**Release Notes for L-Measure v5.2 (06/24/2014)**

**Bug Fixes for L-Measure v5.2**

**Lmv5.2**

**Bug Fixes**

* This bug fix is applicable only for command line execution or batch processing of large #swc files. The executable is crashing when parsing files with spaces, this has been fixed by allowing the use of (a) ‘\*’ to replace space or (b) use quotations to enclose the file name including the path.

**For example:**

*Lm.exe -f0,0,0,10.0 -sC:\Users\user1\Desktop\Lmv5.*

*2\Lmout.txt C:\Users\Romil\Desktop\Lmv5.1\v****\*****e\_moto1.CNG.swc*

**OR**

*Lm.exe -f0,0,0,10.0 -sC:\Users\Romil\Desktop\Lmv5.1\Lmout.txt "C:\Users\Romil\Desktop\Lmv5.1\v****<space>****e\_moto1.CNG.swc"*

* For computing the soma surface area, Surface\_area, section area and volume at the tree level, the PI value from the inbuilt C++ library value (**M\_PI**) is used instead of a hard coded two decimal constant value.

**Help doc**

* LM uses swc format natively for processing the data or for swc conversions. The original reference for SWC format is described here (<http://www.sciencedirect.com/science/article/pii/S0165027098000910>) by its inventor, Robert Cannon.
* More information related to SWC format including the convention followed for arbor type description is found here:

<http://www.neuronland.org/NLMorphologyConverter/MorphologyFormats/SWC/Spec.html>

<http://research.mssm.edu/cnic/swc.html>

**Release Notes for L-Measure v5.1 (01/24/2014)**

**Bug Fixes/New Features for L-Measure v5.1**

**Lmv5.1**

**New Features**

* Added configuration file to the Online L-Measure deployment process. This allows de-coupling the hardcoded paths from the code making the deployment process independent of the host machine environment.

**GUI v5.1**

**Bug Fixes**

* Fixed the online Applet version crashing issue. This fix will now filter out the file names with special characters like Ð,Ñ,Ä,† etc. The GUI will not accept the files with these special characters

**Bug Fixes/New Features for L-Measure v5.0**

**Lmv5.0**

**Bug Fixes**

* The Accepted format of an input SWC file is one which has 7 columns of data namely id, type, x, y, z, radius, pid. If a file has additional columns then it will not be processed and display an error message on the GUI.
* Fixed the online version crashing issue. This fix will now filter out the incompatible input file formats both by checking the file extension and the internal structure. Currently swc, neurolucida and amira versions are the most commonly used formats.
* Fixed Bif\_ampl\_remote angle by removing the decimal point conversion. Only metrics that are a ratio (e.g. Taper\_1, fractal, etc) or length are converted to have decimal point precision. This fix eliminated outlier angles that are too large.
* Fixed the Bif\_ampl\_local angle, which is giving negative values for some of the files. This issue also has been fixed after removing the decimal point precision.
* Fixed the PCA orientation of the neurons such that when Z-resolution is too low, the swc files will be oriented based on only two components (X and Y). This will avoid the swc conversions to orient files that have low resolution jagged looking Z direction in the XY view. This fix, first tests for Z-resolution by checking whether as much as 30% of the z coordinates are same, if true, then the PCA is done only on two axes (X and Y), in the second part of PCA, the orientation is also done based on just two components. For implementing this logic that can conditionally skip Z-coordinate, three new functions ZresolutionEstimator, saveZcoords and setZcoords are implemented in Neuron.cpp and additional data structures like 'datacopy' array and flags like 'zresolution' were created in pca() method. The fix has been tested on the entire Brunjes archive, which was visually verified in CVAPP. Further, entire NMO data was tested in extracting morphometrics using PCA.
* Replaced + with \* in the file path in Neuron.cpp and Morph.cpp, this will now allow the users to choose folders that have a '+' in the path.
* Fixed two linux compiler related bugs. one in converting Neurolucida files to swc in neuron.cpp in the lookFor(tag,in) method. second, in the bif\_torque\_remote method to initialize prev\_next1 and prev\_next2 to NULL
* Fixed ~Neuron() code to ensure all segments are deleted and memory is freed. Updated revision# in morph.h; made changes to Helix, Bif\_ampl\_local, Bif\_ampl\_remote functions in Func.h to restrict decimal points to 2 digits.
* Fixed the code to filter invalid file types for input neurons. Made changes to the LookForFileType() function to correctly identify .swc files and to filter out other invalid file types.

**GUI v5.0**

**New Features**

* Two different versions of the lmeasure executable are made available for 32-bit and 64-bit Linux operating systems.
* A new FAQ has been added to the install.html to mention the valid SWC input file parameters.

http://cng.gmu.edu:8080/Lm/FAQ/install.html#LM5.0\_1

* Added the *svnRevision* entry to the properties file. This will reflect the latest code revision of LM GUI, which is intended for development purposes.
* Added the code to calculate the version number using the *svnRevision* entry from the properties file.

**Bug Fixes**

* Corrected code for placing the LMSearchin.txt and LMSearchout.txt in the proper session folder in online version. This is desired to keep log of all LM input files systematically inside the corresponding session folder.
* Changed the *homeUrl* entry in the properties file to point the online version to the correct location. This will also ensure that all the session folders are created in the designated folder that is assigned to *homeUrl.*
* Changed the code for ‘Analyze Subtrees’ option both in the local and online versions. This fixed the ‘subtree analysis’ function and synchronized with the ‘subtree generation’ option too. Both options, now refer to the subtrees saved into *Apical, basal* and *axon* folders.
* Modified the code to replace space (“ “) with star (“\*”) in the pathname of an input SWC file. This will allow the user to have ‘+’ symbol in the input file path.

