

**Dec 16 2010**

- updated FISH to use Motic colour camera on Savant system.
- Updated Panview to display colour buffers
- starting conversion for regcalc to create colour cells.

**Dec 20**

- changed cell list files from meta\_y\_x.cmg to clist\_y\_x.cmg in RegCalc
- changed same for PanView
- changing Display to load cell and data files from regcalc, merge them and then save them.
- Load merged files if present.
- Display uses 'h' to toggle display of cell contours.
- Mouse can be used to draw a persistent contour.
- Still missing something for Motic colour camera at work...

**Dec 21**

- Motic camera working on cyto savant but unuseable due to saturating
- added colourmap to display for cell group colours
- added celllist and feat list to display model so program loads both in loader
- overrides loader if meta files are present.
- added optseg options for polygons in overlay.
- added Cell.isContained(int,int) to locate cell by coordinates.
- Added delete option
- added append option
- removed filenotfoundexception from celllist load

**home:**

- fixed regcalc to load colour images and create colour cell files

**Dec 22**

- added cell frame
- Mouse click on main panel locates containing cell to update cell frame
- fixed centering for cell append
- added JDQuery
- added data change query to program close

**Dec 23**

- replaced jifCell with JDCellEdit
- adding buttons to toolbars:
- close dialog, delete cell, toggle contours, clear lines
- added JPCellEdit to display cell and editable contours
- append will now delete contained cells.
- Regcalc now trims cell sizes before saving cell data

**Dec 29**

- changed cluster to use distance transform growing to grow nuclei as seeds to fill original mask.
- Added relocate to trim cells down again. Rejects objects < 100 pixels.
- Fixed ciraster loadChain(int xpos, int ypos, int fill) to check fill values
- CIRelocator has new constructor public CLRelocator(double sobel) with sobel threshold.
- Changed regcalcthread to remove redundant first reloc

**Jan 3**

- added cell constructor with padding for relocation
- changed clrelocator to use padded cell

**Jan 4**

- moved and tested FISH system to end room
- worked on segcluster
- added cell(cell,border) test for screen x,y for objects on leading frame edges.

**Jan 5**

- intro for student
- worked on segcluster
- setup timecourse on axio
- run overnight
- studying new relocation
- testing regcalc

**Jan 6**

- some updates for timecourse to work with classify
- New serial cable working on savant system with the FISH program
- testing regcalc
- updated prosilica to use camera properties
- note that the prosilica cameras have significant shading in vertical direction especially at low exposures.
- Time course running on Axio, Savant and getafics

**Jan 12**

- added box to select a nucleus for stats
- added focus and x,y centroids to stats
- updated time course display to show additional features
- fishmodel now saves / loads the focuschannel
- displays now synch with edit
- startup now moves to proper filter
- edit will now force filter change if necessary

**Jan 12**

- created CellCon class to convert old cell format to new one.

**Jan 17**

- changed ciraster genauto to use 2 stds for threshold

**Jan 18**

- working on segmentation
- edge relocation now adds back dilated chain after removing dark material

**Jan 19**

- working on segmentation
- fixed separating nuclei for display
- Features calculated in display if not matching on load.

**Jan 20**

- IOD feature names and checks all updated IOD\_RAW etc.
- barcode stored in feature sets (name\_1 ...3) first export only.
- Fixed registration for display appending chain.

- Finished display edit option 'save'
- fixed a divide by zero in ImLib for less than 10 cells

**Jan 24**

- reloc donut now uses \*.5 of sobel levels rather than (max+min) /2 (more adaptive)
- added jpg save to regcalc
- wrapping RRelocator in DSegment seems to help – encapsulated Rcell etc.
- Added hasBorder to Cell to test if any roi in border
- Rcell expanded if necessary
- Dsegment now tests for roi border and used new Cell(cell,border) to expand if necessary
- moved segment to new project SegTools
- new calculator project jcalc

**Jan 25**

- scanning some cervical slides for testing
- fixed directions for fish grid display
- updated fish help for camera adjustment

**Jan 26**

- working on stitching

**Jan 27**

- Stitching may have second minima where material scrolls off the buffer. The process now checks that the cursor copy has a CV at least .3 of the base copy
- After processing, empty points are filled in in spiral that compares the upper.y-left.y and left.x -upper.x for adjacent non empty points. This is iterated till all points are filled.

**Jan 31**

- Threading file save and data open in display
- more adjustments ro Fish grid display
- Fish settings now checks 8,9,10 filter name changes
- FishModel now propagates filter name changes
- Filter panel will now respond to name changes.

**Feb 1**

- improved stitching

**Feb 3**

- started working on inflections
- expanding on distance transform
- preparing for talk next week
- cell class now allows multiple mask rasters

**Feb 6**

- started updating cell for multiple masks

**Feb 7**

- updated FISH help for presentation
- working on distance variation
- working on cell masks

**Feb 8**

- experimenting with distance transform
- expanding junit tests for cell and cb/ciraster classes to test new formats and methods.

- Raster fillchain now uses polygon within extents to ensure all pixels are adjusted without affecting pixels outside the chain.

**Feb 9**

- Cluster segment seems to work fairly well with doublets
- Trying regcalc with two cluster segs. First only on large clusters but second after cell focus.
- Includes edge relocation.
- Appears that distance transform will not work with elongated nuclei.
- Added settings dialog for segtest and regcalc to adjust segcluster threshold and relocater sobel initial threshold

**Feb 10**

- updated stitching algorithm. One stack file had been cleared so corrupted stitching. Need to find out where and how...
- Added sobel thresholding to cluster segment. High sobel values removed from reduced mask. Can make marginal improvement.
- Updated segtest to allow setting values for visual inspection of results.
- Regcalc without watershed seems significant improvement.

