

Requirements

Reqs for addImageOmeTiff:

- The user input overlay, a SpatialOverlay object
- The user input ometiff file path (default NULL)
- The user input the res(olution) image layer to extract from the OMETIFF (default NULL)
- The user can input extra variables for imageExtraction function
- The function outputs a SpatialOverlay object
 - The function outputs extracted RGB image in object
 - The function outputs calculates and scales coordinates if initial image or at a different resolution

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-addimageometiff>

Reqs for addImageFile:

- The user input overlay, a SpatialOverlay object
- The user input imageFile path for non-OMETIFF image (default NULL)
- The user input the res(olution) image layer extracted from the OMETIFF (default NULL)
- The function outputs a SpatialOverlay object
 - The function outputs image in object
 - The function outputs calculates and scales coordinates if initial image or at a different resolution

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-addimagefile>

Reqs for add4ChannelImage:

- The user input overlay, a SpatialOverlay object
- The user input ometiff file path (default NULL)
- The user input the res(olution) image layer to extract from the OMETIFF (default NULL)
- The user can input extra variables for imageExtraction function
- The function outputs a SpatialOverlay object
 - The function outputs extracted 4-channel image in object
 - The function outputs calculates and scales coordinates if initial image or at a different resolution

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-add4channelimage>

Reqs for addPlottingFactor:

- The user input overlay, a SpatialOverlay object
- The user input annots, a NanoStringGeoMxSet, matrix, data.frame, or vector
- The user input the plottingFactor: column or row name from annots
- If using NanoStringGeoMxSet, the user input countMatrix in object to pull counts from (default “exprs”)
- The function outputs a SpatialOverlay object
 - The function outputs plottingFactor in plotFactors
 - The function matches on SampleID or if unnamed vector assumes correct order

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-addplottingfactor>

Reqs for createCoordFile:

- The user input overlay, a SpatialOverlay object
- The user input outline, only outline or all coordinates boolean (default = TRUE)
- The function outputs a SpatialOverlay object
 - The function outputs coordinates in coords
 - The function specifies workflow@scaled and workflow@outline
 - The function only returns outline coords on Geometric datasets
 - The function wraps all coordinate generating functions together to add to SpatialOverlay object

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-createcoordfile>

Reqs for createMask:

- The user input b64string, a base64 encoded string containing AOI position
- The user input metadata, metadata of AOI including height and width
- The user input outline, only outline or all coordinates boolean (default = TRUE)
- The function outputs a binary mask matrix
 - The function outputs binary matrix containing AOI position
 - The function outputs matrix in metadata specified height and width
 - The function outputs only outline coordinates if specified, else all coordinates are output

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-createmask>

Reqs for coordsFromMask:

- The user input mask, binary mask matrix
- The user input metadata, metadata of AOI including X,Y in full image
- The user input outline, only outline or all coordinates boolean (default = TRUE)
- The function outputs a data.frame of coordinate values
 - The function outputs data.frame containing X,Y coordinates of all AOIs in slide
 - The function changes coordinates from 1 base to 0 base
 - The function sorts coordinates if returning outline coords

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-coordsfrommask>

Reqs for pencilCoordSorting:

- The user input coords for an AOI
- The user input rangeWidth, distance to look for closest coord (default = 100)
- The function outputs an ordered data.frame of coordinate values
 - The function outputs data.frame containing X,Y coordinates of all AOIs in slide ordered by proximity to the previous coordinate
 - The function does not repeat coordinates

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-pencilsortingcoords>

Reqs for boundary:

- The user input mat, binary mask matrix
- The function outputs an vector
 - The function outputs vector of number of neighbors each point has

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-boundary>

Reqs for scaleCoords:

- The user input overlay, a SpatialOverlay object
- The function outputs a SpatialOverlay object
 - The function outputs SpatialOverlay object with coordinates scaled to image size
 - The function does not scale coordinates again if already scaled
 - The function does not scale coordinates if no image in object
 - The function only returns unique coordinates

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-scalecoords>

Reqs for imageColoring:

