Plots

A variety of plots are available in ADCI software. Dose estimation automatically generates a plot upon execution, while the other plots are generated upon request.

Zoom and pan functionality

### Feature present since ADCI version 1.9

Zoom

Zoom in and out using the mouse wheel. Note the zoom functionality zooms in on both the x and y axis. Plot axes are rescaled as necessarily while zooming. The default level of zoom ensures all data points are contained within the visible area (viewport). After zooming, please note some datapoints may be present outside the field of view. For example, the two screenshots to the right of this text depict default zoom (upper screenshot) and increased zoom (lower screenshot). The leftmost bar in the lower screenshot extends beyond the top of the plot viewport.

Pan

The plot viewport can be moved without altering the zoom level in a "drag and drop" manner by holding down the mouse button and moving the mouse. When the mouse button is held down, moving the mouse in any direction will move the viewport. When attempting to click and hold the mouse button to begin panning, ensure the cursor is within the boundaries of the plot. Attempting to pan while the cursor is outside of the plot viewport will cause the window itself to be moved instead. If this occurs it may cause the plot area to "pop out" of the main ADCI window and become a separate window. It can be reattached by simply dragging the plot area back into position in the main ADCI window.

Rescale to default position

Click the "Rescale" button above the plot viewport to reset the zoom level and pan
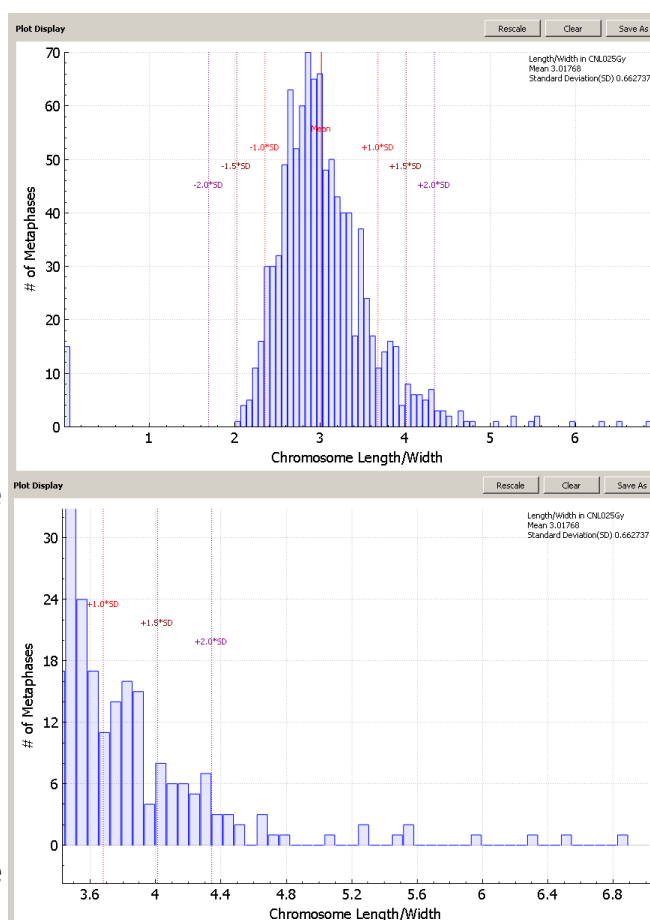
position to default.

Plot types

Calibration curve

<u>Plot generation</u>
Highlight a calibration curve within the main GUI
and click the ✎ icon. Multiple curves can be
plotted simultaneously. A color can be assigned
to a curve by highlighting the appropriate curve,
selecting a color from the color dropdown list in
the Curves section within the main GUI, and
clicking the ✎ icon.

