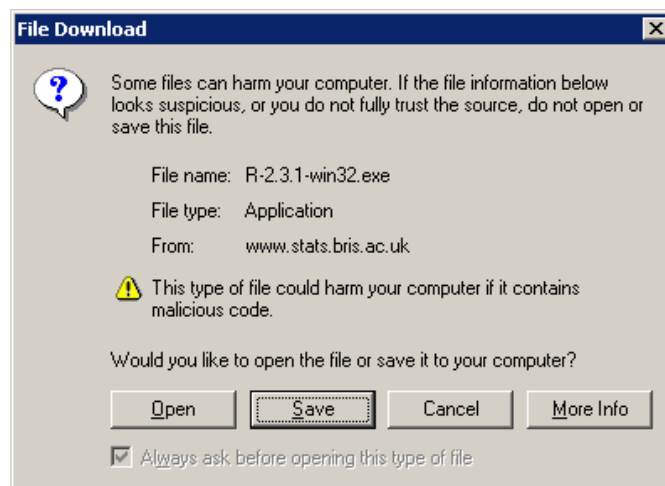


# R Code for Calculating Blood Lactate Endurance markers

Dr. John Newell, August 2006.

A paper detailing the algorithms used to calculate the markers has been submitted to the Journal of Sports Science under the title “Software for Calculating Blood Lactate Endurance Markers” (J. Newell, D. Higgins, N. Madden, J. Cruikshank, J. Einbeck). It is expected that use of this software will be acknowledged by a suitable reference.

The Lactate-R software has been written in R, a powerful free computer language for statistical computing. R is open-source software which can be downloaded at <http://www.r-project.org> . Follow the Cran link under Download and select a mirror site nearest you. The R code described in this tutorial is written for the Windows platform. Click on the Windows (95 and later) option in the ‘Download and Install R’ box, click on Base and then on [R-2.3.1-win32.exe](#). You will be prompted to Open or Save the software



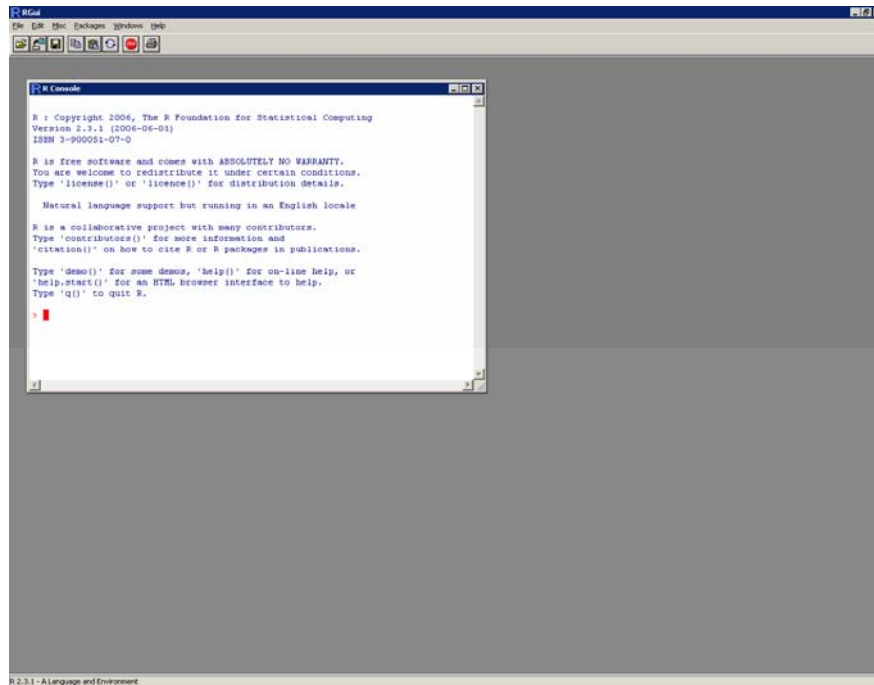
Save the software to a folder of your choice and once the download is completed, double click on the saved file to install the software. Once completed an R icon will appear on

the desktop as  . R is now installed and ready for use.

Before activating R, create a new folder called **Lactatemarkers** on the C drive.

Unzip the *Lactatemarkerscode.zip* file into the **Lactatemarkers** folder you have just created.

