

# Synchronized Nonlinear Motion Trajectories at MAX IV Beamlines

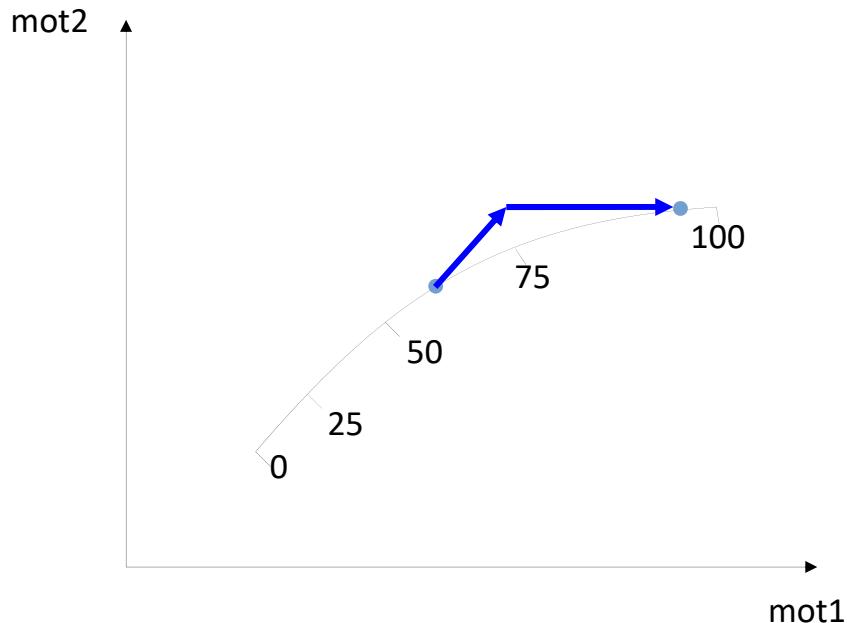
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Two motors started simultaneously but finish independently.

Makes the motion deviate from path.

Typical step scan.

## Standard PseudoMotor

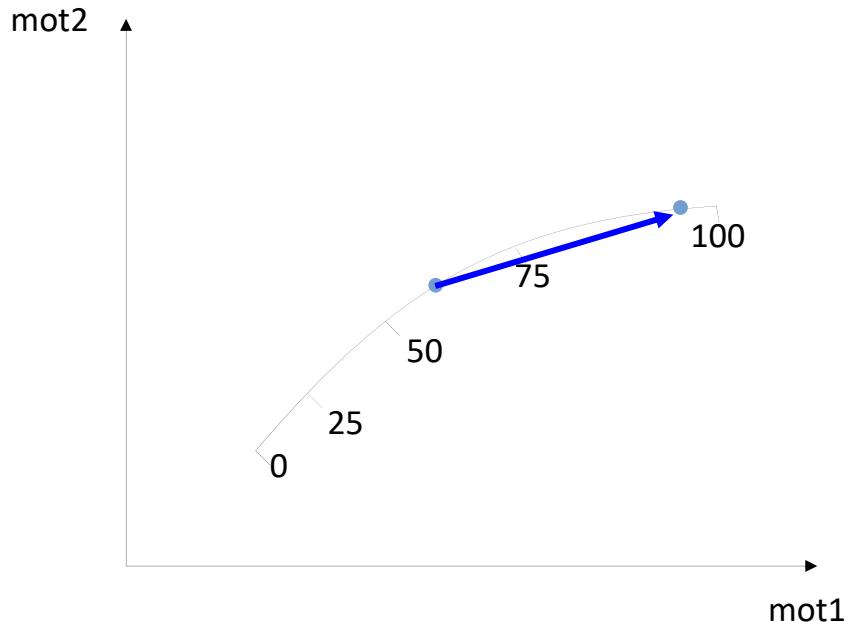


With synchronized linear speed, motors start and finish simultaneously.

Cut corners in the trajectory.

Common in monochromators.