**Bug Fixes for L-Measure v4.0**

* Terminal branches are considered for all Bifurcation remote angles (Bif\_ampl\_remote, Bif\_tilt\_remote, Bif\_torque\_remote). Previously, remote angles were computed only between bifurcating nodes, this fix includes terminal branches also by considering the tip nodes.
* RAW data values are printed for double distribution selection. Previously, the raw data values were printed only for single function, this fix allows printing for double distribution also.
* L-Measure code has been fixed to make it robust enough to accept and process large neurons. Largest file tested so far is ~10MB SWC file, but it can process even larger files.
* Daughter\_ratio and Pk\_classic have been fixed. The functions were returning invalid results when the input file has zero diameter.
* Fragmentation and Taper\_1 were made consistent with contraction and Taper\_2 respectively. Previously, Fragmentation and Taper\_1 were skipping the stem branches, hence the stem compartments were not included in the results.
* Height, Width, Depth functions code has been fixed. Previous version was not using all the points in the SWC for calculation of the result.
* L-Measure was crashing when doing PCA analysis on width, height and depth measures for neurons that has type = 3 or type = 4 (dendrites) defined, but not type = 1 (cell body). This has been now taken care and the code accepts such data without crashing.  
  (please go to FAQ#10 for details about PCA).

**New Functionalities for L-Measure v3.8**

**Major changes:**

* Important changes are made to soma representation in the LM converted SWC formats. Input files that have soma as a single point will be converted into 3 point soma (cylindrical representation). The changes will be reflected in ‘SWC conversion’ selection in the output panel. Please refer here (<http://neuromorpho.org/neuroMorpho/SomaFormat.html>)for more details about the soma format change.
* Neurolucida files that represent soma as a single contour will also be converted to 3 point soma. The first point in the newly converted SWC file is the average of all the points in the single contour.
* Neurolucida files that represent soma as multiple contours will be converted into multiple point cylindrical soma where each contour is averaged to one soma point.
* The soma\_surface function will remain unaffected since the formula for area and sphere and cylinder are adjusted to return the same surface area. The height of the cylinder is set to 2\*radius of the sphere. The files in NeuroMorpho.Org are converted and tested for this change.
* All functions are synchronized with the default specificity condition, which is type > -1, (i.e.) all the functions are applicable to all the arbors of the tree by default. Any specific conditions can be selected in the specificity panel for desired function(s). See the related FAQ: http://cng.gmu.edu:8080/Lm/FAQ/install.html#LM3.8\_6
* AmiraMesh v1.0 format to SWC conversion now supports reconstructions with zero diameters also. This has been tested on automated reconstructions of fly neurons that will be made available on NeuroMorpho.Org, with a constant diameter of 0.5µm
* New command line option “-dx.xx” is introduced in L-Measure for SWC conversions (Amira to SWC only). This allows the user to enter his/her choice of diameter values e.g., –d2, -d3.5, –d0.03467, etc.

Example : -sZ:\Soumya\Test+Folders\Amira+Conv+Problem\_07202011\windows\Lmout.txt -C -p –d0.03467 Z:\Soumya\Test+Folders\Amira+Conv+Problem\_07202011\windows\12070404c1.am

**Minor changes:**

* The output of height/width/depth is made consistent. Now, the total\_sum/max/min/avg all returns the same value. This is because these three functions are calculated at the entire arbor level. Hence, it returns only one value.
* The time of execution for each neuron is logged in the err.txt file as “Current local time and date:Thu Dec 01 13:51:38 2011”. The err.txt file is created by the standalone version in the same location that LM executable is located.
* The ‘Generate Subtrees’ option will generate and organize the subtrees into Axon, Basal and Apical folders locally.
* Bif\_ampl\_local angle at the soma is now changed to return the maximum angle between the soma and one of its stems.
* A new comment header will be added to the Neurolucida to SWC conversions to add details about cell body representation in the original files.

**Bug Fixes for L-Measure v3.8**

* The Bifurcation angle functions were giving erroneous values (value above 360 deg. and sometimes NAN/not a number). This has been fixed now.
* The N\_Branch = N\_bifs+ N\_tips. The functions is edited to return a number same as N\_bifs + N\_tips. See FAQ 6.6 related to this. The comments printed in the SWC converted files had extra empty lines in some cases. This has been fixed.
* The SWC conversion of the files that had soma in the middle (as opposed to the beginning of the file), did not rearrange the soma to the top. This has been fixed.

In the Linux version sometimes multiple files would not get converted at once. This has been fixed with a minor change in the code.

* N\_stems code is fixed. Previously, the function would count change of type anywhere in the tree. But this is now fixed according to the definition (see help: <http://cng.gmu.edu:8080/Lm/help/index.htm>) to return stems (different types) only near the soma area.

**New Functionalities for GUI v4.4**

* The GUI code was changed to support the new sub tree generation functionality. The online GUI can categorize generated sub trees into Axon, Basal and Apical.
* Added a new “remove all” button in LMSearch panel. This button will remove all the files from the input file selection window.

**Bug fixes for GUI v4.4**

* The GUI Search panel’s “load to group2” click was failing. This has been fixed. Also when “load to group2” is clicked the stat\_tests checkbox is automatically highlighted in both function and input panels.

**FAQ for GUI v4.4**

* What is the maximum number of files which can be used in online L-Measure?
* The online L-Measure is not initializing in Linux based OS browsers?