Activate R in Windows by double clicking on the R icon on the desktop. The following screen should now appear. Note that R is command line driven software.



The version of R is given including some useful information for new users, including instructions on how to quit R from the command line. When R starts it automatically searches for any saved work in the current directory. On leaving R it will offer to save the current session allowing you to continue your work from session to session. This is particularly useful in the context described here as once the lactate software has been loaded, the workspace can be saved thus avoiding the necessity to reload the software each time it is needed.

Tutorials on the many features of in R are available on the R homepage. In this article emphasis is on using the R platform to calculate lactate endurance markers.

The first step is to install the pspline library, needed for calculating the D2lmax marker in particular, as follows:

- select the drop down menu **File** and choose **Change Directory**
- select **Browse** and navigate to the **Lactatemarkers** folder on the C drive.
- press **OK**
- select the drop down menu **Packages** and choose **Install package(s) from local zip files**
- select *pspline.zip*
- press **Open**.

Once this is finished and the > prompt returns in the R Console screen, type

```
library(pspline)
```

and press Return. The > prompt returns indicating that the command has been processed and the pspline library is installed.

The next step is to read in the lactate markers code. In the R console copy and paste the following line of code:

```
source('C:\\Lactatemarkers\\lactatecode.txt')
```

and press Return. This command reads in the functions contained in the file **lactatecode.txt** necessary to calculate the markers.

Following this load in the two sample datasets by pasting the following two lines into R

```
sample.runner<-read.table('C:\\Lactatemarkers\\samplerunner.txt', header=TRUE)
sample.squad<-read.table('C:\\Lactatemarkers\\samplesquad.txt', header=TRUE)
sample.timeline<-read.table('C:\\Lactatemarkers\\RunnerTimeline.txt', header=TRUE)
```

and press Return. You have now loaded three sample data sets, which have been given the names sample.runner, sample.squad and sample.timeline respectively into the workspace. The subcommand 'header=TRUE' specifies that the dataset contains variable names. The data represent lactate and corresponding workload measurements collected from a long distance runner. In the R console type

```
sample.runner
```

and press Return, to view the data from the sample runner.

```
> sample.runner
  Workload  JP
1         50 2.8
2         75 2.4
3        100 2.4
4        125 2.9
5        150 3.1
6        175 4.0
7        200 5.8
8        225 9.3
9        250 12.2
10       275  NA
11       300  NA
12       325  NA
```

The data were originally typed in Excel and saved as a text file. Note that the first column contains the Workloads while the second contains the 'Blood Lactate readings corresponding to each workload. The first column is given the label Workload and the athlete in question is given the label JB. A missing value is represented by an NA. Any future datasets that you wish to analyse needs to follow the same convention. The order the columns appear is critical in that the first column is always reserved for the Workload readings!

You are now ready to use the lactate markers code.

