT+|Class2)         0.005 0.027  0.048 0.027
P(Parasitology+|Class2) 0.001 0.033  0.049 0.030

--------------------------------------------------------------------------------
Sensitivities for True.Disease.Status:

             2.5 %  50 % 97.5 %  Mean
FGT          0.345 0.415  0.490 0.416
IFAT         0.238 0.301  0.372 0.302
Parasitology 0.950 0.962  0.987 0.964

Specificities for True.Disease.Status:

             2.5 %  50 % 97.5 %  Mean
FGT          0.953 0.982  0.999 0.980
IFAT         0.952 0.973  0.995 0.973
Parasitology 0.951 0.967  0.999 0.970

--------------------------------------------------------------------------------
Pr(Class|Pattern):

Class 1 (True Disease Status = Pos)

               2.5 % 50 % 97.5 % Mean
P(Class 1|000)  0.01 0.02   0.04 0.02
P(Class 1|001)  0.91 0.95   1.00 0.95
P(Class 1|010)  0.08 0.28   0.71 0.31
P(Class 1|011)  0.99 1.00   1.00 1.00
P(Class 1|100)  0.15 0.48   0.93 0.51
P(Class 1|101)  1.00 1.00   1.00 1.00
P(Class 1|110)  0.67 0.94   1.00 0.92
P(Class 1|111)  1.00 1.00   1.00 1.00

Class 2 (True Disease Status = Neg)

               2.5 % 50 % 97.5 % Mean
P(Class 2|000)  0.96 0.98   0.99 0.98
P(Class 2|001)  0.00 0.05   0.09 0.05
P(Class 2|010)  0.29 0.72   0.92 0.69
P(Class 2|011)  0.00 0.00   0.01 0.00
P(Class 2|100)  0.07 0.52   0.85 0.49
P(Class 2|101)  0.00 0.00   0.00 0.00
P(Class 2|110)  0.00 0.06   0.33 0.08
P(Class 2|111)  0.00 0.00   0.00 0.00
```

```
================================================================================
                              Model diagnostics

================================================================================

 Expected
 frequency of each test profile:
    2.5 % 50 % 97.5 % Mean Observed
000   100  116    132  116      116
001    64   77     91   77       95
010     2    4      7    4        4
011    24   32     41   32       15
100     2    4      7    4        3
101    42   52     64   52       36
110     0    1      1    1        3
111    16   22     30   23       37

 Expected agreement between each pair of tests (E):

Class 1 (True Disease Status = Pos)

                    2.5 %  50 % 97.5 %  Mean
FGT & IFAT          0.455 0.534  0.611 0.534
FGT & Parasitology  0.328 0.422  0.522 0.422
IFAT & Parasitology 0.226 0.315  0.411 0.316

Class 2 (True Disease Status = Neg)

                    2.5 %  50 % 97.5 %  Mean
FGT & IFAT          0.898 0.958  0.992 0.954
FGT & Parasitology  0.893 0.952  0.992 0.951
IFAT & Parasitology 0.886 0.945  0.992 0.944

 Observed agreement between each pair of tests (O):

Class 1 (True Disease Status = Pos)

                    2.5 %  50 % 97.5 %  Mean
FGT & IFAT          0.697 0.713  0.727 0.713
FGT & Parasitology  0.396 0.412  0.432 0.412
IFAT & Parasitology 0.284 0.301  0.321 0.301

Class 2 (True Disease Status = Neg)

                    2.5 %  50 % 97.5 %  Mean
FGT & IFAT          0.943 0.966  0.991 0.965
FGT & Parasitology  0.898 0.951  0.992 0.949
IFAT & Parasitology 0.887 0.941  0.983 0.939

--------------------------------------------------------------------------------
P(Expected>Observed):

       FGT & IFAT FGT & Parasitology IFAT & Parasitology
Class1      0.000              0.553               0.591
Class2      0.289              0.466               0.525

================================================================================
Run time: 9:22 min
```

Output of Example 3:

```
Wed Oct 17 09:27:15 2007                              BayesLatentClassModels 1.0
================================================================================
                        Problem description / Prior input
================================================================================

Test 1 (FGT)
        95% prior credible interval for
        - sensitivity: uniform distribution
        - specificity: uniform distribution  --- truncated on [0.95, 1]

        latent variable: L

Test 2 (IFAT)
        95% prior credible interval for
        - sensitivity: uniform distribution
        - specificity: uniform distribution  --- truncated on [0.95, 1]

        latent variable: L

Test 3 (Parasitology)
        95% prior credible interval for
        - sensitivity: uniform distribution  --- truncated on [0.95, 1]
        - specificity: uniform distribution  --- truncated on [0.95, 1]

        latent variable: True Disease Status

--------------------------------------------------------------------------------
Data file: D:\data\Software\Interface Development\Manual\Rex\VL3.dat.txt
--------------------------------------------------------------------------------

