An implementation decoupling the storage representation from the in-memory representation

July 26, 2024, 3rd "Get Your Brain Together" Hackathon

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SpatialData is a solution for working with spatial multiomics datasets that bridges existing communities



Data representation is abstracted as a modular combination of reusable elements



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Coordinate transformations enable alignment to common coordinate systems



Example: joint visualization of 2 Xenium + 1 Visium datasets

Transformations are defined both for raster and vector types





Coordinate transformations





Deep learning interface



Spatial aggregations



Example use case



SpatialData APIs: set_transformation() vs transform()



from spatialdata.transformations import Translation, Scale, Affine, Sequence

```
translation = Translation([1, 2], axes=("x", "y"))
scale = Scale([2, 1], axes=("y", "x"))
affine = Affine(
        [4, 5, 6],
        [1, 2, 3],
        [0, 0, 1],
    ],
    input_axes=("x", "y"),
    output_axes=("y", "x"),
sequence = Sequence([translation, scale, affine])
print(sequence)
print(sequence.to_affine(input_axes=('x', 'y'), output_axes=('x', 'y')))
```

Sequence Translation (x, y) [1. 2.] Scale (y, x) [2. 1.] Affine (x, $y \rightarrow y$, x) [4. 5. 6.] [1. 2. 3.] [0. 0. 1.]

Affine (x, y \rightarrow x, y) [1. 4. 12.] [4. 10. 30.] [0. 0. 1.]

```
from spatialdata.transformations import Scale, MapAxis
```

```
map_axis = MapAxis({"x": "y", "y": "x"})
scale = Scale([2], axes=("z",))
sequence = Sequence([map_axis, map_axis, scale]).to_affine(
    input_axes=("x", "y", "z"), output_axes=("x", "y", "z")
)
print(sequence)
```

```
Affine (x, y, z \rightarrow x, y, z)

[1. 0. 0. 0.]

[0. 1. 0. 0.]

[0. 0. 2. 0.]

[0. 0. 0. 1.]
```

```
from spatialdata import read_zarr
from spatialdata.transformations import get_transformation,
set_transformation
```

```
sdata = read_zarr('data.zarr')
```

```
my_image = sdata['my_image'] # e.g. cyx image
my_points = sdata['my_points'] # e.g. xy points
```

```
t = get_transformation(my_image, to_coordinate_system='Sample 1')
set_transformation(my_points, transformation=t,
to_coordinate_system='Sample 1')
```



First implementation, mirroring the NGFF specification: coordinate systems

https://github.com/scverse/spatialdata/blob/main/src/spatialdata/transformations/ngff

```
ngff_coordinate_system.py
from spatialdata.transformations.ngff.ngff coordinate system import NgffAxis, NgffCoordinateSystem
axes = [
    NgffAxis(name="x", type="space", unit="micrometer"),
    NgffAxis(name="y", type="space", unit="micrometer"),
    NgffAxis(name="z", type="space", unit="micrometer"),
coordinate_system = NgffCoordinateSystem(
    name="volume micrometers",
    axes=axes,
```

First implementation, mirroring the NGFF specification: coordinate transformations

https://github.com/scverse/spatialdata/blob/main/src/spatialdata/transformations/ngff

ngff_transformations.py

__all__ = [

]

"NgffBaseTransformation", "NgffIdentity", "NgffMapAxis", "NgffTranslation", "NgffScale", "NgffAffine", "NgffRotation", "NgffSequence", "NgffByDimension",

class NgffIdentity(NgffBaseTransformation):

"""The Identity transformation from the NGFF specification."""

lef __init__(

self

input_coordinate_system: Optional[NgffCoordinateSystem] = None, output_coordinate_system: Optional[NgffCoordinateSystem] = None,) → None:

....

Init the NgffIdentity object.

Parameters

```
input_coordinate_system
    Input coordinate system of the transformation.
output_coordinate_system
    Output coordinate system of the transformation.
"""
super().__init__(input_coordinate_system, output_coordinate_system)
```

@classmethod

def _from_dict(cls, _: Transformation_t) → Self: # type: ignore[valid-type]
 return cls()

def to_dict(self) → Transformation_t: d = { "type": "identity", } self._update_dict_with_input_output_cs(d) return d

Possible improvement: using pydantic (see work from Davis Bennet for v0.4: JaneliaSciComp/pydan tic-ome-ngff)

Adding functionalities to the NGFF transformation classes

class NgffBaseTransformation(ABC):

```
"""Base class for all the transformations defined by the NGFF specification.""" \# ...
```

@abstractmethod

```
def inverse(self) → NgffBaseTransformation:
    """Return the inverse of the transformation."""
```

@abstractmethod

```
def _get_and_validate_axes(self) → tuple[tuple[str, ...], tuple[str, ...]]:
    """
```

```
Get the input and output axes of the coordinate systems specified for the transformation, and check if they are compatible with the transformation.
```

.....