### **Single Analysis Example.**

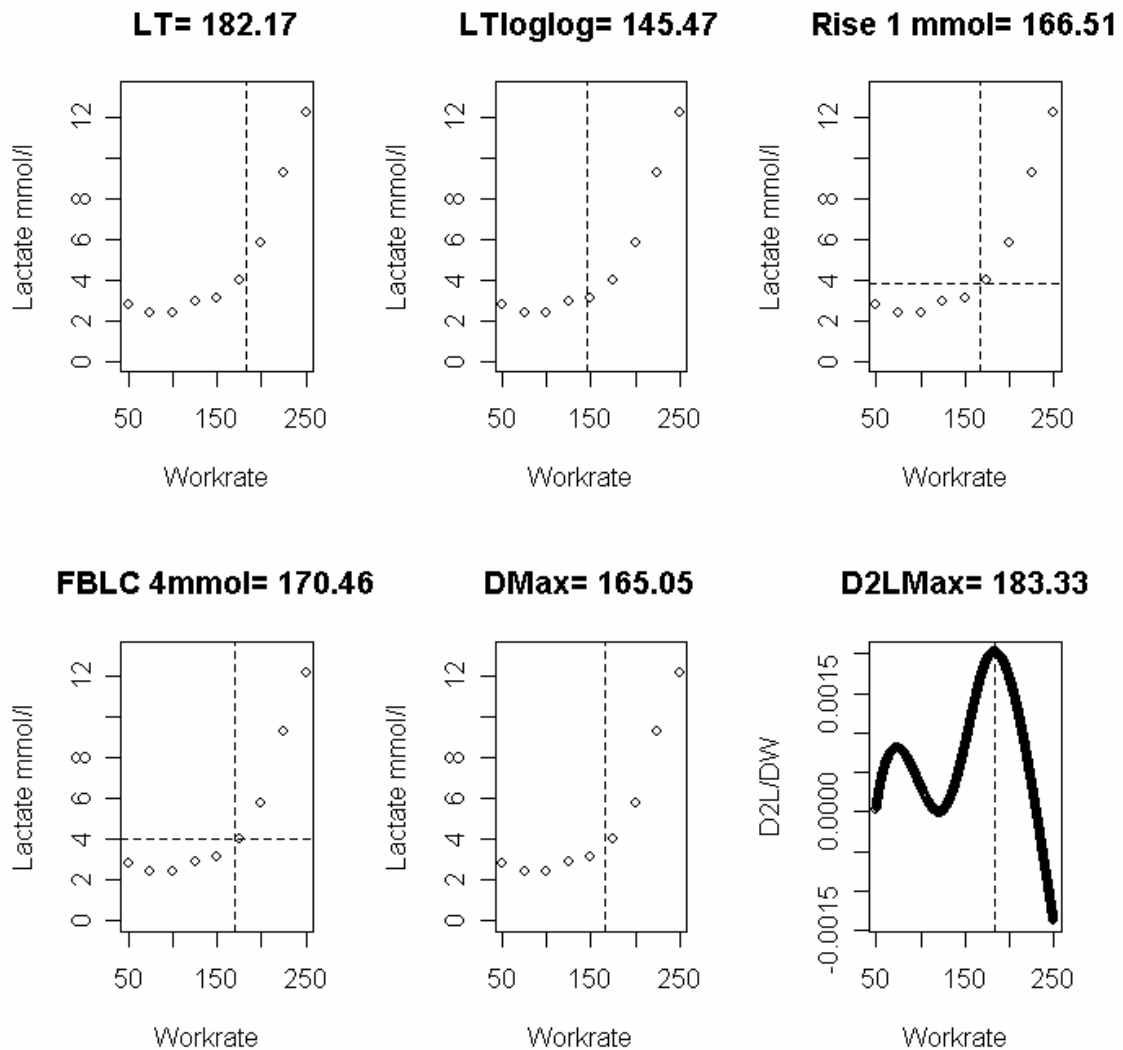
To calculate Lactate Markers for the sample athlete type

```
Lactate.markers(sample.runner)
```

and press Return. The following output should now appear

	Workrate
LT	182.17
LT.log.log	145.47
4mmol	170.46
Rise1mmol	166.51
Dmax	165.05
D2LMax	183.33
D2LMax Discrete	175.00

with the accompanying graph (overleaf).



The graph can be copied into the clipboard and pasted into a word processor if necessary. To export the results as a dataset the results must first be saved as an object within R and then the object written to a file. This can be carried out using the following commands:

```
results1<-Lactate.markers(sample.runner)
write.table(results1, "results1.txt")
```

The results will be written to a file called results.txt which will be located in the C:\Lactatemarkers folder.

## Team Analysis

In the R console type

```
sample.squad
```

and press Return, to view the data from the sample squad.

```
> sample.squad
  Workload  DA  JP  LL  DB  CS  MM  JT  AB  RG  WH  DR
1      50  2.7  2.8  2.3  2.1  2.5  2.3  2.2  2.2  2.3  2.8  3.0
2      75  2.9  2.4  2.0  1.9  2.4  2.4  2.0  1.6  2.5  3.0  3.2
3     100  2.6  2.4  1.8  1.8  2.7  1.7  1.4  1.8  2.9  3.0  3.0
4     125  2.7  2.9  1.8  1.6  3.6  1.8  1.6  1.5  2.6  3.2  2.0
5     150  2.8  3.1  2.1  2.0  4.8  2.1  2.0  1.4  3.3  3.8  1.7
6     175  3.8  4.0  2.3  2.8  5.8  1.6  2.2  1.6  7.1  3.7  2.1
7     200  5.4  5.8  3.5  4.3 10.4  1.9  3.2  1.6  9.3  4.1  2.3
8     225  9.1  9.3  5.6  5.7 12.4  1.8  4.0  2.4 11.4  5.5  5.1
9     250 13.2 12.2  7.9  9.6 14.4  3.4  5.0  4.2 21.4  6.2  5.6
10    275   NA   NA 10.4 11.6   NA  4.4  8.8  7.6 22.8  7.8  8.8
11    300   NA   NA 12.6 13.6   NA  6.5 10.9   NA   NA  9.4 12.0
12    325   NA   NA   NA   NA   NA  8.6 13.0   NA   NA   NA   NA
```