## Standard PseudoMotor

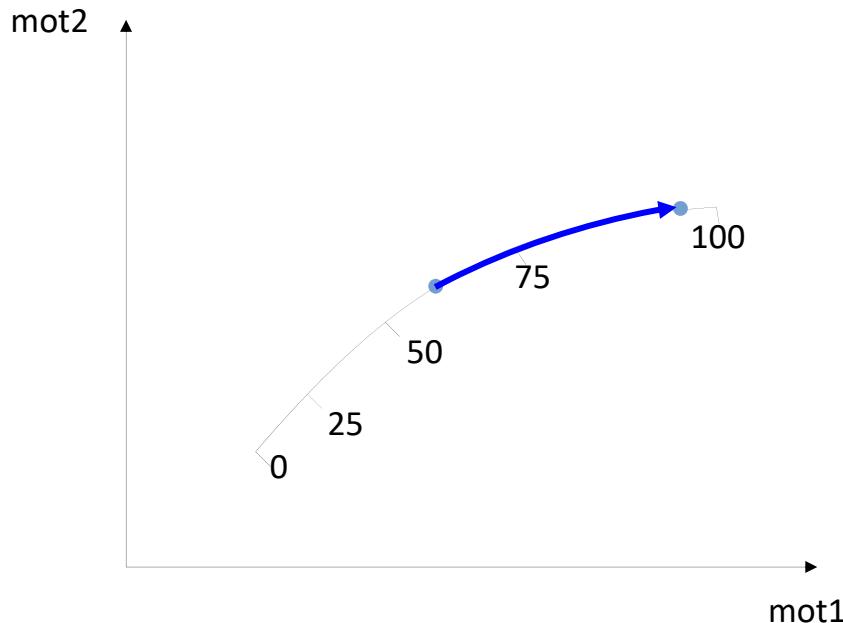


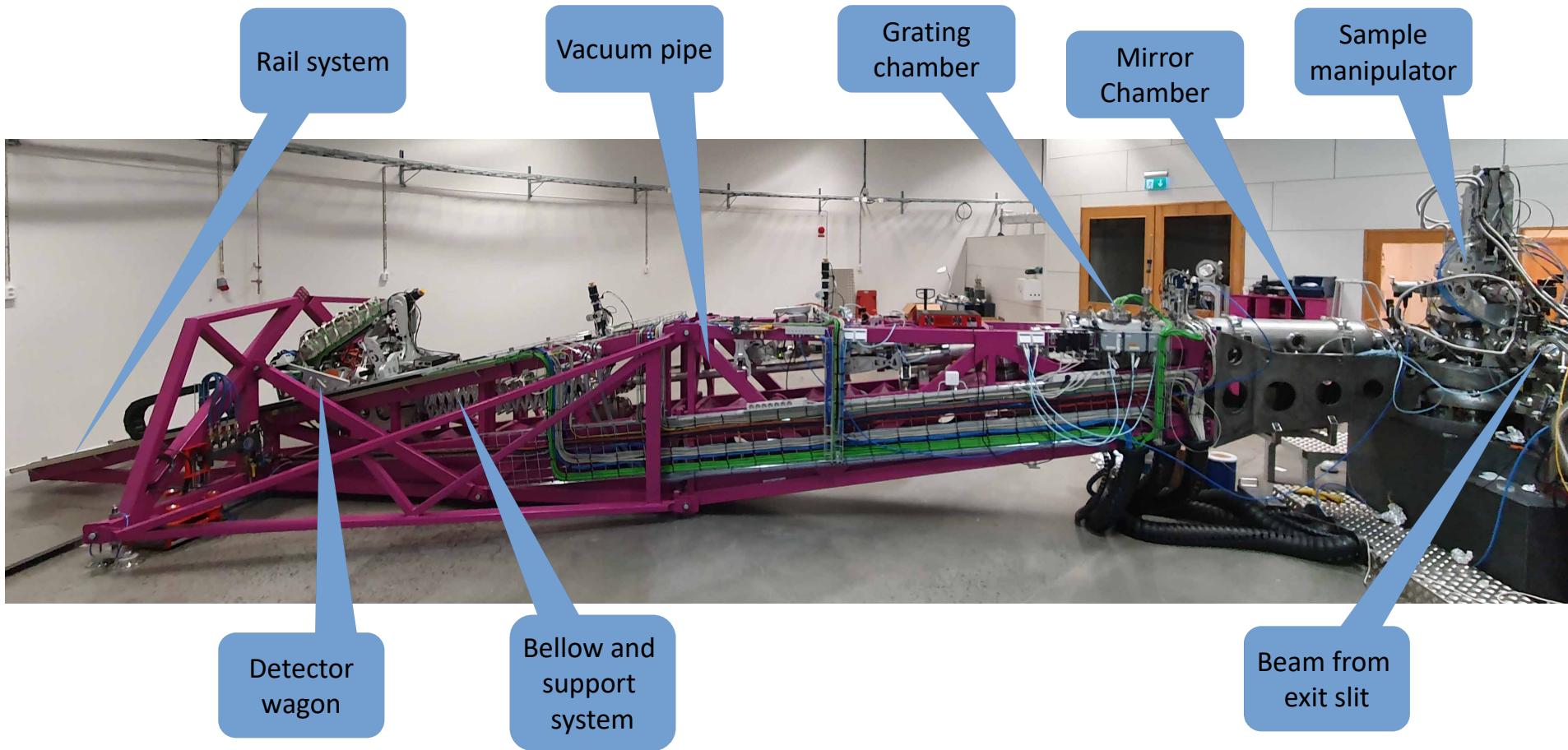
A trajectory is followed when start, stop, speed and acceleration is adjusted along the path.