@abstractmethod

```
def transform_points(self, points: ArrayLike) → ArrayLike:
    """
```

Transform points (coordinates).

Notes

This function will check if the dimensionality of the input and output coordinate systems of the transformation are compatible with the given points.

∂abstractmethod

def to_affine(self) \rightarrow NgffAffine: ""Convert the transformation to an affine transformation, whenever the conversion can be made."""

In the new implementation we have a separate transform() function

Drawbacks:

- 1. our APIs were too verbose:
 - a. the users had to specify (or import) the axes, units, coordinate systems
 - b. c vs non-c axes had to be specified
- 2. transformations could not be moved around: e.g. from xy points to a cyx image
- 3. Ambiguity around sequence transformations due to the possibility of specifying sub-transformations without an input/output coordinate system <u>link</u>

```
link to this old code
   cvx cs.
   yx_cs,
cyx_to_xy = Affine(
    np.array(
   input coordinate system=cyx cs,
    np.arrav(
            [0, 0, 0],
           [1, 0, 0],
   input_coordinate_system=xy_cs,
    output_coordinate_system=cyx_cs,
transformation = Sequence(
       cyx_to_xy,
       ByDimension(
           transformations=[
               MapAxis({"x": "x", "y": "y"}, input_coordinate_system=xy_cs, output_coordinate_system=yx_cs),
               Affine(
                   np.array([[0, 0], [0, 1]]),
                   output_coordinate_system=c_cs,
           input_coordinate_system=xy_cs,
           output_coordinate_system=cyx_cs,
       MapAxis({"x": "x", "y": "y"}, input_coordinate_system=cyx_cs, output_coordinate_system=xy_cs),
       Translation(np.array([1, 2])),
       Scale(np.array([3, 4])),
       xy_to_cyx,
```

Simplification:

 Transformations are defined independently of the input/output coordinate systems they will be eventually applied to
 For the next to react a set if there is only translate it by 5".

E.g. $x \mapsto x + 5$ reads as "if there is an x, translate it by 5"

Implementation:

- 1. We don't use coordinate systems to define transformations
- 2. Transformations require extra arguments. Examples:

```
Translation([5.], axes=(`x',))
Affine([[1, 2]], input_axes=(`i', `j'), output_axes=(`c'))
```

What didn't change:

- Transformations are n-dimensional: any order of axes and any number Detail: in spatialdata we use only `c', `z', `y', `x'; so we actually validate against these axes during __init__()
- 2. IO is done via NGFF transformations thanks to conversions: BaseTransformation ↔ NgffBaseTransformation

Simplifications:

• All transformations can be turned into Affine. This can be relaxed!

Implementation:

- We skipped byDimension and Rotation
- We always know the input axes thanks to our element schemas:
 - 2d images cyx
 - 3d images czy
 - 2d labels yx
 - 3d labels zyx
 - 2d points xy
 - 3d points xyz
 - 2d shapes xy

```
def _get_current_output_axes(
    transformation: BaseTransformation, input_axes: tuple[str, ...]
) → tuple[str, ...]:
```

translation = Translation([5, 3], axes=("x", "y"))
print(translation.to_affine(input_axes=("x", "y", "c"), output_axes=("c", "z", "y", "x")))

Affino	(~		$ \rightarrow $	~	7	v	~)	
ATTTHE	(^,	у,		с,	۷,	у,	~)	
[0.	0.	1.	0.]					
[0.	0.	0.	0.]					
[0.	1.	0.	3.]					
[1.	0.	0.	5.]					
[0.	0.	0.	1.]					

c is "passed through" (because it is present both as input and output axes but not defined in the transformation) z is "ignored" (because it is present only in the output axes)

ValueError: Input axes must be a subset of output axes.
translation.to_affine(input_axes=("x", "y", "c"), output_axes=("y", "x"))

ValueError: The axis y is not an input of the affine transformation but it appears as output.
Probably you want to remove it from the input_axes of the to_affine_matrix() call.
affine = Affine(np.array([[1, 0], [2, 0], [0, 1]]), input_axes=("x",), output_axes=("x", "y"))
affine.to_affine(input_axes=("x", "y"), output_axes=("x", "y"))

We use transformations to map elements to coordinate systems

"Pixel" coordinate system



- Same for vector elements
- A coordinate system is just a string
- We store transformations in the element's metadata

```
my_element.attrs['transform'] = {
    'global': Identity(),
    'Sample 1': Affine(...)
}
```

 We plan to store (optional) coordinate system information

sdata.coordinate_systems = {
 'Sample 1': NgffCoordinateSystem(...)