**Feb 14**

- working on inflections. Seems a range of positive changes can define an inflection reasonably well.

**Feb 15**

- scanned one dapi slide
- some adjustments for stitching fluorescent images
- working on segmentation for fluorescent images
- some updates to FISH program for filters dialog to ensure focus channel is valid

**Feb 16**

- added thresholds to new regcalc prop file
- some testing for segcluster with fluorescent images
- some adjustments to regcalc thread for border nuclei exclusion

**Feb 17**

- Fish edit region now ensures at least one filter always selected.
  - If only one selected, it will be set as the focus filter
- Edge relocation adjusted to invert fluorescent images
- Fish path change dialog cancel leaving interminate state – fixed.

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**Feb 18**

- working on stitch test

**Feb 21**

- checking flavin and dapi slides on scanner
- Some updates to Fish program to load calib files on startup
- expanding stitch test

**Feb 22**

- working on stitching – need changes for fluorescent images

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**Feb 23**

- working on Display program
  - not loading cells and feature for stacks if main file exists – faster load 3 min down to 2.

- **developing cluster segment dialog**
- **added thumbnail for navigation**
- **added arrow keys to shift one camera frame**

**Feb 24**

- **working on Display**
- **extending cluster dialog for cluster**
- **added area classify from polygon**
- **extending cell edit**
- **added groupmodel for group selections**

**Feb 25**

- **added group list dialog with pop ups and actions**

**Feb 28**

- **implementing group dialog functions**
- **adding reclassify to popups**
- **append now accepts group**
- **splits now promote existing group number**

**Feb 29**

- **adding histogram with dialog, panel and model**
- **more work on features and groups dialogs**

**Mar 1**

- **some testing and updating for stitching**
- **some updates for display program**
  - **simplified cell edit dialog and messaging to speed up**

**March 2**

- **regedit calculator now stores feat file extension in the region prp file**
- **display now gets the feat file extension from the region prp file**
- **starting work on display scatterplot**
- **rangemodel now holds feature indexes for scatterplot. Features dialog can now change these in the menu system**

**March 7**

- **working on display scatterplot**

**March 8**

- **right click on scatterplot selects nearest cell and adjusts main frame to centre the cell.**
- **Some fixes for colour images / frames**
- **working on stitch with colour frames.**

**March 9**

- **working on graphs**

**March 10**

- **working on graphs and popups for hist, scatter, feats**
- **threaded voronoi load process**
- **voronoi lines now drawn in cell group colours**

**March 14**

- **starting on binary tree dialog**

**March 15**

- **added setting for regcalc second cluster threshold – seems to do a better job at .6 , .5 too aggressive**
- **added export to display features dialog for centres**

- started unit class with xml persist

**March 16**

- working on unit class
- starting Dunit display
- moved display dialogs to gui project

**March 17**

- filling in Dunit display

**March 21**

- Started the Thumb program to pick areas for Units.
  - Has grid and sizeable box to create units.
  - Unit file loads to DUnit
- Added some connections for Dunit gui components

**March 22**

- working on Dunit
- added membrane and roi models
- Dunit now collects, saves and reads membrane and roi files

**March 23**

- added roi export to Dunit
- Dunit now allows two membranes for ducts
- can collect ROI as a series of points

**March 24**

- Moved Fish calibration to a separate thread and progress dialog.
- Adjusted camera stop to shorten timing.
- Testing Fish program on old CytoSavant hardware.

**March 28**

- working on Fish on CytoSavant

**March 29**

- Some progress on CytoSavant using slide holder with gripper
- experimenting with thread pools

**March 30**

- implemented thread pool for cluster segment
- 1 thread at 271 and 64 at 7 seconds to segment a unit area

**March 31**

- working on Dunit segmentation
- processing scanned data

**April 4**

- working on thread pool. Very large blobs still consume much time – probably in the chain dilation. This needs to be profiled.
- Added flag to disable relocation during cluster seg. Seg process now disables for first pass and enables for second pass.

**April 5**

- profiling dilate
  - timing largely due to ArrayList access
- Changing Fish to persist fluor / white level mode
- profiling chain coding found collection very slow – changed to ArrayIntList.
  - 10 x improvement
- Profiling found fillChain using polygon to check all pixels when only first one was needed.

- 100 x improvement

**April 6**

- fixed fish messaging to close stage monitor thread before first scan
- Fixed fish thumb not inserting frames
- Updated fluor calculator with white calculator features using inverted image
- fixed display and dunit updating rangemodel when feature length changes.
- Added jpg export to scatter dlg
- Started thresh operator dialog

**April 11**

- working on threshold operator dialog
- added locks to groupmodel and group panel. Menu and popup have submenus for lock, unlock and unlock all

**April 12**

- finished threshold operator dialog
- working on edge relocation
  - using  $2 * CV$  of top max for range value
- working on segcluster.
  - Was not operating on single relocations

**April 13**

- added min area to dunit segment, model and settings dialog
- dunit segment will now focus twice and all filters.
- Histogram now has popup
- some work on segtest
- clrelocator now uses 2 SD below upper peak but above mid point to add light pixels
- calculator thread pool: 1: 31 sec, 32: 1.2 sec

**April 14**

- added program to convert single tifs to units
- also added models to read / write existing roi files.