<u>Plot description</u>

- **x-axis**
  Radiation exposure in gray (Gy)
- **y-axis**
  Number of DCs per image
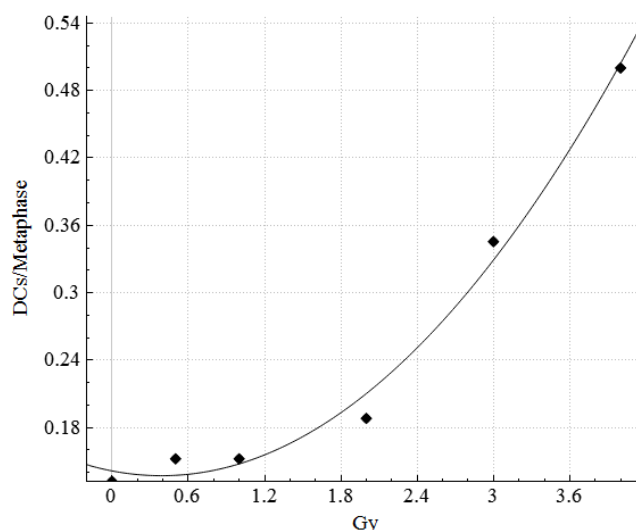
The curved line represents the value (in Gy)
which will be assigned to a sample during dose
estimation based on its calculated DC frequency.
A diamond (♦) symbol is present for each
calibration sample, based on calculated DC
frequency and the physical dose input during
calibration curve creation. If curve confidence
intervals are shown (see the calibration curve
page for more details), upper and lower 95%
confidence intervals appear as dashed lines
above and below the curve.

Dose estimation

<u>Plot generation</u>
This plot will appear when the dose estimation
process is complete.
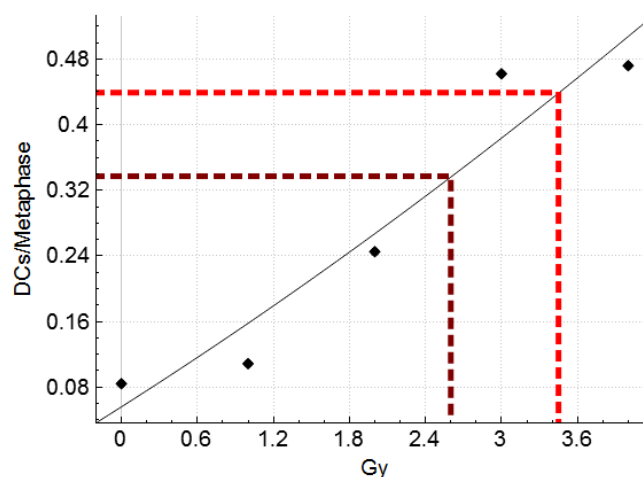
<u>Plot description</u>

- **x-axis**
  Radiation exposure in gray (Gy)
- **y-axis**
  Dicentric chromosomes per metaphase
  images

- **dotted lines**

  Each dotted line represents a DC frequency input in the Dose Calculator.

  Each DC frequency (dotted line) is colored differently. To determine which DC frequency a dotted line corresponds to, consult the output appearing in the console.

Distribution of detected DCs in Sample

<u>Plot generation</u>
Highlight a single sample within the main GUI and click the icon.

<u>Plot description</u>

- **x-axis**
  Number of dicentric chromosomes
- **y-axis**
  Frequency of metaphase images

Green bars represent the frequency at which DCs appear in metaphase images in the sample. In this example, ~26% of images in the sample contain 1 DC. The Red dashed line represents the theoretical Poisson distribution (probability of a number of independent events occurring in a fixed time interval).
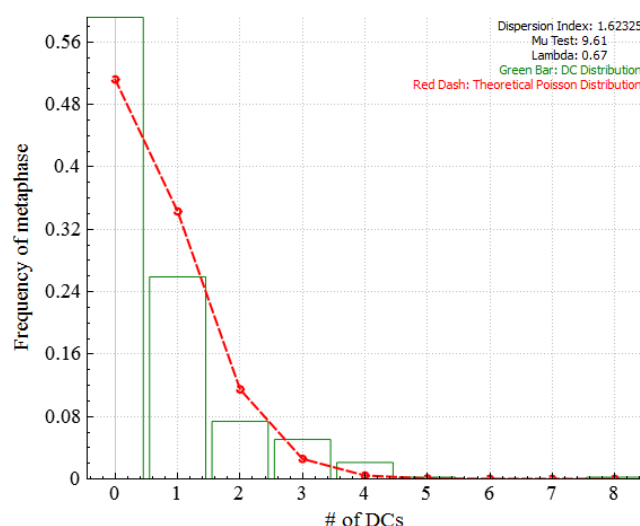
The dicentric cell distribution under full body X or gamma ray radiation is expected to form a Poisson distribution. Dispersion index and Mu test are used to test this compliance. For a Poisson distribution, the dispersion index is one. Mu test higher than 1.96 indicates over-dispersion. Mu test lower than -1.96 means under-dispersion, which is likely to indicate problems in data sampling. The theoretical Poisson distribution with the average number of DCs as Lambda is the result of fitting a Poisson distribution to the actual DC distribution using maximum likelihood estimation. The chi-square goodness of fit is calculated for the Poisson and the actual DC distribution. The result is the p-value of the hypothesis that the DC distribution