- The user input omeImage, a 4-channel AnnotatedImage object
- The user input scanMeta, scan metadata including fluorescence info
- The function outputs a AnnotatedImage object
 - The function outputs an RGB AnnotatedImage object
 - The function scales to min and max intensity if given in scanMeta
 - The function adds 4-channel RGB together for final RGB matrix
 - The function normalizes RGB matrix

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-imagecoloring>

Reqs for changeImageColoring:

- The user input overlay, a SpatialOverlay object with 4-channel image
- The user input color, new color hex or R color name
- The user input dye, Dye or DisplayName to change color of
- The function outputs a SpatialOverlay object
 - The function outputs SpatialOverlay object with fluorescence ColorCode updated
 - The function only works on objects with 4-channel images
 - The function only changes valid dye colors

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-changeimagecoloring>

Reqs for `changeColoringIntensity`:

- The user input overlay, a `SpatialOverlay` object with 4-channel image
- The user input `minInten`, new minimum intensity value (default = NULL)
- The user input `maxInten`, new maximum intensity value (default = NULL)
- The user input `dye`, `Dye` or `DisplayName` to change color of
- The function outputs a `SpatialOverlay` object
 - The function outputs `SpatialOverlay` object with fluorescence `MinIntensity` and/or `MaxIntensity` updated
 - The function only works on objects with 4-channel images
 - The function only changes valid dye colors

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-changecoloringintensity>

Reqs for `recolor`:

- The user input overlay, a `SpatialOverlay` object with 4-channel image
- The function outputs a `SpatialOverlay` object
 - The function outputs `SpatialOverlay` object with RGB image
 - The function only works on objects with 4-channel images
 - The function only scales coordinates if needed
 - The function crops to tissue

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-recolor>

Reqs for `flipY`:

- The user input overlay, a `SpatialOverlay` object
- The function outputs a `SpatialOverlay` object
 - The function outputs `SpatialOverlay` object with Y axis flipped
 - The function flips image and coordinates

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-flipy>

Reqs for `flipX`:

- The user input overlay, a `SpatialOverlay` object
- The function outputs a `SpatialOverlay` object
 - The function outputs `SpatialOverlay` object with X axis flipped
 - The function flips image and coordinates

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-flipx>

Reqs for cropSamples:

- The user input overlay, a SpatialOverlay object
- The user input sampleIDs, sampleIDs of AOIs to include
- The user input buffer, percent of image to add on each edge (default = 0.1)
- The user input sampsWithOnly, only show given samples (default = TRUE)
- The function outputs a SpatialOverlay object
 - The function outputs SpatialOverlay object with cropped image and coordinates only showing given samples
 - The function only works on valid sampleIDs
 - The function only works on RGB images
 - The function requires coordinates to be generated
 - The function requires image in overlay
 - The function generates min/max coords to crop on given sampleIDs
 - The function filters coordinates to only given sampleIDs if desired

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-cropsamples>

Reqs for cropTissue:

- The user input overlay, a SpatialOverlay object
- The user input buffer, percent of image to add on each edge (default = 0.05)
- The function outputs a SpatialOverlay object
 - The function outputs SpatialOverlay object with cropped image and coordinates minimizing black background around tissue
 - The function can work on 4-channel or RGB image
 - The function requires coordinates to be generated with RGB image
 - The function requires image in overlay
 - The function generates min/max coords to crop on tissue

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-croptissue>

Reqs for xmlExtraction:

- The user input ometiff, file path
- The user input saveFile, boolean (default = FALSE)
- The function outputs a list
 - The function outputs list containing all xml info
 - The function only works on valid paths
 - The function saves file to same folder as ometiff if desired

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-xml extraction>

Reqs for imageExtraction:

- The user input ometiff, file path
- The user input res(olution), image layer to extract from the OMETIFF (default = 6)