The transform() function

Implementation:

Lazy and chunk-wise (but can be optimized)

- Uses dask_image.ndinterp.affine_transform for raster data.*
- Uses geopandas.GeoSeries.affine_transform for vector data.

Need to use dask-geopandas at some point

Examples from the docs (note: here actually we use matplotlib.transforms, but the output is analogous)

Translation

The spatialdata.transformations.Translation transformation can be used to apply a translation to the element.

translation = Translation([500, 300], axes=("x", "y"))

set_transformation(sdata.images["raccoon"], translation, to_coordinate_system="global")
sdata.pl.render_images().pl.render_labels().pl.render_shapes().pl.show()



Affine transformation and composition

The <u>spatialdata.transformations.Sequence</u> transformation class can be used to compose transformations. This class allows to compose multiple transformations and it can be used even when the axes do not strictly match.

sequence = Sequence([rotation, scale])

set_transformation(sdata.images["raccoon"], sequence, to_coordinate_system="global")
sdata.pl.render_images().pl.render_labels().pl.render_shapes().pl.show()



Rotation The spatialdata.transformations.Affine transformation can be used to apply an affine transformation to the dements.Left's start with a rotation. theta = math.pi / 6 rotation = Affine([math.cos(theta), -math.sin(theta), 0], [(asth.cin(theta), math.cos(theta), 0], [(asth.cin(theta), math.cos(theta), 0], [, input_axes=("x", "y"), output_axes=("x", "y"), st_transformation(sdata.images["raccoom"], rotation, to_coordinate_system="global") sdata.pl.render_images(),pl.render_labels(),pl.render_shapes(),pl.show()



Limitations of the in-memory classes

Limitations of the in-memory transformations classes:

- So far, for what is implemented, none.
- Need to implement the non-linear transformations.



Limitations of the transform() function

Limitations of their use within spatialdata, and of the transform() function:

- transform() can be optimized (ad hoc algorithms, GPU)
- We allow only `c', `z', `y', `x'. No `t' (workarounds available).
- We allow only specific orders of axes.
- We don't treat `c' as a spatial axis;
 - e.g. embedding a single-channel image into a multi-channel image is not allowed
 - o instead, we just call dask.array.stack()
- No bridge: NGFF transformations \leftrightarrow xarray coordinates.













A bridge: NGFF transformations ↔ Xarray coordinates

The new specs maintain the old v0.4 transformations (scale+translation), used for multi-scale images.

The scale+translation info represents the:

- "Canonical scale for the data"
- "Canonical orientation for the data"
- "Canonical origin for the data"

Implementation:

- After read() turn scale+translation into xarray coordinates.
- Before write() turn the xarray coordinates into scale+translation.
- transform() modifies the data only if necessary E.g. rotation, but not for scale or translation.
- Bonus: scale+translation can be allowed also for vector data; this can be used to define the "canonical orientation"



Conclusions and proposal on how to proceed

What we implemented:

- Ergonomic APIs that address our spatial omics use cases:
- On-disk, still NGFF
- Transformations also for points and shapes

Proposal, move code out of spatialdata into a more general repository:

- Tier 1: NGFFBaseTransformation (in particular read-write APIs)
 - could add a pydantic model
- Tier 2: BaseTransformation (i.e. ergonomic APIs)
- Tier 3: transform()
 - generalize to arbitrary axes
- Extra:
 - Converters between other formats (ITK, matplotlib, napari, ...)

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Good first contributions

- 15 July 2024: Call for abstracts, workshop proposals and sticker contest closes
- 15 August 2024: Early registration fee period ends, regular registration fees start

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Conclusions and acknowledgements



Elvas

Heidari

- established interoperable format for spatial omics based on OME-NGFF
- in-memory multimodal representation
- processing, visualization
- scales to large datasets



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Nature Methods, 2024 First authors are underlined

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