comes from the Poisson distribution.

Dicentric cell distribution will have only one bin
for cells with no DC and the p-value will be 'nan',
not-a-number, if no DC is detected in the
sample. It might be caused by a sigma value
that is too small, too few images in the sample,
or a low exposure dose of the sample.

Distribution of filtering stats for sample

Highlight a single sample and click the ▪️🟡🟢 icon to show information for a specific filtering stats. See
the Image selection model page for explanations of image filtering/selecting stats.
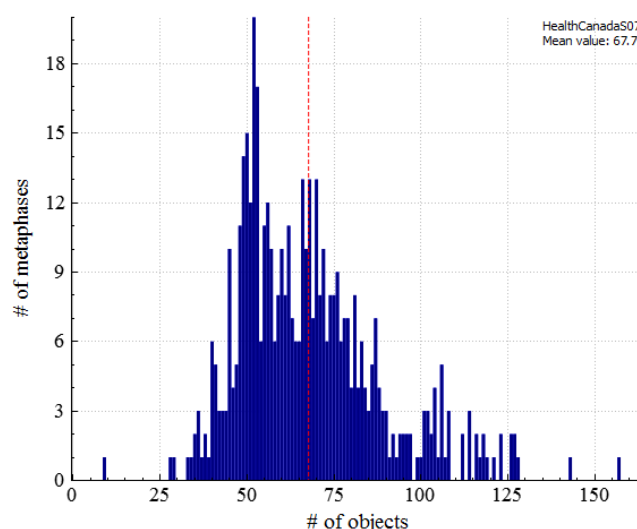
Number of objects

<u>Plot generation</u>
Highlight a single sample within the main GUI,

click the ▪️🟡🟢 icon, and select "Number of
objects" from the dropdown.

<u>Plot description</u>

- **x-axis**
  Number of objects
- **y-axis**
  Number of metaphase images

# of objects is the total number of objects found
in an image, excluding noise and nuclei. Ideally,
the object count would be 46. The plot visualizes
how frequent each object count is within a
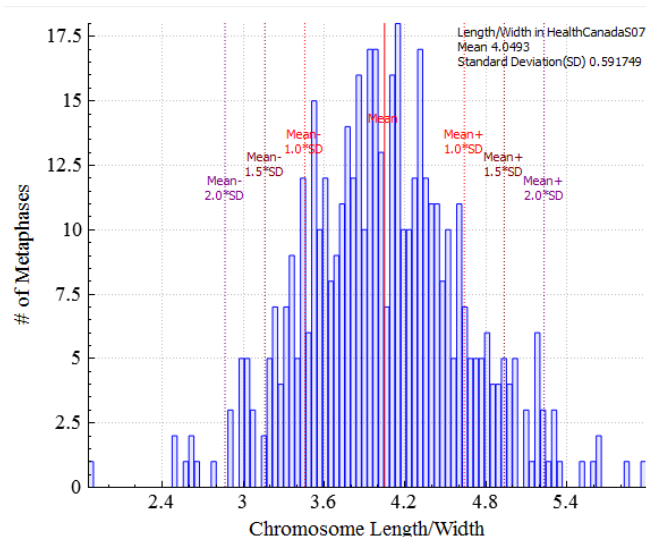sample.

Mean chromosome length/width ratio

<u>Plot generation</u>
Highlight a single sample within the main GUI,

click the ▪️🟡🟢 icon, and select "Mean chromosome
length/width radio" from the dropdown.