**April 18**

- added multiple tifs to tifunit conversion program
  - uses focus calc to determine best plane
- adjusting genauto background thresholding. Using 1/3 of CV of background peak
- dunit save data also saves old .roi file

**April 19**

- working on import asterix data
  - importing cells and creating features
- working on segtest
  - to implement watershed

**April 20**

- added simple inflections option to dunit
- added option to save plane images to dunit

**April 21**

- added versions and prod info dialogs
- fixed tifunit and dunit to manage colour files
- tested with H&E stain from internet jpg file

**April 26**

- created CamView and added to Dunit interface.

**April 27**

- **debugging cluster / relocate / raster**

**April 28**

- **working on SVN**

**April 29**

- **SVN working**
- **trying camview on cytosavant system**
- **working on adding dynamic focussed frames**
- **unable to init stage on skop2 system...**

**May 2**

- **working on skop2 system**

**May 3**

- **working on stage – maybe blown a fuse**
- **updates for raster relabel to use area reset rather than flood which may not be working**

**May 4**

- **some work on raster fill operations**
- **Started work on dunit on-line help**
- **repackaged old classify**
- **added single mouse click to classify objects in dunit**

**May 5**

- **working on dunit on-line help**
- **fixed add/delete problems with cell edit**
- **main panel RMB not active if not in a cell contour or a polygon is not visible**
- **added focus frames display to dunit popup**
- **put fuses in another axio and they work ok.**

**May 9**

- **Working on threading**
- **trying to compile asterix**

**May 10**

- **adding gallery to dunit**
- **added Objective class**
- **tifunit now uses Objective class to enter lens and mag in unit**
- **Dunit now inserts lens and mag in cells after segment**
- **added cell settings dialog for debugging**

**May 11**

- **working on on-line help for dunit**
- **tested and finished Threshold operator dialog**
- **Groups clear now clears feature locks along with the group locks.**
- **Fixed group change in showall gallery.**

**May 12**

- **fixed dunit append for colour buffers**
- **added cell trim to celllist**
- **cell edit now trims save on single nucleus.**
- **Added relocate to cell popup**

**May 16**

- **working on junit for celllist and fstack**
- **dunit will assemble faux colour for up to 3 filters.**



**May 17**

- added lines/mm to griddisplay program
- added version prod info dialogs to test programs
- dunit fixed name references for focus frames in multiple filters.
- fstack accessor method for name of focus frame by filter and focal number
- tnal now assembles colour from multiple filters.
- Working on FISH reading  $z = -1$  after scan

**May 18**

- working on magnification for 63x oil objective
- update to gridmodel after mag change now fixed.
- FISH reading  $z = -1$  ignored for fishmodel / region updates.
- Modified stage read positions thread for closing.
- Started work on linear operator
- Worked on Fish mag for 63x

**May 19**

- updated classify and utilites for cimg
- put cimg in SVN
- updated iutils merge – removed test for readonly
- working on linear operator and stepwise

**May 24**

- FeatureCalculator is now an ICalculator
- Classify will now use Icalculator
- CalcFactory now loads featurecalculator if calculate.prp has calc=fb5 for non-fluorescent
- Dunit now has normalize option in histogram.
- Fixed histogram initial limits now set by setRangeModel() - should have featIndex set first.
- Histogram stats now respect hidden records.
- Cell edit moved split button above save button to shorten distance.

**May 25**

- added calibrate dialog to camview
- added import tifunit to dunit
- added fb5 calculator dll calculate.prp has "calc=features"

**May 26**

- working on OS/2 machines
- Started on Reset Operator

**May 30**

- working on Reset
- Integrating operators and binary tree display
- added 10 temp\_x features to java calculators
- adding setTitle(index,name) to FeatureSet

**May 31**

- working on binary tree integration
- working on voronoi
- added voronoi feature for cytoplasm area approximation.

**June 1**

- fixed binary tree insert

- changed voronoi raster to int version to fill with sequential numbers
- extracting distance to next nucleus of given group
- extracting number of nuclei between these

**June 2**

- fixed raster draw for oob wrapping

**June 6**

- fixed findeexchain to find external chain
- ciraster finds connected cells
- stats adds borderCells feature for count of connected cells
- stats reports mean number of conected cells.
- Icalculator now has setResolution so calculators now convert area and radius features to microns.
- Stats reports spanning distance and cytoplasm area in microns.
- Added magnification to Dunit settings dialog.
- Unitmodel saves unit on exit with any changes to mag.
- Tifunit saves / reloads default directory

**June 7**

- added mag\*2 to cell edit window

**June 8**

- adding print option to main menu
- added prod info to camview
- added min iod to dunit segment thread and model / settings

**June 9**

- added Report form
- added edge cell detection

**June 13**

- working on report / stats

**June 14 – 16**

- working on OS/2 systems
- working on serial port problems

**June 20**

- working on R
- working on axio serial ports

**June 21**

- working on dunit help
- working on reclassify in dunit – aborting for no reason
- updating fb5 calculator and jcalc. Need 64 bit compiler.
- Ran fluorescent slide for Ivana – no spots
- ran stitch program on Anita's slides to correct stitching. Copied to f drive

**June 22**

- interface to R now working
- 

**June 23**

- presentation
- 

**June 27**

- tried out canny segmentation

- added interface and factory for segmentation algorithms
- added halogen setting dialog to CamView to test systems.
- No light level on MEH but works fine on BABA

**June 28**

- camView now persists the halogen level to the stage.prp so dialog will load and save this value on start and end. Halogen menu item disabled til stage is initialized.
- Mskop stage now initializes the halogen level from stage.prp – default 100.
- added thread and dialog to rjava project and dunit
- Added reclassify to dunit and classify as global

**June 29**

- installed Visual Studio
- working on feature calculator
- Updated classify to work with rjava

**June 30**

- added settings to calculator for mag, low and mid thresholds
- updated cb0 calculators for 32 and 64 bits
- classify now uses thread and dialog for Rclassify

**July 4**

- working on voronoi mode for dunit

**July 5**

- implementing cell and feature lists for voronoi objects
- created voronoi mode for v display
- v data lists updated only on switch out, save or update to save processing time
- v data lists updated when displays are opened.