- The user input scanMeta, scan metadata from XML (default = NULL)
- The user input saveFile, boolean (default = FALSE)
- The user input fileType, image type to save as (default = “tiff”)
- The user input color, turn into RGB image boolean (default = TRUE)
- The function outputs an image
 - If color == TRUE
 - * The function outputs magick-image pointer
 - * The function colors image
 - * The function saves image to same folder as ometiff if desired
 - * The function only saves to valid fileTypes
 - If color == FALSE
 - * The function outputs AnnotatedImage
 - The function only works on valid paths
 - The function only extracts valid res layers
 - The function extracts scanMeta if NULL

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-imageextraction>

Reqs for checkValidRes:

- The user input ometiff, file path
- The function outputs an numeric
 - The function returns highest valid res(olution) value for ometiff

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-checkvalidres>

Reqs for plotSpatialOverlay:

- The user input overlay, file path
- The user input colorBy, coloring factor (default = “sampleID”)
- The user input hiRes(olution) plotting boolean (default = TRUE)
- The user input alpha, opacity value (default = 1)
- The user input legend, show legend boolean (default = TRUE)
- The user input scaleBar, show scale bar boolean (default = TRUE)
- The user input image, show image boolean (default = TRUE)
- The user input fluorLegend, show fluorescence legend (default = FALSE)
- The user input ..., extra values for scale bar plotting
- The user input corner, scale bar corner (default = “bottomright”)
- The user input scaleBarWidth, scale bar width of image percentage (default = 0.2)
- The user input scaleBarColor, scale bar color (default = “black”)
- The user input scaleBarFontSize, scale bar font size value (default = 6)
- The user input scaleBarLineSize, scale bar line size value (default = 1.5)
- The user input textDistance, distance of text from line value (default = 2)
- The function outputs a ggplot object
 - The function recolors image if 4-channel is given
 - The function only works on valid plotFactors unless sampleID is given
 - The function only adds fluorLegend if image = TRUE and desired regardless of plotting call
 - The function adds image to background if image = TRUE

- The function uses image coordinates if image is attached even with image = FALSE
- The function removes legend if desired
- The function adds scalebar if desired
- The function customizes scale bar

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-plotspatialoverlay>

Reqs for scaleBarMath:

- The user input scanMetadata, scan metadata from XML specifically PhysicalX/Y
- The user input pts, coordinate data.frame
- The user input scaleBarWidth, percent of image value (default = 0.2)
- The user input image, image from SpatialOverlay (default = NULL)
- The function outputs a list
 - The function returns list of values to print scale bar
 - The function works with or without image
 - The function calculates scale bar width based on um/pixel ratio
 - The function works on all resolutions
 - The function only creates scale bars with round values

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-scalebarmath>

Reqs for scaleBarCalculation:

- The user input corner, location for scale bar (default = “bottomright”)
- The user input scaleBar, list from scaleBarMath
- The user input textDistance, distance of text from line value (default = 2)
- The function outputs a data.frame
 - The function returns data.frame of coordinates for scale bar
 - The function only works with valid corner
 - The function calculates scale bar coordinates

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-scalebarcalculation>

Reqs for scaleBarPrinting:

- The user input gp, ggplot object
- The user input scaleBar, list from scaleBarMath
- The user input corner, distance of text from line value (default = 2)
- The user input scaleBarFontSize, scale bar font size value (default = 6)
- The user input scaleBarLineSize, scale bar line size value (default = 1.5)
- The user input scaleBarColor, scale bar color (default = “red”)
- The user input textDistance, distance of text from line value (default = 2)
- The user input image, image from SpatialOverlay (default = NULL)
- The user input ..., extra values for scale bar plotting
- The function outputs a ggplot object
 - The function returns ggplot with added scale bar

- The function works with or without image
- The function customizes scale bar

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-scalebarprinting>

Reqs for `fluorLegend`:

- The user input overlay, `SpatialOverlay` object
- The user input nrow, number of rows value (default = 4)
- The user input textSize, font size value (default = 10)
- The user input boxColor, color of background (default = “grey”)
- The user input alpha, opacity value (default = 0.25)
- The function outputs a ggplot object
 - The function returns ggplot of visualization marker legend
 - The function only works with valid nrows
 - The function colors Target based on ColorCode
 - The function adds background based on user input