<u>Plot description</u>

- **x-axis**
  Chromosome length-width ratio
- **y-axis**
  Number of metaphase images

Chromosome length-width ratio is the average length-width ratio of all chromosomes in an image. ADCI software works best with chromosomes which are not too long, or too thin.
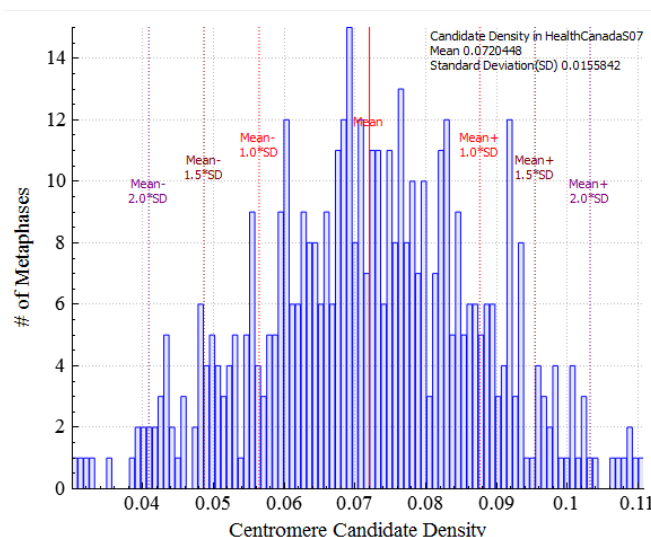

Mean candidate density

Plot generation
Highlight a single sample within the main GUI, click the ▪▌█ icon, and select "Mean candidate density" from the dropdown.

Plot description

- **x-axis**
  Centromere candidate density
- **y-axis**
  Number of metaphase images

Centromere candidate density represents average bending level of chromosomes in an image. Severely bent chromosomes generally reduce the accuracy of DC detection.

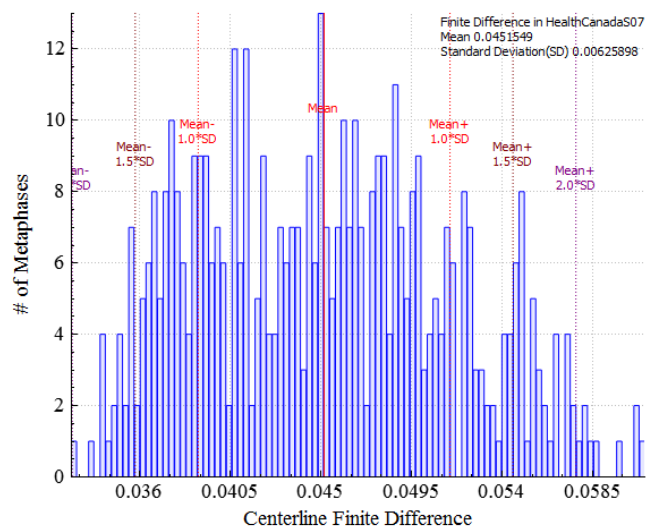## Mean Chromosome finite difference

Plot generation
Highlight a single sample within the main GUI, click the ▪▌█ icon, and select "Mean Chromosome finite difference" from the dropdown.

Plot description

- **x-axis**
  Centerline finite difference
- **y-axis**
  Number of metaphase images

Represents the average concavity level of chromosomes in an image. Chromosomes showing insufficient centromere constriction generally reduce the accuracy of DC detection.
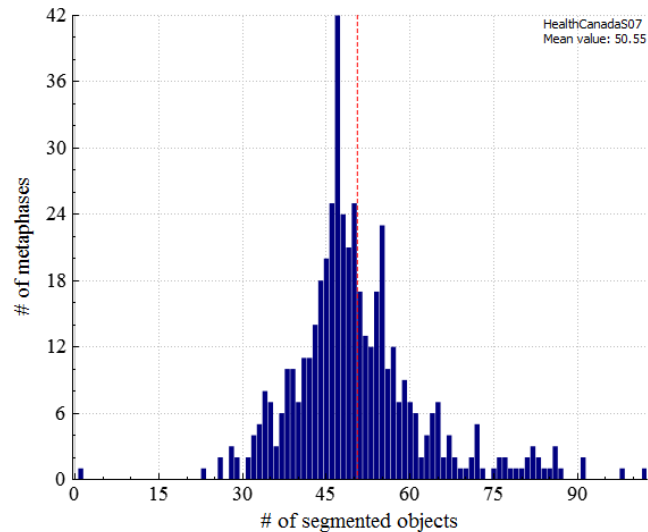

