Overview of procedure to process a STXM stack

Read stack

1. **read~STXM(sdf)** or **read~STXM(NeXus)**
2. **browse to file – click on name**
3. **select region** (1 = I, 2 = Io for example)
4. **select channel** (counter 0, SiPD etc)
5. **click 'OK'** ➔ reads images
6. **define file name** (e.g. use the index 11_100912034 → 34)
7. **choose zoom** (stack_analyze widget size) choose default

Inspect data

1. **play movie** to check quality – remove bad images etc
2. identify Io regions (see below)
3. **Dismiss** stack process

drifts ?

yes

Align data

1. **read in** stack to stacks~analyze~**Zimba**
   OR stacks~analyze~ **Jacobsen stack analyze**
2. **click on Auto alignment** (zimba) or
   file~align~start aligning
3. **save *.aln file** or save new alignment (multiple)
4. **read in** to stack_analyze~axis binary
5. **select *.aln file**
6. **write out** & trim (*a.ncb) [(*.a2.ncb) if twice etc]

no

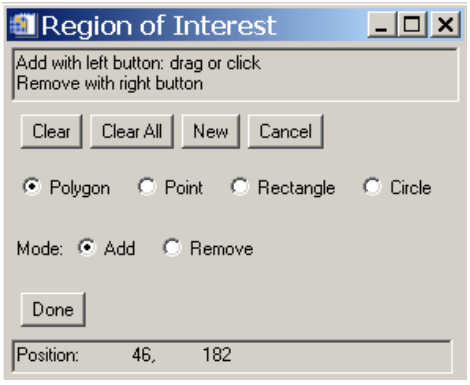
convert to OD & save

2. **select Io region** (if one in stack) OR
   read Io from file (recorded separately, or ROI, etc)
3. **convert to OD**
4. **SAVE stack** (➔ ##jod.ncb) - use systematice naming

use Zimba viewer to view & document

1. **read in aligned, OD stack** to stacks~analyze~Zimba
2. **skip alignment – go to Zstack spectra**
3. **add I region(s)** in areas with different morphologies
4. **screen capture** images, spectra plots to ppt to document
5. **save *.xas** to use as reference spectra in fitting

Further processing - see other manual pages



- Generating quantitative reference spectra
- Fitting stacks to make chemical maps
- Checking quality of fits in spectral space