**July 6**

- working on Voronoi display

**July 7**

- working on Voronoi mode

**July 11**

- working on tiled tiffs

**July 12**

- working on tiled tifs
- swapping power supplies with OS/2 systems

**July 13**

- updated calculators to add voron\_x and voron\_y features.
- Restructuring dunit
- source of nodes to create voronoi now come from
  - a. normal cell list centroids
  - b. existing node points
  - c. voronoi coordinates in v feat list
- unable to read tiles in tiled tiffs.

**July 14**

- fixed voronoi centres for cells
- Fish load slides now loads all regions and inserts the barcodes
- JPSlide mouse clicks now picks correct region if more than one
- load no longer excludes overlapping regions.

**July 18**

- **calcfactory will create prp file with cb0 calculator and detect 64 bit systems to set dll element if prp does not exist**
- **cameraFactory will disable camera in prp file if camera load fails.**
- **Prp will now list supported camera type options**
- **Dunit will persist a directory for saving plane feat and image files.**
- **Calculators now have features "voron\_x" and "voron\_y"**
- **Chains now have neighbours list generated from voronoi but not persisted.**
- **Cell header is now 128 up from 100.**

**July 19**

- **problem with fish camera**
- **fish now waits for stitich to finish from previous region**
- **problem with dunit sizing voronoi**
- **problem with voronoi lines not reaching borders crashing calculator**

**July 20**

- **fixed problem with calculator by not calculating large cells at borders**
- **gallery now resizes to current group in show group mode**
- **dunit now sets groupmodel for voronoi in gallery**
- **Voronoi now calculated at full size so display will resize to current mag.**
  - **Does not require regen on mag changes.**
- **Updated Timecourse to add exposure dialog**
- **running on Fish system to see if some limit to scan number**
- **updated dunit help for voronoi options**

**July 21**

- **Fish camera seems to fail on some time limit.**
- **Altered dll to return data if no errors.**
- **Jai camera class will stop and restart on grab error**
- **Able to read tiled tiffs, make thumbnail, make unit and load to dunit**

**July 25**

- **increased dwell time in camera dll seems to have fixed camera problem**
- **created pannex program to load pannoramic tiled tiffs to expand to region and stack files.**
- **Tiles have a 3 pixel offset**
- **Fixed crash in feature dll – not enough space for error strings.**

**July 26**

- **fixed text buffer errors and chain code size limit in feature calculator dll**
- **fixed grid lines in thumb program**
- **dunit now puts group number in roi architecture file**
- **pannex extracts 256x256 tiles.**
  - **Assumes width includes extra tile if remainder > .5 of tile width**

**July 27**

- **working on segmentation for Pann images with bright clipped.**
- **Pannex now strips first three pixels before loading tiles.**
- **Feature calculator – changed chain code limit from 4k to 120k**
- **Pannex now creates thumbnail at 10x subsample**

**July 28**

- **added settings to tifunit for setting fluorescent mode images**
- **added dunit function to drag points of roi or membranes**

- Ctrl plus mouse click removes nearest point
- Shift plus mouse click adds a point

**August 2**

- report now hides selected groups. Has menu options to toggle.
- Cell now has both boundary and edge attributes set automatically to groups 10 and 11.
- report now can scale to fit roi / membranes. Has menu options to toggle.

**August 3**

- fixed calc pool with each thread creating it own calculator
- test on 600 cell file – 2: 15010,8: 3814, 16: 2020, 32: 1135
- restructuring to remove dependancies between cmodel and ciutils and hardware.
- Hide / unhide in report now reflected in main panel and groups display
- implemented aspect ratio in report form while fitting region
- fixed no roi for roi export

**August 4 to 15**

- working on voronoi
- split off vormodel

**August 16**

- implementing R classifier

**August 17**

- dunit gallery now has zoom in / out
- polygon with negative Y now makes bisecting line inside boundary
- polygon with negative X now makes bisecting line inside boundary
- changed MST centre to vorx,vory stored in cell header

**August 18**

- working on polygon extraction. Validated for single oob points...

**August 25**

- fixed finding edge cells for voronoi plot
- Group window now in sync with voronoi display
- Rview now tests operator names to enable / disable run and test

**August 29**

- fixing getneighbours
- now hiding contours while moving roi / membranes
- Fish needed focusChannel reset for each collect frames

**August 30**

- working on Voronoi problems
- switched flour feature files to binary (.ib0)

**September 1**

- fixed rgb display of fluor cell images.
- Removed option to load individual feat and img files with stacks.

