|      | <pre>for j in range(0, len(atomplane.atom_list)):     atom=atomplane.atom_list[j]     x_pos,y_pos=atom.get_pixel_position()     intensity=atom.intensity_mask     plane_intensity.append(intensity)     x_values_plane.append(x_pos)     y_values_plane.append(y_pos)     intensity_A.append(plane_intensity)     x_values_append(x_values_plane)     y_values.append(x_values_plane)     y_values.append(y_values_plane)  intensity_A_array = np.zeros([len(intensity_A),len(max(intensity_A,key = lambda x: len(x)))]) intensity_A_array[:] = np.nan for i, j in enumerate(intensity_A):     intensity_A_array[i][0:len(j)] = j  x_values_array[:] = np.nan for i, j in enumerate(x_values):     x_values_array[i][0:len(j)] = j  y_values_array = np.zeros([len(x_values),len(max(y_values,key = lambda x: len(x)))])</pre>  |
|------|---|
| [6]: | <pre>y_values_array[:] = np.nan for i, j in enumerate(y_values):     y_values_array[i][0:len(j)] = j intensity_A=np.stack((intensity_A_array, x_values_array), axis=2) np.save('intensity_A.npy', intensity_A)  The circles represent the atom columns of the sublattice A at their respective positions. But the circle sizes are not the same as the atom column sizes due to the splitting into two sublattices.  Uncomment plt.imshow(s.data, cmap='gray') to additionally plot the original image.  plt.figure() plt.scatter(intensity_A[:,:,1], intensity_A[:,:,2], s=20, c=intensity_A[:,:,0]) plt.colorbar() plt.axis('scaled') plt.axis('scaled') plt.axis('sff') ax_plt.gca() ax.set_ylim(ax.get_ylim()[::-1]) ax.sat_ylim(ax.get_ylim()[::-1]) ax.yaxis.tick_top() ax_yaxis.tick_top() ax_yaxis.tick_top() plt.simbnow(s.data_cmap='gray') plt.simbnow(s.data_cmap='gray') plt.simbnow(s.data_cmap='gray') plt.savefig('intensitymap_sublatticeA.png',dpi=300,transparent=True,bbox_inches='tight')</pre>  |
|      | Figure 2  - 0.090 - 0.085   |
|      | - 0.080   |
| [7]: | For the sublattice B, the same process is followed.  Constructing the zone axes:  sublattice_B.construct_zone_axes(atom_plane_tolerance=0.8)  Selecting the optimal zone axis:  direction=0   |
| 8]:  | <pre>zone_vector = sublattice_B.zones_axis_average_distances[direction] atom_planes = sublattice_B.atom_planes_by_zone_vector[zone_vector] zone_axis = sublattice_B.get_atom_planes_on_image(atom_planes) zone_axis.plot() ax = plt.gca() ax.get_xaxis().set_visible(False) ax.get_yaxis().set_visible(False) sublattice_B  <pre> <sublantice, (atoms:2360,="" planes:6)=""></sublantice,></pre>  Figure 3  Signal  -0.095 -0.090</pre>   |
|      | - 0.085 - 0.080 - 0.075 - 0.070 - 0.065 - 0.060   |
| 9]:  | Selecting the required layers:  first_layer = 0 last_layer = 39  sublattice_B.find_sublattice_intensity_from_masked_image(sublattice_B.image) zone_axis_B = sublattice_B.zones_axis_average_distances[direction] atom_plane_list_B = sublattice_B.atom_planes_by_zone_vector[zone_axis_B] intensity_B=[] x_values=[] y_values=[] y_values=[] plane_intensity=[] x_values_plane=[] y_values_plane=[] y_values_plane=[] y_values_plane=[] for j in range(0, len(atomplane.atom_list)):  |
|      | atom=atomplane.atom_list[j]     x_pos, y_pos=atom.get_pixel_position()     intensity=atom.intensity.mask     plane_intensity.append(intensity)     x_values_plane.append(x_pos)     y_values_plane.append(y_pos)     intensity_B_append(plane_intensity)     x_values.append(x_values_plane)     y_values.append(x_values_plane)  intensity_B_array = np.zeros([len(intensity_B),len(max(intensity_B,key = lambda x: len(x)))]) intensity_B_array[] = np.nan  for i,j in enumerate(intensity_B):     intensity_B_array[i][0:len(j)] = j  x_values_array = np.zeros([len(x_values),len(max(x_values,key = lambda x: len(x)))]) x_values_array[:] = np.nan  for i,j in enumerate(x_values):     x_values_array[i][0:len(j)] = j  y_values_array = np.zeros([len(y_values),len(max(y_values,key = lambda x: len(x)))]) y_values_array[:] = np.nan  for i,j in enumerate(y_values):     x_values_array[:] = np.nan  for i,j in enumerate(y_values):     y_values_array[:] = np.nan  |
| .O]: | <pre>intensity_B=np.stack((intensity_B_array,x_values_array,y_values_array),axis=2) np.save('intensity_B.npy',intensity_B)  Plotting the intensity map of the sublattice B:  Uncomment plt.imshow(s.data,cmap='gray') to additionally plot the original image.  plt.figure() plt.scatter(intensity_B[:,:,1],intensity_B[:,:,2],s=20,c=intensity_B[:,:,0]) plt.axis('scaled') plt.axis('scaled') plt.axis('off') ax=plt.gca() ax.set_ylim(ax.get_ylim()[::-1]) ax.yaxis.tick_left() # plt.imshow(s.data,cmap='gray') plt.tight_layout() plt.show(s.data,cmap='gray') plt.tight_layout() plt.savefig('intensitymap_sublatticeB.png',dpi=300,transparent=True,bbox_inches='tight')</pre>   |
|      | Figure 4  - 0.090 - 0.085   |
|      | - 0.080   |
| I    | Thickness compensation  If the quantum well has only one element in a sublattice, we can use it to perform thickness compensation (for the other sublattice). It is mandatory that the two sublattices have the same dimension because the 2D array of the group III sublattice will be divided element-by-element by the normalized 2D array of the group V sublattice. $I_{comp_{i,j}} = \frac{I_{gIII_{i,j}}}{I_{gV norm_{i,j}}}$ group_III_sublattice and group_V_sublattice must be selected between intensity_A and intensity_B.  |