Specifications:

Reqs for `readSpatialOverlay`:

- The user input ometiff, file path
- The user input annots, file path or `GeomxSet` object
- The user input slideName, name of slide
- The user input image, add image boolean (default = FALSE)
- The user input res, image layer to extract from the OMETIFF (default = NULL)
- The user input saveFile, save file boolean (default = FALSE)
- The user input outline, outline coords only boolean (default = TRUE)
- The function outputs a `SpatialOverlay` object
 - The function returns starting point `SpatialOverlay`
 - The function annotations can be `NanostringGeomxSet`, `labWorksheet`, or `DSPDA` output
 - The function is a wrapper for extracting XML, add scan metadata, add overlay attrs, determine dataset segmentation, add image, generate coordinates

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-readspatialoverlay>

Reqs for `removeSample`:

- The user input overlay, `SpatialOverlay` object
- The user input remove, sampleIDs to remove
- The function outputs a `SpatialOverlay` object
 - The function returns a `SpatialOverlay` without sampleIDs to remove
 - The function only works on valid sampleIDs
 - The function removes samples across all parts of the `SpatialOverlay` object
 - The function determines if dataset segmentation type

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-removesamples>

Reqs for bookendStr:

- The user input x, string
- The user input bookend, length of bookend value (default = 8)
- The function outputs a string
 - The function returns a string small enough to be legible
 - The function returns first bookend ... last bookend (# total char)

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-bookendstr>

Reqs for readLabWorksheet:

- The user input lw, labworksheet file path
- The user input slideName, slide name
- The function outputs a data.frame
 - The function returns a data.frame with AOI annotations
 - The function only works on valid lw
 - The function only works with valid slide name

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-readlabworksheet>

Reqs for downloadMouseBrainImage:

- The function outputs a tiff file path
 - The function returns a cached tiff file path for Spatial Organ Atlas Mouse Brain OMETIFF
 - The function downloads and untars file if not already cached

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-downloadmousebrainimage>

Reqs for parseScanMetadata:

- The user input omexml, xml list
- The function outputs a list
 - The function returns a list of scan metadata including panel, physical size and fluorescence data
 - The function can handle omexml being the file path to ometiff

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-downloadmousebrainimage>

Reqs for parseOverlayAttrs:

- The user input omexml, xml list
- The user input annots, data.frame of annotations
- The user input labworksheet, is annot labworksheet boolean
- The function outputs a SpatialPosition

- The function returns a list of AOI metadata including AOI height, width, and location
- The function can handle xml files from multiple software versions
- The function only returns AOIs in both XML and annots

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-parseoverlayattrs>

Reqs for physicalSizes:

- The user input omexml, xml list
- The function outputs a list
 - The function returns a list of PhysicalSizes from xml

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-physicalsizes>

Reqs for fluorData:

- The user input omexml, xml list
- The function outputs a data.frame
 - The function returns a data.frame of fluorescence data from xml including: dye, displayname, color, wavelength, target, exposure time, colorcode, and min/max intensities if available.
 - The function can work if fluorescence data takes 1 or 2 slots in XML

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-fluordata>

Reqs for decodeB64:

- The user input b64string, base 64 location string
- The user input width, width of AOI
- The user input height, height of AOI
- The function outputs a vector
 - The function returns a binary vector of AOI position

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-decodeb64>

Reqs for annotMatching:

- The user input annots, data.frame of annotations
- The user input ROI num, ROI number from xml
- The user input maskNum, number of masks in ROI
- The user input maskText, segment name
- The function outputs a data.frame
 - The function returns a data.frame of the matching sampleID
 - The function only works on valid ROI numbers
 - The function can work on multiple versions of the software

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-annotmatching>

Reqs for SpatialOverlay-class:

- The class contains all info pertaining to image
 - The class contains slideName
 - The class contains scanMetadata
 - * List of panel, physicalsize, and fluorescence
 - The class contains overlayData
 - * SpatialPosition
 - The class contains coords
 - The class contains plottingFactors
 - * Added individually
 - The class contains workflow
 - * Workflow booleans that affect downstream analysis: outline, labworksheet, scaled
 - The class contains image
 - * list of image related info: filePath, imagePointer, resolution
- The class contains accessors and replacers where necessary