**December 19**

- roi exports border cells
- Opening another file will now prompt for saving changes
- Centre mouse key will now toggle the group.
- Voronoi menu item disabled if no cells in celllist
- Fixed mark outer

- roi export dialog now uses name

**December 20**

- mark outside now uses node x,y in polygon
- working on specs and testing docs

**December 22**

- data save now uses thread and progress dialog
- Saving changed data now logs version, user and date
- working on specs and testing docs
- "Version .978 20111222"

**2012**

**November 7**

- program now checks tree features when switching to/from fluorescent units
- program now saves tree data when saving settings to a new directory

**November 8**

- program now checks window positions against screen resolution to ensure they are visible
- program will create logs, calib and test folders if not already created.
- Added print option for main page with file path and name at the top

**November 13**

- started working on new relocation
- Dunit will now copy groups from cell list to feat list on loading in case feature sets are different

**2013**

**August 13**

- added check for stack plane count in dunit and runit
- added plane count set to stacks in saveunitthread
- selfeat now updates model index for histogram
- program now updates histogram when new data file loaded.
- Shape adding can now be ended by pressing right or centre key.
- Version 1.21.40 20130813

**August 14**

- changed cell read / write buffer sizes to 2000000 bytes – about 10% faster.

**August 15**

- program will now retain the names of the last 10 files loaded
- Version 1.21.50 20130815

**August 27**

- added (C)apture option to sample 12x128 areas of the frame
- Holding the Alt key down will allow panning the frame
- Some updates to on-line help
- Added optional distance transform before edge relocation

**August 29**

- made changes to cluster merging
- re-tested distance transform
- removed treea

- **Version 1.22.00 201300929**

**September 3**

- **updating segcluster with one distance transform after relocation**
- **some more work on distance – setting threshold to 70.**
- **Version 1.23.00 201301003**

**September 5**

- **added neighbour features to cb1 calculator for min, max, mean and variance**
- **shifted calculations in segthread to after voronoi generation.**
- **Working on updating runit**
- **Version 1.24.00 201301005**

**September 10**

- **Updated runit to match changes to dunit**
- **Runit Version 1.08 20130910**
- **dunit now has ctrl / shift 'D' to change dot size.**
- **Some updates to dunit help**
- **dunit normalize will now run the tree if enabled and loaded**
- **Version 1.24.00 20130910**

**September 11**

- **fixed neighbour assignments**
- **'N' will now show connections to neighbours of selected cell.**
- **Normalize will now show the 'Processing' in red on the menu bar until finished.**
- **Starting a mouse drag with the Shift key down will allow drawing a boundary around a region of the screen. The popup presents a "classify" option to re-classify all objects inside the boundary to the selected group.**
- **Version 1.26.10 201300911**

**September 16**

- **fixed name error for radius+m**
- **fixed calc for area\_m**
- **trimmed cells now inherit features from original cells.**
- **Added feature slider to mark groups 0 or 1 depending on feature value.**
- **Fixed cell getclass(int index)**
- **added feature "nb\_layer" to cb1 features, nodes and cells.**
- **Version 1.26.10 201300916**

**September 17**

- **added method to assign layers**
- **fixed nb feats for different input methods and group delete and normalize**
- **fixed ascii export in featuresetlist**
- **jdfeatslider now has append lower / upper to pass thresholds to threshold operator**
- **Ctrl 'L' will toggle display of layers as groups.**
- **Version 1.26.20 201300917**

**September 18**

- **mark shapes now assigns roi borders to zeros.**
- **Ctrl will now determine layers**
- **Alt 'L' will now determine layers after shapes are marked.**

**September 19**

- **added finding 0 layer for membranes**
- **Alt 'L' will now find layers for shapes**

**September 23**

- cell now persists layer
- Dunit won't re-assign layers by default.
- White calculator will now pass cell layer to feature layer
- Shapes export cells now passes original features list with trimmed cells.
- Fixed voronoi mask copied to cytometry mask in reseg
- removed remask option as it was not working as intended.

**September 24**

- mark shapes will now also assign layers
- reseg on adding nuclei/voronoi will now assign mask even if vorx/y not in mask
- first pass for cluster uses 1/2 the min area process to allow edge relocation
- Version 1.26.30 201300924

**september 25**

- changing the groupmodel and colormap to use arraylists instead of fixed arrays
- Requires a lot of changes to Classify

**September 26**

- testing latest changes
- groups now dynamic depending on group feature
- Version 1.26.30 201300926

**October 2**

- moved segthread removing small cells before the voronoi calc.
- Version 1.26.50 20131001

**October 8**

- added raster function to find dark objects and find centre of largest one for voronoi point
- added feature for angle to the nearest basal layer cell
- Version 1.26.70 20131008

**October 10**

- added 2 points to cell header- 2 bytes per value gives limit of 64k.
- dunit shape-mark now sets the nearest shape line segment end points in the cells headers
- segthread now uses border(4) and segborder(0) so blobs touching border are not eliminated.
- Started class
- Version 1.26.80 20131010

**October 16**

- Cell gallery should now resize by ignoring hidden groups
- Version 1.26.80 20131016
- unit testing basal class for angles and distances

**October 17**

- working on layering, nearest segment
- fixed messaging to gallery for group change
- Version 1.26.90 20131017

**October 22**

- validated nearest segment
- each group will find the nearest segment for the group
- group zero (no shape) will find the nearest shape



- **Version 1.27.00 20131022**

**October 23**

- **Nearest segment should now work with groups working within shapes**
- **group zero should find nearest shape**
- **Nearest distance is working much better**
- **reset segthread segborder back to 3**
- **no longer removing faint nuclei that failed get centroid in ciraster**
- **added hide others to Groups popup and unhide all to menubar**
- **basal distance still failing on some nuclei.**
- **A few nuclei still not finding nearest basal segment – fixed**
- **added move shape to popup on main window**
- **move ended with mouse key other than the LMB**
- **Version 1.27.00 20131023**

**October 29**

- **reseg of neighbours for insertion being over segmented by old edge relocation**
- **inserted now segs new cell only once as not marked for background process**
- **Version 1.28.00 20131029**