Possible to scan e.g. energy in constant speed.

Trajectories is now a function available in the IcePAP motion system through its collaboration.

## Following trajectory





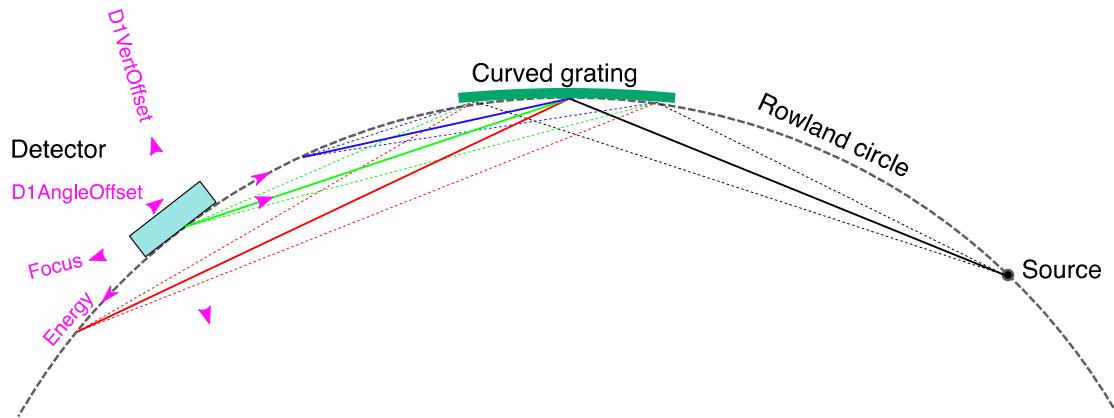
# Veritas Rowland Spectrometer

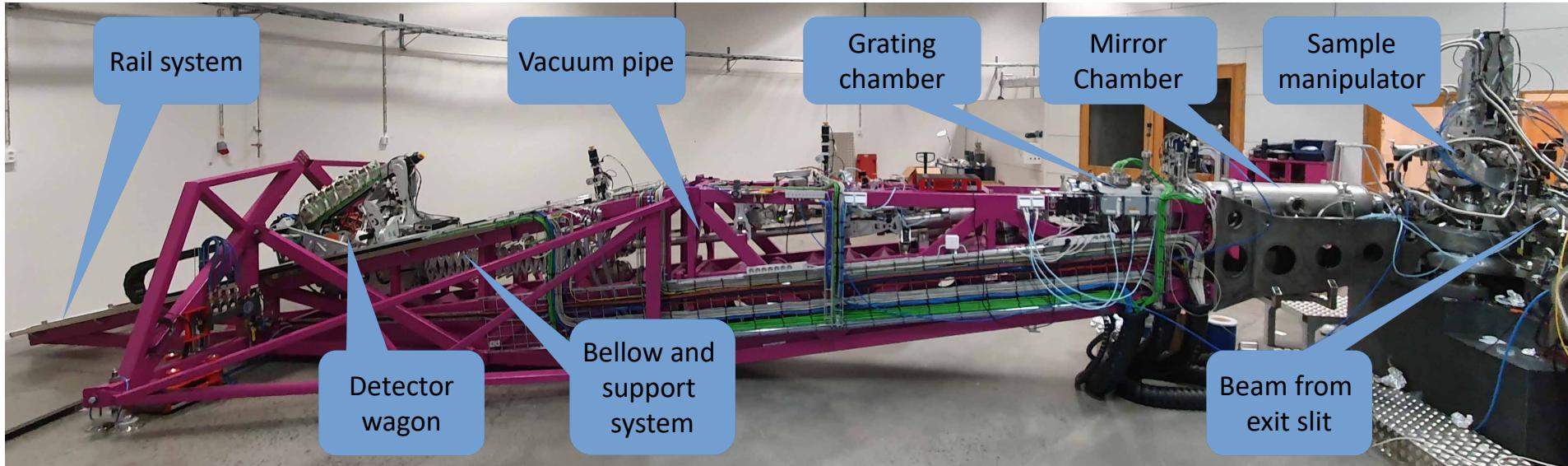
MAX IV

# Rowland Spectrometer

With a curved grating with radius  $2R$ , the detector will be in focus if the source, grating center and detector is on the same circle with radius  $R$ .

Great example where trajectories are useful.