Initial values for

        test 1  sensitivity: 0.8
                specificity: 0.97
        test 2  sensitivity: 0.8
                specificity: 0.97
        test 3  sensitivity: 0.97
                specificity: 0.97

--------------------------------------------------------------------------------

Dirichlet prior parameters and initial values for prevalences for each Latent Class:

        Latent  Latent  Dirichlet       Prevalence
        Class 1 Class 2 parameter       initial value

        Pos     Pos     1               0.25
        Pos     Neg     1               0.25
        Neg     Pos     1               0.25
        Neg     Neg     1               0.25

where:
        Latent variable 1 is: L
        Latent variable 2 is: True Disease Status

In the output below, Class<number> refer to the following classes combinations:

  Class1:      L = Pos, True Disease Status = Pos
  Class2:      L = Pos, True Disease Status = Neg
  Class3:      L = Neg, True Disease Status = Pos
  Class4:      L = Neg, True Disease Status = Neg

Number of parameters:  9
Degrees of freedom: 7
Rank of the Jacobian:  7
The model is not identifiable.
(Informative priors are needed on a minimum of 2 parameters to make the model identifiable)
```

```
================================================================================
                    Summary of the posterior distributions
       of latent variable prevalence and diagnostic test characteristics

================================================================================


Iteration:  501 -- 10500
--------------------------------------------------------------------------------
Prevalence:

       2.5 %  50 % 97.5 %  Mean
Class1 0.251 0.319  0.398 0.321
Class2 0.001 0.018  0.048 0.019
Class3 0.200 0.274  0.345 0.274
Class4 0.328 0.386  0.447 0.386

--------------------------------------------------------------------------------
Pr(Test+|Class):

Class 1 (L = Pos, True Disease Status = Pos)

                         2.5 %  50 % 97.5 %  Mean
P(FGT+|Class1)           0.594 0.732  0.863 0.732
P(IFAT+|Class1)          0.399 0.517  0.633 0.515
P(Parasitology+|Class1) 0.951 0.977  0.999 0.976

Class 2 (L = Pos, True Disease Status = Neg)

                         2.5 %  50 % 97.5 %  Mean
P(FGT+|Class2)           0.594 0.732  0.863 0.732
P(IFAT+|Class2)          0.399 0.517  0.633 0.515
P(Parasitology+|Class2) 0.001 0.025  0.049 0.025

Class 3 (L = Neg, True Disease Status = Pos)

                         2.5 %  50 % 97.5 %  Mean
P(FGT+|Class3)           0.001 0.013  0.044 0.016
P(IFAT+|Class3)          0.004 0.028  0.048 0.028
P(Parasitology+|Class3) 0.951 0.977  0.999 0.976

Class 4 (L = Neg, True Disease Status = Neg)

                         2.5 %  50 % 97.5 %  Mean
P(FGT+|Class4)           0.001 0.013  0.044 0.016
P(IFAT+|Class4)          0.004 0.028  0.048 0.028
P(Parasitology+|Class4) 0.001 0.025  0.049 0.025

--------------------------------------------------------------------------------
Sensitivities for L:

             2.5 %  50 % 97.5 %  Mean
FGT          0.594 0.732  0.863 0.732
IFAT         0.399 0.517  0.633 0.515
Parasitology 0.852 0.926  0.971 0.922

Specificities for L:

             2.5 %  50 % 97.5 %  Mean
FGT          0.956 0.987  0.999 0.984
IFAT         0.952 0.972  0.996 0.972
Parasitology 0.503 0.581  0.664 0.582

Sensitivities for True.Disease.Status:

             2.5 %  50 % 97.5 %  Mean
FGT          0.329 0.399  0.473 0.400
IFAT         0.227 0.289  0.359 0.290
Parasitology 0.951 0.977  0.999 0.976
Specificities for True.Disease.Status:
```

```
             2.5 %  50 % 97.5 %  Mean
FGT          0.903 0.952  0.987 0.950
IFAT         0.916 0.950  0.978 0.949
Parasitology 0.951 0.975  0.999 0.975

------------------------------------------------------------------------------
Pr(Class|Pattern):


Class 1 (L = Pos, True Disease Status = Pos)

               2.5 % 50 % 97.5 % Mean
P(Class 1|000)  0.00 0.00   0.01 0.00
P(Class 1|001)  0.05 0.13   0.28 0.14
P(Class 1|010)  0.00 0.07   0.29 0.09
P(Class 1|011)  0.61 0.85   0.98 0.84
P(Class 1|100)  0.01 0.17   0.59 0.20
P(Class 1|101)  0.88 0.97   1.00 0.96
P(Class 1|110)  0.01 0.28   0.85 0.32
P(Class 1|111)  0.99 1.00   1.00 1.00

Class 2 (L = Pos, True Disease Status = Neg)