**October 30**

- **fixed relocfactory to use only the new edge relocation**
- **added distance transform max to settings parameter def = 0.7**
- **'c' key will store region around mouse position while Ctrl 'c' will save selected cell to selected file**
- **inverted distance transform factor now seedDistance.**
- **Fixed popup for moving shapes to consider concentric shapes**
- **Version 1.28.00 20131030**

**November 4**

- **added distance seed distance to settings menu**

**November 6**

- **program now exposed edge relocation parameters to props\relocate.prp**
- **Version 1.28.10 20131107**

**November 7**

- **set defaults to be a bit more aggressive.**
- **Version 1.28.20 20131107**

**November 14**

- **added function to mark duct cells between the membranes**
- **Version 1.28.30 20131114**
- **added block at 200 grids**
- **fixed Sobel display in jdmono**
- **Version 1.28.31 20131114**

**November 21**

- **added progress indication to data load thread**
- **added keyboard option Ctrl R to add roi**

**November 25**

- **removed two int[] buffers to reduce footprint**
- **changed ciraster int[] model to cbraster byte model in segthresh to reduce footprint**
- **Version 2.28.40 20131125**
- **clearing buffers and raster after use to reduce footprint**

**November 26**

- testing on data with 26x20 1.3kx1k mono frames – generates a 6 gig image file; takes 15 minutes to load/save the data. Used 11 gig of memory
- main screen popup now has roi shape add, move and remove menu items
- Group window will now show all groups after shape-mark groups/ducts
- cbraster seems to have some problem with large areas so currently using ciraster.
- Version 2.29.00 20131126

**November 28**

- fixed cbraster problem so replaces ciraster for lower footprint
- added isDll() method to feature calculators
- added thread pool for generatefeatures for non dll features
- changed frame magnification from int to float.
- Popup to zoom in/out will change by .5
- Version 1.29.10 20131128

**December 2**

- fixed roi scaling error from mag change
- fixed speed problem in white features sub\_nuc\_number
- Version 1.29.20 20131202

**December 4**

- fixed membrane scale factor
- Version 1.29.22 20131204

**January 8**

- fixed getHistogram() in ciraster
- updated Thumb program to allow multiple selection
- updated mb0 to include dunit voronoi features

**2016****February 24**

- added new toolbar
- 

**March 4**

- added buttons to toolbar for edit and rgb
- added offsetmin and offsetmax to cameras
- microscope will now reset the camera offset from the camera.prp file
- e2v camera has working exposure and will disable auto exposure and shows full frame. Camera is 12 bit using 16 bit data.
- Rgb dialog will now keep singular checkboxes in each column and will update the main screen for each change and close.
- Fixed allegro offset in dialog and startup.
- Fixed alternate tool bar displays for camera view.
- Increased Previous size to 15.
- d/l latest Apperio driver and camera now runs a consistent 66 fps.
- Updated illum offset for apperio camera

**March 5**

- added offset to Dunit camera toolbar

**March 6**

- fixed getOffset() native mismatch

**April 13**

- fixed toolbar switch after unit save from camera view.

**April 26**

- updated Pannex to read xposition,yposition and xresolution in case they are present and store them in the stacks.

**June 17**

- fish – added dialog to centre the camera using the spot on the Motic slide.

**June 22**

- added video dialog
- updated positions to revisit nuclei.
- Added stage initialize option.
- Added stage halogen persist.

**June 30**

- updated tifunit to process a list of tiff files to generate unit structures.
- Added max size for edge relocation to skip objects > 500000 pixels

**July 13**

- programs now create prp file for last settings used on data sets. Dunit will now display the file from the help menu.

**July 19**

- added feature calculator selector to the Program Settings dialog.
- For a new calculator.prp file, the program will set the calc to martial
- Version 1.39.00 20160719

**September 20**

- adjusted boundary detection to use scale of 1 to get continuous line.
- added Boundary to shape menu
- updated help to reflect changes to menus.

**September 22**

- updated mskop2
- added check for valid string from getHalogenLevel()
- Version 1.39.00 20160922
- created 32 bit martial dll and updated class to select based on 64 bit.

**September 27**

- changed flag for new segment to integer with comobox in setttings. This will allow addition of Calum's segment option.
- Version 1.39.00 20160927

**October 7**

- changed eraster findDir16 to use lookup table rather than time consumimg atan().

**November 15**

- updates to Nunit settings dialog for fixed output stage file
- updates to Pannex to export only jpg file for Nunit.
- Updates to Pannex for colour output in jpg.

**Nov 29**

- changed thumb to drag first grid rectangle or last to define area
- updated Classify for normalizing to a different feature set. Version 2.28.6 20161128

**December 6**

- updated 2 feature calc dlls to use 512 instead of 256 for max size

**January 5 2017**

- Gallery Sort now using thread and progress dialog

**January 23**

- **Version 1.39 20170123**

**January 24**

- updated nunit to add previous files menu items

**January 25**

- Dunit changes to feature selection in threshold dialog will now pass to histogram
- Histogram now responds to group hide options
- JDTree now has 'New' option
- **Version 1.39 20170123**

**January 26**

- - **Version 1.39 20170126**

**January 30**

- Dunit fixed rgb selection for multiple coloured image buffers abd rgb
- added thread / progress dialog for normalizing

**January 31**

- fixed progress indicator for image file loading
- nunit added features and histogram displays with positions save / restore

**February 6**

- updated cell and features to include the stack x,y positions
- Implemented roi subshapes.