Number of segmented objects

Plot generation
Highlight a single sample within the main GUI, click the icon, and select "Number of segmented objects" from the dropdown.

Plot description

- **x-axis**
  Number of segmented objects
- **y-axis**
  Frequency of metaphase images

The number of objects processed by GVF algorithm in an image. Segmented objects (processed by GVF) are a subset of total objects. Ideally, it would also be 46. It is similar to object count, but more stringent.
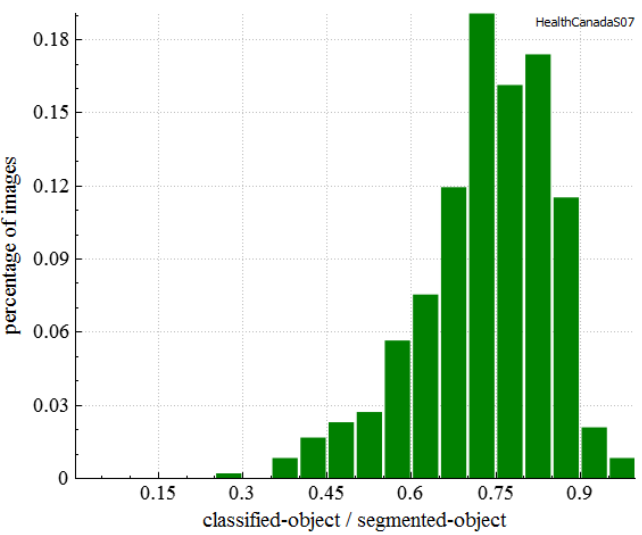
Classified object/segmented objects

Plot generation
Highlight a single sample within the main GUI, click the icon, and select "Classified object/segmented objects" from the dropdown.

Plot description

- **x-axis**
  Classified object/segmented object ratio
- **y-axis**
  Percentage of metaphase images

The ratio of objects recognized as chromosomes and segmented objects. Classified objects (recognized as chromosomes) are subset of segmented objects.
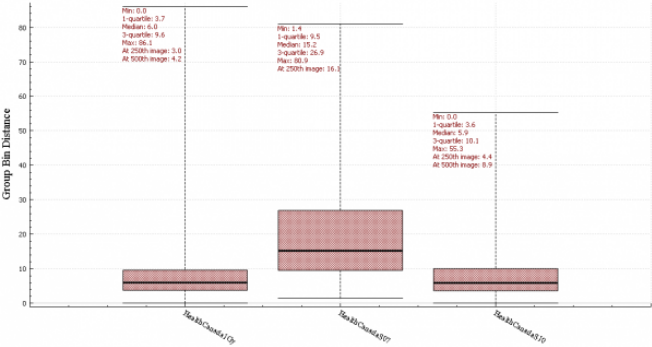

Group bin distance

Plot generation
Highlight a single sample within the main GUI, click the ▪◧▮ icon, and select "Group bin distance" from the dropdown.

Plot description

- **x-axis**
  Sample(s) in the plot
- **y-axis**
  Group bin distance

This plot is a whisker box graph demonstrating statistics of metaphase image group bin distances in sample(s). A box shows positions of the first quartile, the median and the third quartile of group bin distances in a sample. The two whiskers indicate the minimum and maximum. Text boxes display the numerical values of these stats, as well as group bin distances of the 250th image and the 500th image sorted in ascending order of group bin distances, if applicable. Multiple samples can be plotted together for comparison. If the current plot is not a group bin distance plot, it will erased and the new whisker box will be drawn. If the the current plot is a group bin distance plot, the new whisker box will be drawn as the rightmost box.