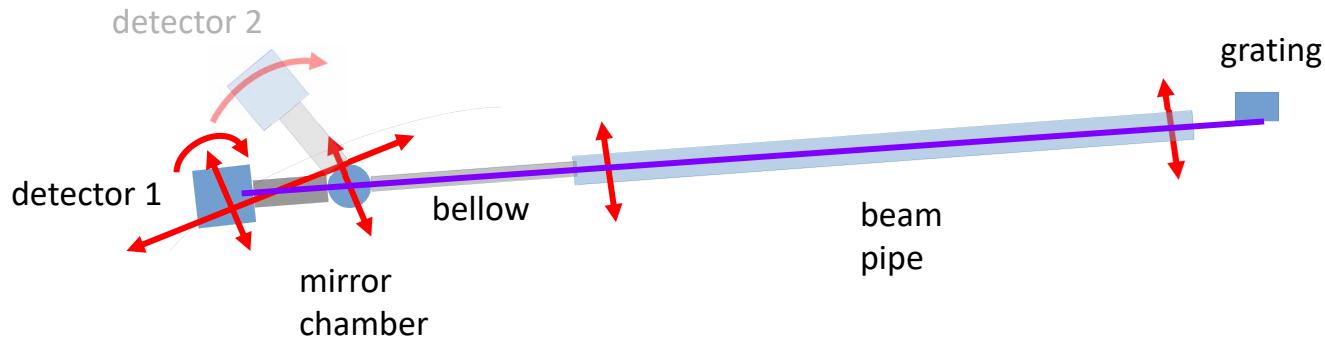


# Veritas Rowland Spectrometer

MAX IV

# Veritas Rowland Spectrometer

## What to move?



### Parameters

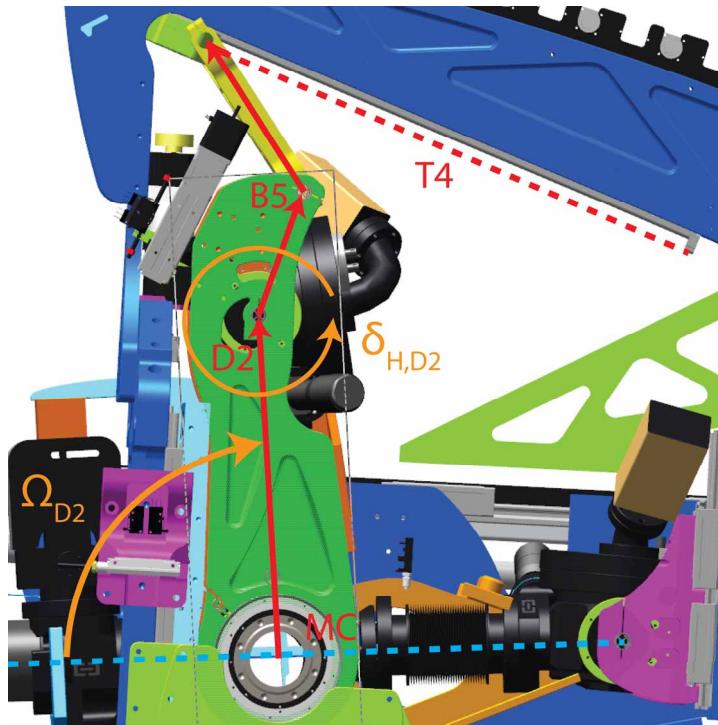
- Energy
- Detector 1 angle adjust
- Detector 1 distance adjust
- Detector 1 height adjust
- Grating line density
- Detector 2 angle

Each motion needs to have its equation.

Trajectories makes updates easy.

Blue beam path travel through mirror camber to two detectors while motion and joints keep them aligned.

## Detector wagon detail Objects are interlinked



# How to make a trajectory move

Function  $f(energy)$  calculates positions for mot1 and mot2

Function  $units2steps()$  converts from units to motor steps

Make the tables:

```
energytable = []
```

```
mot1table = []
```

```
mot2table = []
```

for energy in range(0,100):

- mot1, mot2 = f(energy)
- energytable.append(energy)
- mot1table.append(units2steps(mot1))
- mot2table.append(units2steps(mot2))

# The structure of a active trajectory uploaded in IcePAP

# How to make a trajectory move

1. Upload table to each motor using pylcePAP:

```
ipap[mot1axis].clear_parametric_table()  
ipap[mot2axis].clear_parametric_table()  
ipap[mot1axis].set_parametric_table(energytable, mot1table, mode='LINEAR')  
ipap[mot2axis].set_parametric_table(energytable, mot1table, mode='LINEAR')
```

2. Move onto trajectory:

```
ipap.movevp(energytable[0], [mot1axis, mot2axis], group=True)
```

Or 'SPLINE'

3. Set velocity:

```
ipap[mot1axis].parvel = vel  
ipap[mot2axis].parvel = vel
```

Can be different!

4. Move along trajectory:

```
ipap.pmove(75.3, [mot1axis, mot2axis], group=True)
```

Important!

# Various notes

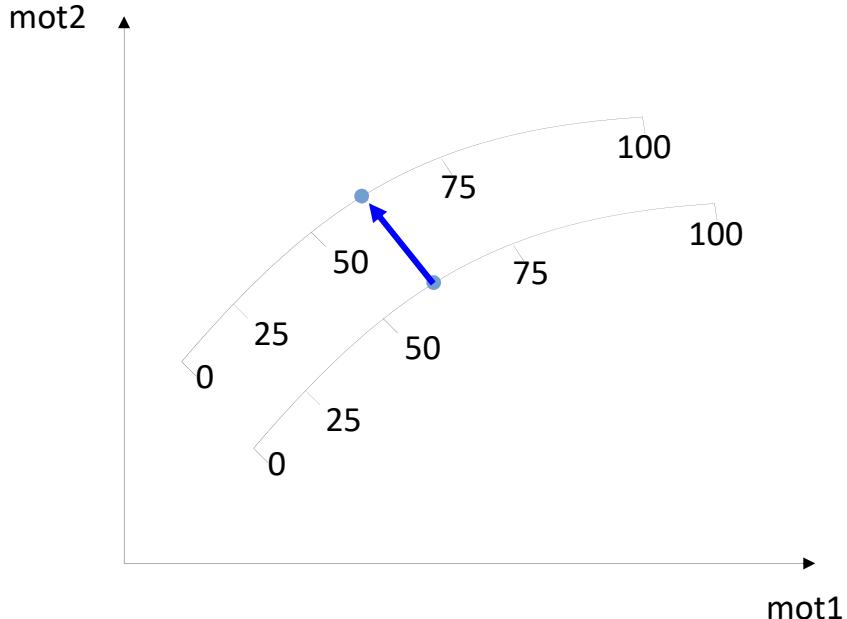
- Each motor can have a different parametric velocity.
- Without group mode: If one motor stops due to some error the others continue.
- It's still possible to move each motor individually, doing so breaks the trajectory "magic" and it's necessary to do a MOVEP to get them back in sync.
- Trajectory coordinate can be read from any axis:  
 $\text{Pos} = \text{ipap}[\text{mot1axis}].\text{parpos}$
- If a motor is not on the trajectory this will raise an exception.