| .1]: | <pre>Uncomment plt.imshow(s.data,cmap='gray') to additionally plot the original image.  group_III_sublattice=np.copy(intensity_A) group_V_sublattice=np.copy(intensity_B)  from atomap.atom_finding_refining import normalize_signal normalized_V = normalize_signal(hs.signals.Signal2D(group_V_sublattice[:,:,0])) compensated_III=np.divide(group_III_sublattice[:,:,0],normalized_V.data) group_III_sublattice[:,:,0]=np.copy(compensated_III) plt.figure() plt.satter(group_III_sublattice[:,:,1],group_III_sublattice[:,:,2],s=20,c=group_III_sublattice[:,:,0]) plt.colorbar() plt.axis('scaled') plt.axis('scaled') plt.axis('sff') ax_plt.gca() ax.set_ylim(ax.get_ylim()[::-1]) ax.saty.lim(ax.get_ylim()[::-1]) ax.xaxis.tick_top() ax.yaxis.tick_left() bt.fight_layout() plt.show() data_a,cmap='gray') plt.sight_layout() plt.show() intensitymap_groupIII_compensated.png',dpi=300,transparent=True,bbox_inches='tight')</pre>   |
|      | np.save('group_V_sublattice.npy',group_V_sublattice)  Figure 5  - 0.110 - 0.105   |
|      | - 0.095<br>- 0.090<br>- 0.085   |
| 7    | Composition maps The composition map of the segregated element present in the sublattice III is very similar to the intensity map, since to obtain it, the intensity map must be normalized according to the nominal composition of the element.  To obtain the composition map, the average intensities of two reference regions (the quantum well and the barriers) are calculated. Then, the intensity map is normalized with these two values and the nominal composition $x_0$ (Han et al., 2015):   |
| .2]: | $x = \frac{x_0(I_{czp} - I_{Ga})}{I_{GaIn} - I_{Ga}}$ First, we select the <code>required_sublattice</code> : required_sublattice=np.copy(group_III_sublattice)  To get the average intensities, we select the upper and lower limit using the histogram of the average intensity plot: $avg\_i=np.mean(required\_sublattice[:,:,0], axis=0) \\ avg\_ax=np.mean(required\_sublattice[:,:,1], axis=0)*s.axes\_manager[0].scale$ from scipy.stats <code>import</code> binned_statistic from scipy.signal <code>import</code> find_peaks count_binned_statistic(avg\_i, avg\_i, 'count', bins=10) bin_centers=(count_binned[statistic(avg_i, avg\_i, 'mean', bins=10)) pos_peaks_peaks[n_argsort(count_binned[0], height=0) pos_peaks_sorted=mean_binned[0][n_argsort(count_binned[0)][pos_peaks])] peaks_sorted=mean_binned[0][pos_peaks_sorted] maxi_pos_max2_pos=np.sort(peaks_sorted][0] == max1[0], np.where(mean_binned[0] == max2)[0]   |
|      | <pre>lower_limit=count_binned[1][max1_pos+1] upper_limit=count_binned[1][max2_pos]  fig, (ax1, ax2) = plt.subplots(2, 1) ax1.plot(avg_ax,avg_i,'*') ax1.set(xlabel='Position ['+s.axes_manager[0].units+']',ylabel='Average intensity') label1='Lower limit: %.5f' % (lower_limit) label2='Upper limit: %.5f' % (upper_limit) ax1.plot(avg_ax, [lower_limit]*len(avg_i), linestyle='', color='red', alpha=0.5, label=label1) ax1.plot(avg_ax, [upper_limit]*len(avg_i), linestyle='', color='orange', alpha=0.5, label=label2) ax1.legend(), patches = ax2.hist(avg_i, bins=count_binned[1], color='lightblue') for i in (np.where(np.arange(0, len(patches))&lt;=max1_pos))[0]:     patches[int(i)].set_fc('lightcoral') for i in (np.where(np.arange(0, len(patches))&gt;=max2_pos))[0]:     patches[int(i)].set_fc('lightsalmon') ax2.plot(bin_centers, count_binned[0],'*') ax2.plot(bin_centers, count_binned[0],'*') ax2.plot(bin_centers, count_binned[0], '*') ax2.plot(bin_centers, count_binned[0], '*') ax2.set(xlabel='Average intensity', ylabel='Histogram (Count)') fig.tight_layout() plt.show() positions_l=np.where(avg_i<lower_limit) i_barriers="np.nanmean(avg_i[positions_l])&lt;/pre"></lower_limit)></pre>  |
|      | positions_u=np.where(avg_i)=upper_limit) i_quantum_well=np.anmean(avg_i[positions_u]) print('Mean intensity of the barriers: '+str(i_barriers)) print('Mean intensity of the quantum well: '+str(i_quantum_well))  Figure 6  0.096 -  |
|      | 0.088 - Lower limit: 0.08980 Upper limit: 0.09502 Upper limit: |
|      | Mean intensity of the barriers: 0.08861379186574508 Mean intensity of the quantum well: 0.09665842778213221 Finally, we can obtain the composition map using the nominal_composition:  nominal_composition=0.28  composition_map=np.copy(required_sublattice) composition_map[:,:,0]=nominal_composition*(required_sublattice[:,:,0]-i_barriers)/(i_quantum_well-i_barriers)  |
|      | plt.figure() plt.scatter(composition_map[:,:,1],composition_map[:,:,2],s=20,c=composition_map[:,:,0]) plt.colorbar() plt.axis('scaled') plt.axis('scaled') plt.axis('scaled') ax.set_ylim(ax.get_ylim()[::-1]) ax.xaxis.tick_top() ax.yaxis.tick_left() #plt.imshow(s.data,cmap='gray') plt.tight_layout() plt.show() plt.savefig('composition_map.png',dpi=300,transparent=True,bbox_inches='tight') np.save('composition_map.npy',composition_map)  Figure 7  |
|      | - 0.6   |
|      | - 0.0<br>0.2  |
|      | Composition profile  In addition to the composition map, we can average the perpendicular layers to the growth direction in order to get the composition profile:  avg_intensity=np.mean(composition_map[:,:,0], axis=0) avg_axis=np.mean(composition_map[:,:,1], axis=0)*s.axes_manager[0].scale plt.figure() plt.plot(avg_axis, avg_intensity,'*',linestyle='') plt.xlabel('Position ['+s.axes_manager[0].units+']') plt.ylabel('Average composition') plt.show()  Figure 8   |
|      | 0.30 - 0.25 - 0.20 - 0.15 - 0.10 -  |
|      | 0.00 -<br>-0.05 -   |