               2.5 % 50 % 97.5 % Mean
P(Class 2|000)  0.00 0.01   0.02 0.01
P(Class 2|001)  0.00 0.00   0.00 0.00
P(Class 2|010)  0.01 0.16   0.63 0.21
P(Class 2|011)  0.00 0.00   0.00 0.00
P(Class 2|100)  0.04 0.43   0.88 0.44
P(Class 2|101)  0.00 0.00   0.01 0.00
P(Class 2|110)  0.10 0.70   0.97 0.65
P(Class 2|111)  0.00 0.00   0.01 0.00

Class 3 (L = Neg, True Disease Status = Pos)

               2.5 % 50 % 97.5 % Mean
P(Class 3|000)  0.00 0.02   0.04 0.02
P(Class 3|001)  0.68 0.84   0.93 0.83
P(Class 3|010)  0.00 0.01   0.03 0.01
P(Class 3|011)  0.02 0.14   0.37 0.16
P(Class 3|100)  0.00 0.00   0.02 0.01
P(Class 3|101)  0.00 0.03   0.12 0.04
P(Class 3|110)  0.00 0.00   0.00 0.00
P(Class 3|111)  0.00 0.00   0.00 0.00

Class 4 (L = Neg, True Disease Status = Neg)

               2.5 % 50 % 97.5 % Mean
P(Class 4|000)  0.95 0.97   0.99 0.97
P(Class 4|001)  0.00 0.03   0.07 0.03
P(Class 4|010)  0.20 0.75   0.93 0.70
P(Class 4|011)  0.00 0.00   0.02 0.01
P(Class 4|100)  0.02 0.34   0.78 0.36
P(Class 4|101)  0.00 0.00   0.01 0.00
P(Class 4|110)  0.00 0.01   0.10 0.02
P(Class 4|111)  0.00 0.00   0.00 0.00
```

```
================================================================================
                              Model diagnostics
================================================================================

 Expected frequency of each test profile:

    2.5 % 50 % 97.5 % Mean Observed
000    98  114    131  114      116
001    79   95    111   95       95
010     2    4      7    4        4
011     9   16     24   16       15
100     2    5      8    5        3
101    26   35     47   35       36
110     1    3      6    3        3
111    26   36     48   36       37

 Expected agreement between each pair of tests (E):

Class 1 (L = Pos, True Disease Status = Pos)
                     2.5 %  50 % 97.5 %  Mean
FGT & IFAT          0.398 0.509  0.629 0.510
FGT & Parasitology  0.560 0.722  0.870 0.720
IFAT & Parasitology 0.367 0.515  0.667 0.516

Class 2 (L = Pos, True Disease Status = Neg)

                     2.5 % 50 % 97.5 %  Mean
FGT & IFAT               0 0.50      1 0.508
FGT & Parasitology       0 0.25      1 0.285
IFAT & Parasitology      0 0.50      1 0.489

Class 3 (L = Neg, True Disease Status = Pos)

                     2.5 %  50 % 97.5 %  Mean
FGT & IFAT          0.893 0.962  1.000 0.957
FGT & Parasitology  0.000 0.035  0.101 0.039
IFAT & Parasitology 0.000 0.047  0.117 0.050
Class 4 (L = Neg, True Disease Status = Neg)
                     2.5 %  50 % 97.5 %  Mean
FGT & IFAT          0.902 0.959  1.000 0.957
FGT & Parasitology  0.903 0.965  1.000 0.960
IFAT & Parasitology 0.891 0.951  0.992 0.949

 Observed agreement between each pair of tests (O):

Class 1 (L = Pos, True Disease Status = Pos)

                     2.5 %  50 % 97.5 %  Mean
FGT & IFAT          0.462 0.514  0.578 0.515
FGT & Parasitology  0.622 0.730  0.835 0.730
IFAT & Parasitology 0.441 0.510  0.570 0.509

Class 2 (L = Pos, True Disease Status = Neg)

                     2.5 %  50 % 97.5 %  Mean
FGT & IFAT               0 0.571   1.00 0.588
FGT & Parasitology       0 0.333   0.75 0.301
IFAT & Parasitology      0 0.429   1.00 0.406

Class 3 (L = Neg, True Disease Status = Pos)

                     2.5 %  50 % 97.5 %  Mean
FGT & IFAT          0.897 0.961  1.000 0.957
FGT & Parasitology  0.000 0.036  0.103 0.040
IFAT & Parasitology 0.000 0.047  0.115 0.050
```

Class 4 (L = Neg, True Disease Status = Neg)

	2.5 %	50 %	97.5 %	Mean
FGT & IFAT	0.943	0.967	0.992	0.967
FGT & Parasitology	0.919	0.967	1.000	0.966
IFAT & Parasitology	0.906	0.956	0.991	0.952

P(Expected>Observed):

	FGT & IFAT	FGT & Parasitology	IFAT & Parasitology
Class1	0.437	0.417	0.508
Class2	NA	NA	NA
Class3	0.424	0.394	0.417
Class4	0.294	0.333	0.404

==========

Run time: 14:36 min