# Changing other parameters

## Method 1: keep trajectory coordinate

Most requests result in small changes in trajectory.

The new setpoint will be the same value on the new trajectory.



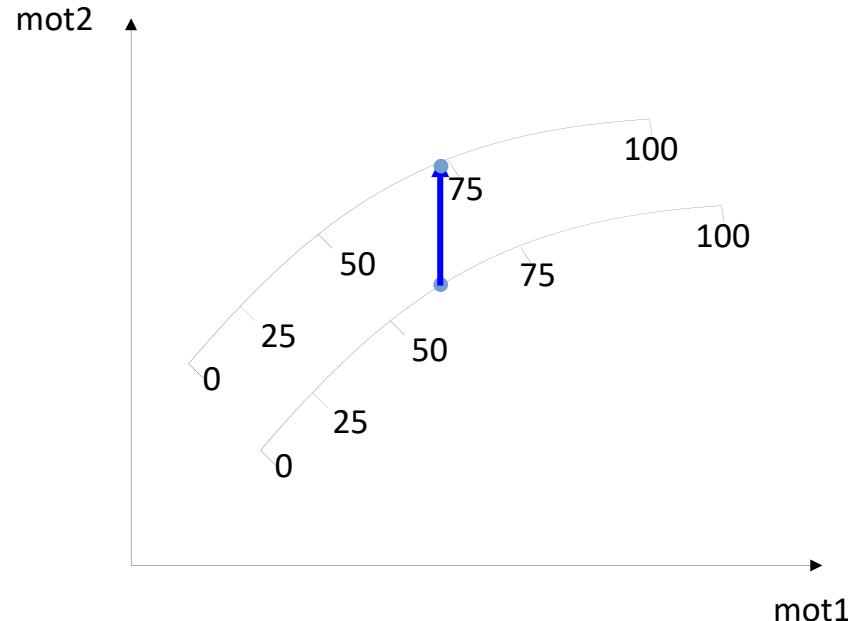
With a new trajectory resulting in a large time consuming motion, a new setpoint is defined as the physically closest point.

The way between them are traveled through a temporary trajectory

Automatically uploaded, removed and replaced with the final trajectory when the change is completed.