**February 14**

- added process and settings dialog options for spct
- added spct thread
- thread sorts cells into groups based on centroid distances from stack coordinates.
- Cells with too few stacks are removed and the voronoi regenerateted.
- Cells are now expanded by the prescibed dilations.
- Cell nuclei are now dilated by prescribed dilation amount
- 

**February 15**

- implemented feature regeneration for General Settings calculator changes.
- Added ROI project types to General Settings.
- Added menu item name changes for selected ROI project changes.
- Names now stored / retrieved from dunit.prp and dunitproj.prp
- **Dunit Version 1.39.00 20170215**

**February 20**

- spct now adds third mask buffer with dilated cytometry mask.
- Histology now cycles mask contours with 'O' key.
- **Histology Version 2.00 20170220**
- Dunit now forked to Histology installed in [c:\oncology](#).

**February 21**

- updated cmodel cell conversion to set mask number to 1.
- updated imaging cell to reset 0 to 1 mask buffer

**February 22**

- extended shape mark to add menuitems for mark current shape or all shapes
- Histology cell loading will enforce rgb mapping to monochrome for single buffer mono types.
- Added tree dialog to NUnit Version 00.91.00 20170122
- default tree path set to project name

- added Threshold dialog to Nunit
- added Reset dialog to Nunit. Reset now enforces default extension.

**February 27**

- added discr fn to nunit
- added dilate count to nunit settings and added dilations to segthread

**February 28**

- added popup options for rescale zooms
- added popup option for cell edit
- added disable / enable to main menu items for data loaded.
- Fixed finding nearest cell in frame. For classification and boundary export.

**March 1**

- added thread / progress dlg to loading jpg
- added transitions to data loading dlg.
- Adjusted file sources to <c:\oncology>
- updated gif for Histology
- updated gif for NUnit
- coordinated chain display modes to model value in nunit and histology
- Nunit Version 00.93.00 20170301
- Histology Version 2.00 20170301

**March 2**

- Nunit settings dlg now forces dilations between 0 and 5.

**March 7**

- updated ROI add menu items
- DUnit Version 1.39.01 20170307
- Histology Version 2.00 20170307

**March 8**

- added roid addshape 'All' to dunit popup
- now trapping empty or faulty shapes before addShape();
- processed Acceptance Testing
- DUnit Version 1.39.01 20170308

**March 13**

- Histology added dialog for Relocation, Inflect.
- Updated Inflect to new design
- Updated segparams for new parameters.
- Added histology gif for program title icon

**March 20**

- merged edge relocation parameters to main segparams
- Version 2.00 20170320

**April 10**

- implemented Dproject to hold project settings
- implemented JFProject program to edit project and parameter settings.
- Updated dunit and histology to load project files from drag drop

**April 13**

- further testing Version 1.39.01 20170413

**April 18**

- added subtypes to shapes add for membrane, roi and ducts.
- Now deleting incomplete shapes on shape collection ending.

- **Version 1.39.01 20170418**
- **updated requirements and tests**

**May 10**

- **added menu item for 5<sup>th</sup> roi shape add**
- **Version 1.39.01 20170510**

**May 18**

- **shape point remove will no longer remove end points**

**May 23**

- **added fb7 calculator CalcFactory will now use on calculate.prp or by extension.**
- **Histogram now always displays stats**
- **if histogram is displaying raw iod, mean value is passed to data model and used for normalizing. Default is set from first cell header on celllist loading**
- **calculators with dlls now bypass the thread pool with a single calculator instance.**

**July 17**

- **changed inflections parameters to add range for inflection angles and indents**
- **updated segtest to display inflection points.**
- **Added Ctrl-Z to inflection display dialog for**

**July 20**

- **added background dialog to histology camera view in Histology**

**Aug 3**

- **working on inflection**
- **created basaltest in segqtest.**

**Aug 04**

- **updated Rldf dialog**
- **operator dialogs now notify changes to treepath. UnitModel now saves / restores treePath on close and open.**

**August 16**

- **added BOPE for Estella's R operator**

**August 28**

- **added areaiod feature to Martial's feature dll.**

**August 29**

- **changed jdCSet to use arraylist to load text.**
- **Main panel 'N' no longer moves the screen to centre the cell.**
- **Updated Inflection mfrom imaging**
- **Updated basal from imaging**
- **Added circularity from chain code to Cell Settings**
- **SegCluster now uses circularity limit from sobSeg.**

**August 30**

- **added cluster type name to program title.**

**September 6**

- **added Cytometry Gallery to Histology to display smaller cell list.**

**September 11**

- **added print options to histology scatter and histogram plots.**
- **Updated req and test docs.**
- **Tiffu will now optionally scale tiff files which have more than 255 values.**

**September 12**

- **added MonoIntBuffer and ColourIntBuffer to provide integer size data buffers.**

**October 18**

- renamed .jars for histology

**October 30**

- updated calcpool, calcthreads to pass segparams

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**October 31**

- updated jfeat(s)
  - added parameters for segment defaults and cell composite
  - added drag drop for project short cut, project file and settings file
  - changed cell composite to checkbox
  - added persist for window size / position
- updated calculators and cell class to use cell composites and cell defaults

**November 1**

- finished working on cell composite for both forks
- Updated Dunit to use primary and composite settings.
- Updated Histology to use primary and composite settings.
- Composite images now clipped to 0 – 255
- Histology new edge relocation will use composite images

**November 2**

- added iod thresholds for histology with cell defaults checkbox in settings
- updated layout for jdsobsegsettings

**November 20**

- fixed Display + unitmodel loading project and its propfile for Histology and DUnit
- added scrollPane to jdmGroup.
- Added 'T' to clip groups.
- Trapped image size in cmfeatures.
- Added jpeg save to settings dialog to both