Once again the data were originally typed in Excel and saved as a text file. The first column contains the Workloads while the remaining contains the blood lactate readings for each workload for each squad member. A missing value is represented by an NA.

To calculate Lactate Markers for a Squad type

```
Lactate.markers.squad (sample.squad)
```

and press Return. The following output will now appear.

```
> Lactate.markers.squad (sample.squad)
      DA      JP      LL      DB      CS      MM      JT      AB      RG
LT      172.26 182.17 185.60 182.24 124.77 230.43 214.96 267.70 160.81
LT.log.log 162.39 145.47 146.94 141.17  98.49 217.02 160.77 206.44 137.00
4mmol     178.69 170.46 201.23 191.17 135.11 267.28 219.56 244.41 146.76
Riselmol   173.26 166.51 187.51 174.52 126.32 253.32 202.63 233.89 135.22
Dmax       174.16 165.05 179.28 170.60 133.68 219.78 197.63 196.55 165.12
D2LMax     202.75 183.33 187.89 220.42 168.72 290.04 246.55 146.85 218.02
D2LMax Discrete 175.00 175.00 150.00 200.00 150.00 200.00 225.00 225.00 200.00

      WH      DR
LT      198.62 230.63
LT.log.log 188.67 174.16
4mmol     182.15 223.77
Riselmol   171.66 223.77
Dmax       199.02 200.02
D2LMax     266.72 266.22
D2LMax Discrete 175.00 225.00
```

To export the results as a dataset the results must first be saved as an object within R as in the previous example as outlined below:

```
resultssquad<- Lactate.markers.squad (sample.squad)
write.table(resultssquad, "resultssquad.txt")
```

The results will be written to a file called resultssquad.txt which will be located in the C:\Lactatemarkers folder.

### Timeline Analysis

The same function as used in the squad analysis can be used to calculate the markers for an athlete over time. For example, in the R console type

```
sample.timeline
```

and press Return, to view the data from the sample squad.

	Workload	Subject1Lactate1	Subject1Lactate2	Subject1Lactate3
1	12.5	0.70	0.80	0.60
2	13.0	0.70	0.80	0.35
3	13.5	0.70	0.90	0.60
4	14.0	0.70	0.80	0.50
5	14.5	1.15	0.95	0.60
6	15.0	1.30	1.00	0.80
7	15.5	1.75	1.60	0.95
8	16.0	2.50	2.00	1.15
9	16.5	3.25	2.45	1.80
10	17.0	4.40	3.40	2.40
11	17.5	5.65	5.00	3.40
12	18.0	NA	NA	4.85

Once again the data were originally typed in Excel and saved as a text file. The first column contains Workload while the remaining columns contain the blood lactate readings for the same athlete at different times e.g. beginning, middle and end of the season and missing values are represented by an NA.

To calculate the Lactate Markers for this individual over time type

```
Lactate.markers.squad(sample.timeline)
```

and press Return.

The following output will now appear

```
Lactate.markers.squad (sample.timeline)
```

	Subject1Lactate1	Subject1Lactate2	Subject1Lactate3
LT	15.62	16.26	16.23
LT.log.log	13.87	14.73	14.73
4mmol	16.84	17.18	17.72
Rise1mmol	15.40	15.93	16.38
Dmax	15.32	15.61	15.89
D2LMax	16.77	17.00	17.48
D2LMax Discrete	13.50	16.50	12.50

As before the results can be exported as a dataset in a similar manner as follows:

```
resultstime<- Lactate.markers.squad (sample.timeline)  
write.table(resultstime, "resultstime.txt")
```

The results will be written to a file called `resultstime.txt` which will be located in the `C:\Lactatemarkers` folder.