## Changing other parameters

### Method 2: keep master position

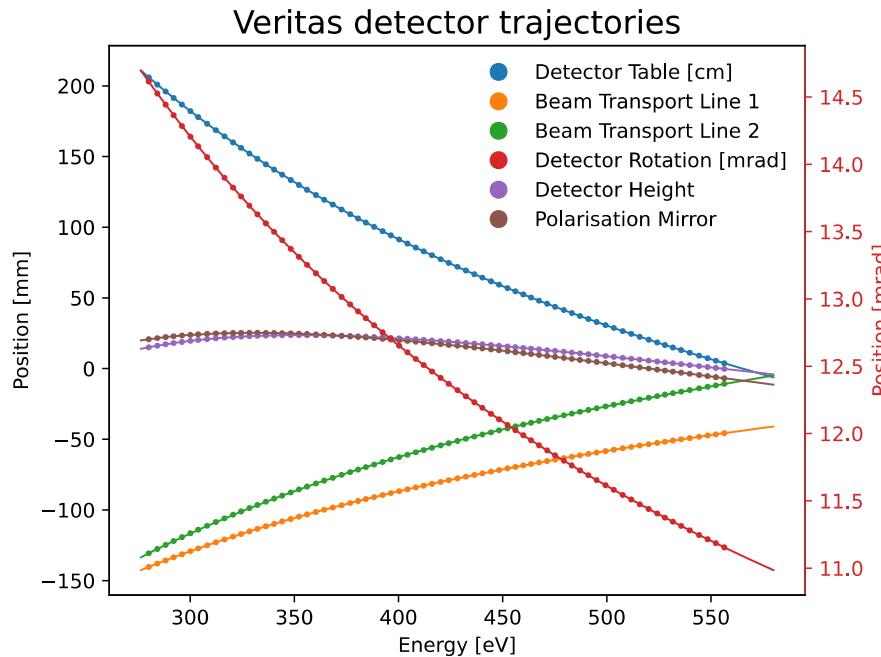


Prior motion, the trajectory is calculated and uploaded and here plotted as a solid line.

During motion, the tango attribute position is plotted as dots and laid in the same graph.

The two datasets matches well with each other.

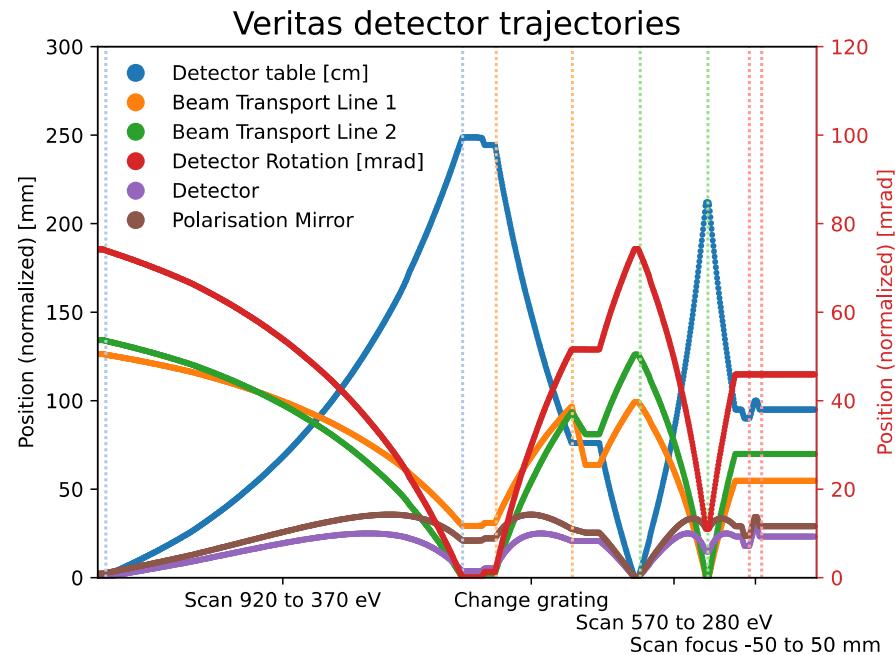
## Measured position and uploaded trajectory



During operation, the trajectories need to be followed at all time.

1. Energy scan
2. Grating exchange
3. Energy scan
4. Focus scan

## Trajectories at work



## User Parameters

- Detector height offset
- Detector rotation offset
- Detector focus offset
- Grating line density
- Grating curvature

## Fitting routine

- The exact trajectory of the Rowland geometry is very sensitive to parameters such as grating radius and line density.
- By finding a few known points along the energy scale, by using samples with well-known emission, it's possible to fit the parameters.
- Given the recorded detector positions at these known points, the routine optimizes the Rowland parameters to generate a trajectory that gets as close as possible to these positions, at the correct energies.
- The output is a set of adjusted parameters that can be entered in the Sardana motor controller.

# Summary

- Trajectories successfully brings new capabilities to MAX IV motion systems in terms of motion along non-trivial and non-linear paths.
- Parameter to follow can be arbitrarily chosen as e.g. energy or a curvature in space.
- A large set of motors can be treated as one unit and the complex motion is solved without the need of interference from the user.
- They are deployed in production at several instruments including
  - SCANIA spectrometer at Balder beamline
  - flight tube at CoSAXS beamline
  - monochromators at FlexPES and FinEstBeAMS beamlines
  - Veritas Rowland Spectrometer