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-spatialoverlay-class>

Reqs for SpatialPosition-class:

- The class contains all info pertaining to position in space
 - The class contains ROILabel
 - The class contains Sample_ID
 - The class contains Height
 - The class contains Width
 - The class contains X
 - The class contains Y
 - The class contains Segmentation
 - The class contains Position
 - * Base64 encoded string
- The class contains accessors and replacers where necessary

Specifications

Specifications: <https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/main/specs.md#specs-for-spatialposition-class> ##### Specs for addImageOmeTiff:

1. The function outputs a list in the image slot containing the expected filePath, imagePointer, and resolution.

test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_addImage.R#L11 2. The imagePointer is a magick-image with the correct dimensions.

test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_addImage.R#L26 3. The function scales the coordinates.

test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_addImage.R#L42 4. The function produces reproducible results.

test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_addImage.R#L36

Specs for add4ChannelImage:

1. The function outputs a list in the image slot containing the expected filePath, imagePointer, and resolution.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addImage.R#L77
2. The imagePointer is an AnnotatedImage with the correct dimensions.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addImage.R#L92
3. The function scales the coordinates.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addImage.R#L101

Specs for addImageFile:

1. The function outputs a list in the image slot containing the expected filePath, imagePointer, and resolution.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addImage.R#L130
2. The imagePointer is a magick-image with the correct dimensions.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addImage.R#L140
3. The function scales the coordinates.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addImage.R#L151
4. The function produces reproducible results.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addImage.R#L146

Specs for addPlottingFactor:

1. The function only works on one factor at a time regardless of input type.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addPlottingFactor.R#L16
2. The function gives warning for annotation missing for samples in object regardless of input type.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addPlottingFactor.R#L30
3. The function works with a data.frame input, column name plotting factor.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addPlottingFactor.R#L18
4. The function works with a data.frame input, row name plotting factor.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addPlottingFactor.R#L32
5. The function works with a matrix input, column name plotting factor.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addPlottingFactor.R#L46
6. The function works with a matrix input, row name plotting factor.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addPlottingFactor.R#L59
7. If vectors aren't named they must be the same length as number of samples in object.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addPlottingFactor.R#L71

8. The function only matches vectors if they are named, otherwise assumed in correct order.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addPlottingFactor.R#L77
9. The function works with character vectors.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addPlottingFactor.R#L79
10. The function works with factor vectors.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addPlottingFactor.R#L97
11. The function works with numeric vectors.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addPlottingFactor.R#L116
12. The function works with a NanostringGeomxSet input, column name plotting factor.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addPlottingFactor.R#L139
13. The function works with a NanostringGeomxSet input, row name plotting factor.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addPlottingFactor.R#L148

Specs for decodeB64:

1. The function produces same values as python truth.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_coordinateGeneration.R#L19

Specs for createMask: When outline == FALSE,

1. The function creates mask in correct dimension.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_coordinateGeneration.R#L31
2. The function produces same values as python truth.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_coordinateGeneration.R#L33
3. The function produces mask of only 0 & 1.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_coordinateGeneration.R#L35
4. The function creates matrix.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_coordinateGeneration.R#L37

When outline == TRUE,

1. The function creates mask in correct dimension.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_coordinateGeneration.R#L59
2. The function has fewer matches with the python truth.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_coordinateGeneration.R#L61
3. The function produces mask of only 0 & 1.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_coordinateGeneration.R#L64

4. The function creates matrix.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_coordinateGeneration.R#L66
5. The function create mask with < 0.1% of points with 7 or more neighbors.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_coordinateGeneration.R#L69

Specs for coordsFromMask: When outline == FALSE,

1. The function creates coordinates for mask = 1 points. Coordinates are put into full image range and changed from base1 to base0.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_coordinateGeneration.R#L42