**November 21**

- Histogram settings now has bin entry
- bin size is now persisted by histmodel

**November 22**

- added Histology user log to c:\oncology\scans\users.log

**November 23**

- added combobox and Motic to tifunit settings
- changes to cellvor trim sizing
- added counts and progress to segthread progress window
- changed logging to use username for log file in f:\cytometry\users

**November 27**

- re added save cell popup in Histology
- re updated Inflection multi
- added segBorder to segparams to setting for all algorithms.
- Updated genvoronoi and updateCell to extract with segBorder. Image is expanded to allow segborder for cytometry and voronoi masks.
- Updated inflection, segdistance and ereloc for dynamic border size

**November 29**

- updated Inflect for dunit and histology
- fixed ciraster draw() to add first point in dunit and histology

- added toolbar buttons for groups and features to Histology
- fixed save / restore for general settings for border value
- added dialog for inflect settings to dunit. Updated segparams for new settings
- jcalc now logs to f:\cytometry\users

**November 30**

- crippled inflection in Dunit to use a single pass.
- Added cell list export to cytometry gallery
- added cell boundary setting to all segs in Histology
- copied segdistance from imaging source

**December 11**

- added settings dialog to tifunit save unit to prompt users to assign values.
- Added up / down arrows to Histology groups display

**December 12 – 15**

- fixed groupmodel setGroups
- fixed multi colour display
- updated jfeat dialog window to split calc with file count
- updated inflect with pre filter to clean edges.
- Split white calc to a cb0 (cytometry) and cb1 (histology).
- updated calcfactory to enable all calculators

**December 24**

- updated Patch for cells in edge relocation.
- Added clipped as a bit to both systems.
- Added patch settings to segparams
- 

**December 25**

- updated Patch for eraster.labela
- added patch to sobcluster

**December 31**

- moved calibrated to bit 3 of image header 64. Now uses boolean.
- added patch reloc setting
- updated new reloc to use new patch setting for reloc only
- fixed some issues with patch raster function
- added Patch to segcluster
- added upper limit of 1.4 to resulting circularity as new segparams setting
- disabled debugging

**January 3**

- added Stagecoord to distance and inflect for no clustering

**January 10**

- finished repack and rename for feature dlls
- switched settings for linear report between normal and jackknife.

**January 31**

- updated Inflection to check for separation near end of the chains.
- Updated Histology and Dunit to accept deleting nodes on membrane shapes.
- Added BOPE1 to tree loading for Histology and Dunit.
- Added more checks for keyboard changes to cells for modifications.

**February 1**



- changed Mskop2 to avoid setting microscope light manager options to avoid crashes.

**February 5**

- added primary band to cell header at 111
- 

**February 6**

- changed move for membranes to check lengths of appropriate side.
- Added fb5 option and updated fb5,fb6,fb7,fb8 to change using image[1] as mask value.
- Changed dunit data save to refill featlist.
- Updated req and test docs.
- Added primary band to Normalize pre dialog from first cell header
- Added primary band display to cell settings.
- Calculators now have a set cell defaults and set composite with setthresholds.
- Dunit and histology will now save primary band in cell headers.
- Normalization dialog will now update to use the primary band value in the first cell header.
- Jfeat will now assert the primary band from the first cell header in the settings.

**February 13**

- changed Histology Exposure low slider to use max 100 for units of 1/10 th msec units for finer control.
- Updated Inflections and added pdf description.

**March 20**

- Updated jfeat to fix calculator
- updated new edge relocation to restore images that are destroyed if the original is greater than twice the min area. Some valid images were being lost.

**March 21**

- updating merge to extract group counts and clear group names to defaults.

**March 26**

- updated Thumb to save / restore shapes
- Review tree disabled tree update for viewing operators.

**April 4**

- updated jclass to manage more than 19 groups for the tree display.

**April 5**

- Batch normalize now checks that the tree features matches the feature files.
- Now at Version 1.00.20180405
- updated Thumb to use a thread and progress dialog for loading the region data files.

**April 10**

- updated jdnormalize and groupmodels to ignore unloaded tree
- Histology Version 2.00 20180410
- Dunit Version 1.39.01 20180410

**April 16**

- added Cnote dialog to Histology and Review
- started thumb create thumb image with new model and tthead

**April 17**

- updated thumb creating thumbnail tif.
- Added thumb settings for colour and fluorescent
- Added settings to thumb to set colour and fluorescent settings.
- Region and settings is now persisted.

- Histology will now discard objects larger than 1m area after resegmenting. Too large objects are too time consuming.
- Fixed histology for display of rgb fluorescent main display and cell creation in colour

**April 19**

- ran tests for batch and review normalizing. Both now log the normalizing iods.
- Created doc Histology Test to track such changes.
- 

**April 24**

- added feature names dialog to jfeat
- 

**May 1**

- Thumb will now display the created thumb immediately.
- Thumb will now hide / unhide the grid with the 'H' key

**May 8**

- updated Histology to accept input from a project file to load that settings and ignore settings from data files. Otherwise, settings will be loaded from the data set.
- A project file or a file shortcut can be used to drag and drop on the Histology icon.
- Program Hproject in c:\histology\java should be used for the latest settings dialog.

**May 16**

- added Tiff Import option to the Batch program.
- Now writes cell images to disc as they are created to use less memory.
- Added option to subsample at 2, 4 or 8.

**May 27**

- merged main, relocate and inflections settings to one dialog
- If started with a project file, the program will only provide read only settings.

**May 31**

- fixed colour display for multiple bands
- fixed sync for inflections enable
-