*Zirmi README*

This is opensource written in MATLAB 2015b. It builds upon other opensource tools, in particularly *PhagoSight* package for an automated quantitative evaluation of cell kinetics and oxidative stress in zebrafish tails after injury.

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1. Zirmi Module 1
   1. Script A - reformats raw data from ZEN microscope outputs so as to be compatible with *PhagoSight tools* and *Zirmi* analysis pipeline
   2. Script B0 - Defines tools and parameters such as algorithm values and directories for automation in future modules and saving
   3. compatible.
2. Zirmi Module 2
   1. Script D0 determines unwounded or baseline fluorescent intensity values
   2. Script D1 determines wounded fluorescent intensity values
   3. Supplementary D will call values from user-selected subjects for visualization Plots
3. Zirmi Module 3
   1. (B0 and B1 – need to be ran; B2 and B3 are to amend MATLAB workspace inputs but not save 🡪 re-run B0 and B1 if you would like to re-save inputs)
   2. NOTE 1: To run B1 user needs to have already performed *PhagoSight* “neutrophlanalysis( )”; please see *PhagoSight* elegant URL to access the package and instructions: <http://phagosight.org/>
   3. NOTE 2: Script A reformats raw data so that directory inputs into PhagoSight are
   4. Script C1 – Find PhagoSight “handles” to determine temporal and spatial domain cell kinetic computations.
   5. *Zirmi* Cell kinetic quantitative measures include: absolute velocity, meandering index, static ratio, Forward Index, Backward Index, Backward to Forward Index, distance traveled, net distance traveled.
   6. Cell kinetic measures are automatically exported in a time and space manner with Script C2
   7. Visualization - dowloand Zirmi provided shortcuts for quick and easy
   8. Generated Plots can be automatically exported to Powerpoint with Script F2A-C
4. Zirmi Module 4
   1. Script F’s permit automated excel database generation.