When outline == TRUE,

1. The function creates coordinates for mask = 1 points. Coordinates are put into full image range and changed from base1 to base0.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_coordinateGeneration.R#L74

Specs for pencilSortingCoords:

1. The function sorts outline coordinates by proximity. >99% of differences between adjacent coordinates is 1.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_coordinateGeneration.R#L101
2. The function sorts outline coordinates by proximity. The max difference is <100.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_coordinateGeneration.R#L104

Specs for createCoordFile:

1. The function places coordinates in correct location.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_coordinateGeneration.R#L118
2. The function produces same values as python truth.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_coordinateGeneration.R#L125
3. The function only returns outline coordinates on Geometric data.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_coordinateGeneration.R#L136

Specs for Boundary:

1. The function returns expected number of neighbors.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_coordinateGeneration.R#L145

Specs for scaleCoords:

1. The function scales the coordinates based on the size of the image.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addImage.R#L46
2. The coordinates are all smaller than the image size.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addImage.R#L54
3. There are no duplicated coordinates.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addImage.R#L61
4. Coordinates can't be rescaled.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addImage.R#L67
5. An image must be in object to scale coordinates.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_addImage.R#L69

Specs for xmlExtraction:

1. The function only works with valid ometiff file.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_extraction.R#L4
2. The function returns a valid list with the expected names.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_extraction.R#L12
3. The function saves xml file in expected location, if desired.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_extraction.R#L19
4. The function doesn't save file when not asked.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_extraction.R#L28

Specs for imageExtraction:

1. The function only extracts valid res layers.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_extraction.R#L38
2. The function extracts expected res layer.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_extraction.R#L40
3. The function saves file in expected location and in correct & valid fileType.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_extraction.R#L50

Specs for checkValidRes:

1. The function returns expected value.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_extraction.R#L85

Specs for cropTissue:

1. The function returns smaller image.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L10
2. The function returns all original coordinates.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L16
3. The function produces reproducible results.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L19

Specs for cropSamples: When sampOnly = TRUE,

1. The function returns smaller image.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L28
2. The function returns all coordinates of only the given samples.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L34
3. The function produces reproducible results.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L39

When sampOnly = FALSE

1. The function returns smaller image.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L44
2. The function returns all coordinates of the given samples.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L50
3. The function returns coordinates within dimensions of cropped image.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L55
4. The function produces reproducible results.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L66
5. The function only works with valid sampleIDs.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L69

Specs for flipX:

1. The function returns expected coordinates.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L80
2. The function produces reproducible results.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L85

Specs for flipY:

1. The function returns expected coordinates.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L90
2. The function produces reproducible results.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L95

Specs for changeColoringIntensity:

1. The function only works on 4-channel images.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L100
2. The function changes min/max intensity values of only correct fluor.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L110

Specs for changeImageColoring:

1. The function only works on 4-channel images.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L103
2. The function changes ColorCode values of only correct fluor.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L132

Specs for imageColoring:

1. The function creates RGB image arrays.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L157
2. The function produces reproducible results.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L162

Specs for recolor:

1. The function scales coordinates.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L170
2. The function creates RGB image arrays.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L178
3. The function produces reproducible results.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_imageManipulation.R#L184

Specs for parseScanMetadata:

1. The function works on ometiff variable instead of expected xml.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_parsing.R#L12
2. The function returns a list with all of the expected names.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_parsing.R#L18

Specs for fluorData:

1. The function works on xmls where fluor data takes up 1 or 2 lines.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_parsing.R#L44
2. The function returns a data.frame with all of the expected values.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_parsing.R#L72

Specs for physicalSizes:

1. The function works returns list with expected names & values.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_parsing.R#L91

Specs for parseOverlayAttrs:

1. The function requires correct labworksheet boolean.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_parsing.R#L105
2. The function only works with valid sample names.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_parsing.R#L112
3. The function returns SpatialPosition with correct column names.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_parsing.R#L122

Specs for annotMatching:

1. The function matches sampleIDs correctly between xml and annots.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_parsing.R#L138

Specs for plotSpatialOverlay:

1. The function requires valid colorBy variable.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_plotting.R#L22
2. The function returns a ggplot object for high resolution, low resolution and outline graphing.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_plotting.R#L30

3. The function returns a ggplot object without legend if desired.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L51
4. The function returns a ggplot object with fluorescence legend if desired.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L58
5. The function works on with both 4-channel and RGB images.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L250
6. The function produces reproducible figures. test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L37

Specs for scaleBarMath:

1. The function expects size to be between 0-1.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L113

Without image

2. The function returns a list with the expected names and values.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L117
3. The function returns a um value in valid sizes.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L135
4. The function calculates the number of pixels for scale bar correctly.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L141

With image

2. The function returns a list with the expected names and values.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L288
3. The function returns a um value in valid sizes.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L306
4. The function calculates the number of pixels for scale bar correctly.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L312

Specs for scaleBarCalculation:

1. The function only works with valid corner value.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L147

Without image

2. The function returns a list of numeric values.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L150
3. The function calculates the scale bar points the same across the different corner options.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L154

With image

2. The function returns a list of numeric values.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L321
3. The function calculates the scale bar points the same across the different corner options.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L325

Specs for scaleBarPrinting: Without image,

1. The function only works with valid corner value.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L224
2. The function produces a ggplot object.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L228
3. The function produces reproducible figures. test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L232

With image

2. The function produces a ggplot object.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L395
3. The function produces reproducible figures. test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L399

Specs for fluorLegend:

1. The function only works on valid nrow values.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L405
2. The function produces reproducible legends. test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_plotting.R#L408

Specs for readSpatialOverlay:

1. The function works with either a labworksheet or a geomxset object as annotation.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e308/longtests/testthat/test_readSpatialOverlay.R#L13

2. The function only returns samples in both xml and annotation.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_readSpatialOverlay.R#L25

With all points

1. The function returns a SpatialOverlay object.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_readSpatialOverlay.R#L32
2. The function returns a SpatialOverlay object with the expected values in the correct locations.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_readSpatialOverlay.R#L35

With image

1. The function returns a SpatialOverlay object.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_readSpatialOverlay.R#L62
2. The function returns a SpatialOverlay object with the expected values in the correct locations.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_readSpatialOverlay.R#L65
3. The function returns a SpatialOverlay object with image in expected location.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_readSpatialOverlay.R#L82
4. The function returns a SpatialOverlay object with scaled coordinates to image.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_readSpatialOverlay.R#L88

With boundary points

1. The function returns a SpatialOverlay object.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_readSpatialOverlay.R#L97
2. The function returns a SpatialOverlay object with the expected values in the correct locations.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_readSpatialOverlay.R#L100

Specs for removeSamples:

1. The function only works on valid sample names.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_removeSamples.R#L25
2. The function works before adding coordinates and plotting factors.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_removeSamples.R#L31
3. The function works after adding coordinates and before plotting factors.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_removeSamples.R#L49
4. The function works after adding coordinates and plotting factors.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e30longtests/testthat/test_removeSamples.R#L67

Specs for SpatialOverlay-class:

1. The class is formatted correctly.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_SpatialOverlay.R#L17
2. The class accessors work as expected.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_SpatialOverlay.R#L45
3. The class replacers work as expected.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_SpatialOverlay.R#L89

Specs for SpatialPosition-class:

1. The class is formatted correctly.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_SpatialPosition.R#L11
2. The class accessors work as expected.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_SpatialPosition.R#L32

Specs for bookendStr:

1. The function returns a string in the expected format.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_utils.R#L3

Specs for readLabWorksheet:

1. The function only works on correct file paths.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_utils.R#L24
2. The function only works on correct slide names.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_utils.R#L26
3. The function only returns annotations from the specified slide.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_utils.R#L29

Specs for downloadMouseBrainImage:

1. The function downloads the mouse brain tiff and returns a valid file path.
test: https://github.com/Nanostring-Biostats/SpatialOmicsOverlay/blob/c427265120cc9835f1443541d68a22901195e300longtests/testthat/test_utils.R#L49