Import the required libraries

atom\_lattice = am.load\_atom\_lattice\_from\_hdf5('atom\_lattice\_qw.hdf5')
s=hs.load('data.hspy')
sublattice\_A=atom\_lattice.sublattice\_list[0]
sublattice\_B=atom\_lattice.sublattice\_list[1]

To select the optimal zone axis, the parameter **direction** is varied until the optimum is found.

Figure 1

Signal

zone\_vector = sublattice\_A.zones\_axis\_average\_distances[direction]
atom\_planes = sublattice\_A.atom\_planes\_by\_zone\_vector[zone\_vector]
zone\_axis = sublattice\_A.get\_atom\_planes\_on\_image(atom\_planes)

sublattice\_A.construct\_zone\_axes(atom\_plane\_tolerance=0.8)

Starting with the sublattice A, it is necessary to construct a 2D array with the intensities of every atom column in this sublattice. Therefore, we need to select the required planes from a zone axis.

0.095

- 0.090

**Intensity Maps** 

First, we load the atom lattice:

Constructing the zone axes:

direction=0

zone\_axis.plot()

sublattice\_A

ax = plt.gca()
ax.get\_xaxis().set\_visible(False)
ax.get\_yaxis().set\_visible(False)

<Sublattice, (atoms:2419,planes:6)>

In [2]:

In [3]:

In [4]: