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# **probeinterface**

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probeinterface is a Python package to handle probe layout, geometry and wiring to a device for neuroscience experiments.

The package handles the following items:

- probe geometry (2D or 3D layout)
- probe shape (contours of the probe)
- shape and size of the shank
- probe wiring to the recording device
- combination of several probes: global geometry + global wiring

The probeinterface package also provides:

- basic plotting functions with matplotlib
- input/output functions to several formats (PRB, NWB, CSV, MEArec, SpikeGLX, ...)

Here is a schema for the naming used in the package:



orphan



## EXAMPLES

Start here with a tutorial showing probeinterface.

## 1.1 Generate a Probe from scratch

This example generates a probe from scratch.

```
import numpy as np
import matplotlib.pyplot as plt

from probeinterface import Probe
from probeinterface.plotting import plot_probe
```

First, let's create dummy positions for a 24-contact probe

```
n = 24
positions = np.zeros((n, 2))
for i in range(n):
    x = i // 8
    y = i % 8
    positions[i] = x, y
positions *= 20
positions[8:16, 1] -= 10
```

Now we can create a *Probe* object and set the position and shape of each contact

The *ndim* argument indicates that the contact is 2d, so the positions have a (n\_elec, 2) shape. We can also define a 3d probe with *ndim*=3 and positions will have a (n\_elec, 3) shape.

Note: *shapes* and *shape\_params* could be arrays as well, indicating the shape for each contact separately.

```
probe = Probe(ndim=2, si_units='um')
probe.set_contacts(positions=positions, shapes='circle', shape_params={'radius': 5})
```

*Probe* objects have fancy prints!

```
print(probe)
```

```
Probe - 24ch - 1shanks
```

In addition to contacts, we can create the planar contour (polygon) of the probe

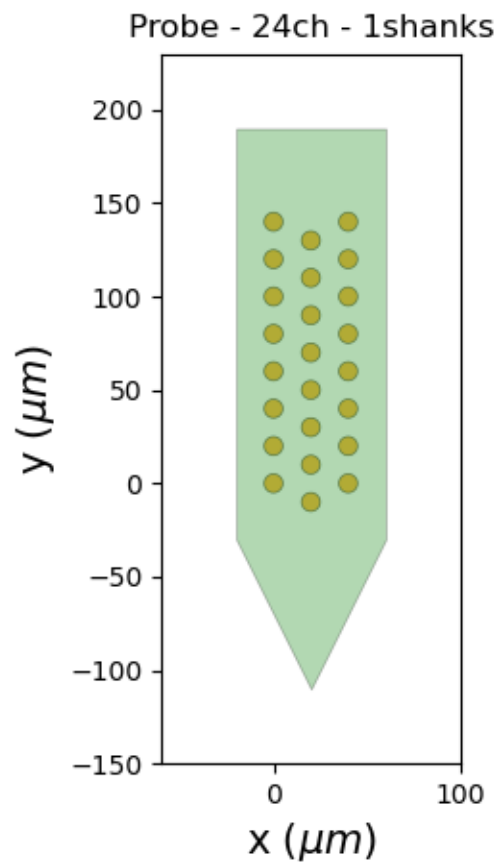
```
polygon = [(-20, -30), (20, -110), (60, -30), (60, 190), (-20, 190)]
probe.set_planar_contour(polygon)
```

If *pandas* is installed, the *Probe* object can be exported as a dataframe for a simpler view:

```
df = probe.to_dataframe()
df
```

If *matplotlib* is installed, the *Probe* can also be easily plotted:

```
plot_probe(probe)
```



```
(<matplotlib.collections.PolyCollection object at 0xffff7ab920f0>, <matplotlib.
collections.PolyCollection object at 0xffff7a1be360>)
```

A 2d *Probe* can be transformed into a 3d *Probe* by indicating the *axes* on which contacts will lie (Here the 'y' coordinate will be 0 for all contacts):

```
probe_3d = probe.to_3d(axes='xz')
plot_probe(probe_3d)

plt.show()
```



Probe - 24ch - 1shanks



Total running time of the script: (0 minutes 0.391 seconds)

## 1.2 2d and 3d Probes

This example shows how to manipulate a probe in 2d or 3d.

Import

```
import numpy as np
import matplotlib.pyplot as plt

from probeinterface import Probe
from probeinterface.plotting import plot_probe
```

First, let's create one 2d probe with 24 contacts:

```
n = 24
positions = np.zeros((n, 2))
for i in range(n):
    x = i // 8
    y = i % 8
    positions[i] = x, y
positions *= 20
```

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```
positions[8:16, 1] -= 10

probe_2d = Probe(ndim=2, si_units='um')
probe_2d.set_contacts(positions=positions, shapes='circle', shape_params={'radius': 5})
probe_2d.create_auto_shape(probe_type='tip')
```

Let's transform it into a 3d probe.

Here the axes are 'xz' so y will be 0 for all contacts. The shape of probe\_3d.contact\_positions is now (n\_elec, 3)

```
probe_3d = probe_2d.to_3d(axes='xz')
print(probe_2d.contact_positions.shape)
print(probe_3d.contact_positions.shape)
```

```
(24, 2)
(24, 3)
```

Note that all “y” coordinates are 0

```
df = probe_3d.to_dataframe()
df[['x', 'y', 'z']].head()
```

The plotting function automatically displays the *Probe* in 3d:

```
plot_probe(probe_3d)
```

Probe - 24ch - 1shanks

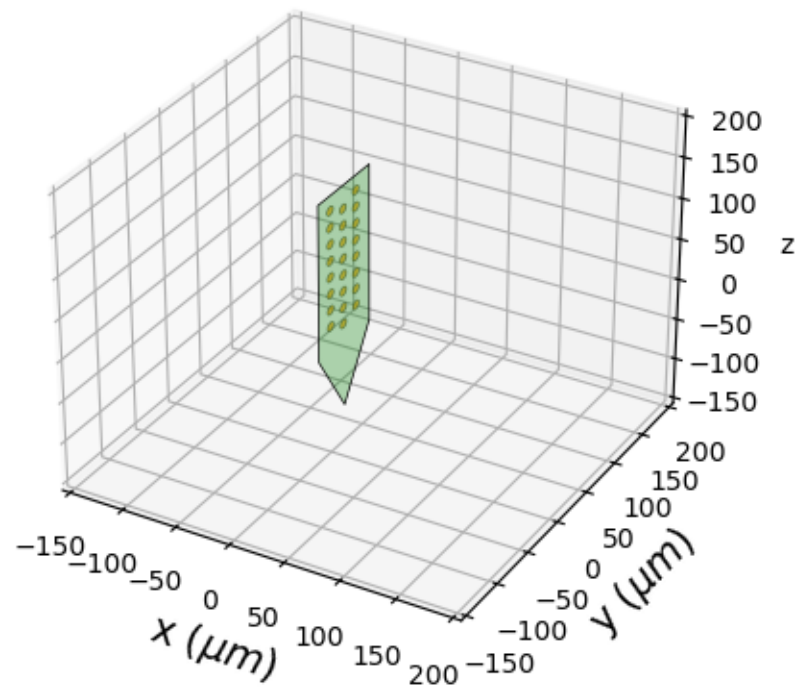


```
(<matplotlib.mplot3d.art3d.Poly3DCollection object at 0xffff77e0e750>, <matplotlib.mplot3d.art3d.Poly3DCollection object at 0xffff77fcef0>)
```

We can create another probe lying on another plane:

```
other_3d = probe_2d.to_3d(axes='yz')
plot_probe(other_3d)
```

Probe - 24ch - 1shanks



```
(<matplotlib.pyplot.art3d.Poly3DCollection object at 0xffff77fe5b50>, <matplotlib.pyplot.art3d.Poly3DCollection object at 0xffff825b85f0>)
```

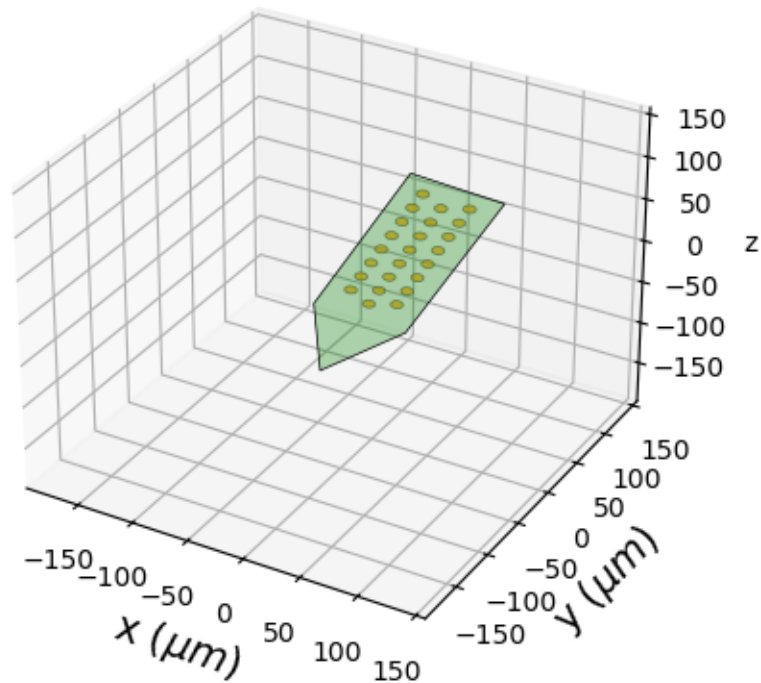
*Probe* can be moved and rotated in 3d:

```
probe_3d.move([0, 30, -50])
probe_3d.rotate(theta=35, center=[0, 0, 0], axis=[0, 1, 1])

plot_probe(probe_3d)

plt.show()
```

Probe - 24ch - 1shanks



Total running time of the script: (0 minutes 0.233 seconds)

### 1.3 Generate a ProbeGroup

This example shows how to assemble several Probe objects into a ProbeGroup object.

Import

```
import numpy as np
import matplotlib.pyplot as plt

from probeinterface import Probe, ProbeGroup
from probeinterface.plotting import plot_probe_group
from probeinterface import generate_dummy_probe
```

Generate 2 dummy *Probe* objects with the utils function:

```
probe0 = generate_dummy_probe(elec_shapes='square')
probe1 = generate_dummy_probe(elec_shapes='circle')
probe1.move([250, -90])
```

Let's create a *ProbeGroup* and add the *Probe* objects into it:

```
probegroup = ProbeGroup()
probegroup.add_probe(probe0)
probegroup.add_probe(probe1)

print('probe0.get_contact_count()', probe0.get_contact_count())
print('probe1.get_contact_count()', probe1.get_contact_count())
print('probegroup.get_contact_count()', probegroup.get_contact_count())
```

```
probe0.get_contact_count() 32
probe1.get_contact_count() 32
probegroup.get_contact_count() 64
```

We can now plot all probes in the same axis:

```
plot_probe_group(probegroup, same_axes=True)
```



or in separate axes:

```
plot_probe_group(probegroup, same_axes=False, with_contact_id=True)

plt.show()
```



Total running time of the script: (0 minutes 0.156 seconds)

## 1.4 Multi shank probes

This example shows how to deal with multi-shank probes.

In *probeinterface* this can be done with a *Probe* object, but internally each probe handles a *shank\_ids* vector to carry information about which contacts belong to which shanks.

Optionally, a *Probe* object can be rendered split into *Shank*.

Import

```
import numpy as np
import matplotlib.pyplot as plt

from probeinterface import Probe, ProbeGroup
from probeinterface import generate_linear_probe, generate_multi_shank
from probeinterface import combine_probes
from probeinterface.plotting import plot_probe
```

Let's use a generator to create a multi-shank probe:

```
multi_shank = generate_multi_shank(num_shank=3, num_columns=2, num_contact_per_column=6)
plot_probe(multi_shank)
```



```
(<matplotlib.collections.PolyCollection object at 0xffff77f48590>, <matplotlib.
collections.PolyCollection object at 0xffff77f57650>)
```

*multi\_shank* is one *probe* object, but internally the *Probe.shank\_ids* vector handles the shank ids.

```
print(multi_shank.shank_ids)
```

```
['0' '0' '0' '0' '0' '0' '0' '0' '0' '0' '0' '0' '1' '1' '1' '1' '1' '1'
 '1' '1' '1' '1' '1' '1' '2' '2' '2' '2' '2' '2' '2' '2' '2' '2' '2' '2']
```

The dataframe displays the *shank\_ids* column:

```
df = multi_shank.to_dataframe()
df
```

We can iterate over a multi-shank probe and get *Shank* objects. A *Shank* is linked to a *Probe* object and can also retrieve positions, contact shapes, etc.:

```
for i, shank in enumerate(multi_shank.get_shanks()):
    print('shank', i)
```

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```

print(shank.__class__)
print(shank.get_contact_count())
print(shank.contact_positions.shape)

```

```

shank 0
<class 'probeinterface.shank.Shank'>
12
(12, 2)
shank 1
<class 'probeinterface.shank.Shank'>
12
(12, 2)
shank 2
<class 'probeinterface.shank.Shank'>
12
(12, 2)

```

Another option to create multi-shank probes is to create several *Shank* objects as separate probes and then combine them into a single *Probe* object

```

# generate a 2 shanks linear
probe0 = generate_linear_probe(num_elec=16, ypitch=20,
                               contact_shapes='square',
                               contact_shape_params={'width': 12})

probe1 = probe0.copy()
probe1.move([100, 0])

multi_shank = combine_probes([probe0, probe1])

```

```

print(multi_shank.shank_ids)

```

```

['0' '0' '0' '0' '0' '0' '0' '0' '0' '0' '0' '0' '0' '0' '0' '1' '1'
 '1' '1' '1' '1' '1' '1' '1' '1' '1' '1' '1' '1' '1' '1']

```

```

plot_probe(multi_shank)

plt.show()

```



**Total running time of the script:** (0 minutes 0.121 seconds)

## 1.5 Handle channel indices

Probes can have a complex contacts indexing system due to the probe layout. When they are plugged into a recording device like an Open Ephys with an Intan headstage, the channel order can be mixed again. So the physical contact channel index is rarely the channel index on the device.

This is why the *Probe* object can handle separate *device\_channel\_indices*.

Import

```
import numpy as np
import matplotlib.pyplot as plt

from probeinterface import Probe, ProbeGroup
from probeinterface.plotting import plot_probe, plot_probe_group
from probeinterface import generate_multi_columns_probe
```

Let's first generate a probe. By default, the wiring is not complicated: each column increments the contact index from the bottom to the top of the probe:

```

probe = generate_multi_columns_probe(num_columns=3,
                                     num_contact_per_column=[5, 6, 5],
                                     xpitch=75, ypitch=75, y_shift_per_column=[0, -37.5, 37.5],
                                     contact_shapes='circle', contact_shape_params={
                                         'radius': 12})

plot_probe(probe, with_contact_id=True)

```



```

(<matplotlib.collections.PolyCollection object at 0xffff82a44320>, <matplotlib.
collections.PolyCollection object at 0xffff7a204470>)

```

The Probe is not connected to any device yet:

```
print(probe.device_channel_indices)
```

None

Let's imagine we have a headstage with the following wiring: the first half of the channels have natural indices, but the order of the other half is reversed:

```

channel_indices = np.arange(16)
channel_indices[8:16] = channel_indices[8:16][::-1]

```

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```
probe.set_device_channel_indices(channel_indices)
print(probe.device_channel_indices)
```

```
[ 0  1  2  3  4  5  6  7 15 14 13 12 11 10  9  8]
```

We can visualize the two sets of indices:

- the prbXX is the contact index ordered from 0 to N
- the devXX is the channel index on the device (with the second half reversed)

```
plot_probe(probe, with_contact_id=True, with_device_index=True)
```



```
(<matplotlib.collections.PolyCollection object at 0xffff825a2540>, <matplotlib.
collections.PolyCollection object at 0xffff7a3f7f20>)
```

Very often we have several probes on the device and this can lead to even more complex channel indices. *ProbeGroup.get\_global\_device\_channel\_indices()* gives an overview of the device wiring.

```
probe0 = generate_multi_columns_probe(num_columns=3,
                                      num_contact_per_column=[5, 6, 5],
                                      xpitch=75, ypitch=75, y_shift_per_column=[0, -37.5,
                                      ↪ 0],
```

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```

contact_shapes='circle', contact_shape_params={
↪ 'radius': 12})
probe1 = probe0.copy()

probe1.move([350, 200])
probegroup = ProbeGroup()
probegroup.add_probe(probe0)
probegroup.add_probe(probe1)

# wire probe0 0 to 31 and shuffle
channel_indices0 = np.arange(16)
np.random.shuffle(channel_indices0)
probe0.set_device_channel_indices(channel_indices0)

# wire probe0 32 to 63 and shuffle
channel_indices1 = np.arange(16, 32)
np.random.shuffle(channel_indices1)
probe1.set_device_channel_indices(channel_indices1)

print(probegroup.get_global_device_channel_indices())

```

```

[(0, 1) (0, 8) (0, 3) (0, 13) (0, 9) (0, 15) (0, 0) (0, 14) (0, 10)
 (0, 11) (0, 6) (0, 4) (0, 7) (0, 12) (0, 5) (0, 2) (1, 16) (1, 19)
 (1, 25) (1, 20) (1, 29) (1, 30) (1, 28) (1, 17) (1, 23) (1, 24) (1, 22)
 (1, 21) (1, 31) (1, 26) (1, 18) (1, 27)]

```

The indices of the probe group can also be plotted:

```

fig, ax = plt.subplots()
plot_probe_group(probegroup, with_contact_id=True, same_axes=True, ax=ax)

plt.show()

```



**Total running time of the script:** (0 minutes 0.197 seconds)

## 1.6 Import/export functions

*probeinterface* has its own format based on JSON. The format can handle several probes in one file. It has a ‘probes’ key that can contain a list of probes.

Each probe field in the json format contains the *Probe* class attributes.

It also supports reading (and sometimes writing) from these formats:

- PRB (.prb) : used by klusta/spyking-circus/tridesclous
- CSV (.csv): 2 or 3 columns locations in text file
- mearec (.h5) : mearec handles the geometry
- spikeglx (.meta) : spikeglx also handles the geometry

Import

```
import numpy as np
import matplotlib.pyplot as plt

from probeinterface import Probe, ProbeGroup
from probeinterface.plotting import plot_probe, plot_probe_group
```

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```

from probeinterface import generate_dummy_probe
from probeinterface import write_probeinterface, read_probeinterface
from probeinterface import write_prb, read_prb

```

Let's first generate 2 dummy probes and combine them into a ProbeGroup

```

probe0 = generate_dummy_probe(elec_shapes='square')
probe1 = generate_dummy_probe(elec_shapes='circle')
probe1.move([250, -90])

probegroup = ProbeGroup()
probegroup.add_probe(probe0)
probegroup.add_probe(probe1)

```

With the `write_probeinterface` and `read_probeinterface` functions we can write to and read from the json-based probeinterface format:

```

write_probeinterface('my_two_probe_setup.json', probegroup)

probegroup2 = read_probeinterface('my_two_probe_setup.json')
plot_probe_group(probegroup2)

```



The format looks like this:

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```

        'geometry': {
            4: [0, 50],
            5: [50, 0],
            6: [0, -50],
            7: [-50, 0],
        }
    }
}
"""

with open('two_tetrodes.prb', 'w') as f:
    f.write(prb_two_tetrodes)

two_tetrode = read_prb('two_tetrodes.prb')
plot_probe_group(two_tetrode, same_axes=False, with_contact_id=True)

plt.show()

```



**Total running time of the script:** (0 minutes 0.131 seconds)

## 1.7 Probe generator

*probeinterface* have also basic function to generate simple contact layouts like:

- tetrodes
- linear probes
- multi-column probes

Import

```
import numpy as np
import matplotlib.pyplot as plt

from probeinterface import Probe, ProbeGroup
from probeinterface.plotting import plot_probe, plot_probe_group
```

Generate 4 tetrodes:

```
from probeinterface import generate_tetrode

probegroup = ProbeGroup()
for i in range(4):
    tetrode = generate_tetrode()
    tetrode.move([i * 50, 0])
    probegroup.add_probe(tetrode)
probegroup.set_global_device_channel_indices(np.arange(16))

df = probegroup.to_dataframe()
df

plot_probe_group(probegroup, with_contact_id=True, same_axes=True)
```



Generate a linear probe:

```
from probeinterface import generate_linear_probe

linear_probe = generate_linear_probe(num_elec=16, ypitch=20)
plot_probe(linear_probe, with_contact_id=True)
```



```
(<matplotlib.collections.PolyCollection object at 0xffff824b3110>, <matplotlib.
collections.PolyCollection object at 0xffff77eadd30>)
```

Generate a multi-column probe:

```
from probeinterface import generate_multi_columns_probe

multi_columns = generate_multi_columns_probe(num_columns=3,
                                              num_contact_per_column=[10, 12, 10],
                                              xpitch=22, ypitch=20,
                                              y_shift_per_column=[0, -10, 0],
                                              contact_shapes='square', contact_shape_
↳ params={'width': 12})
plot_probe(multi_columns, with_contact_id=True, )
```

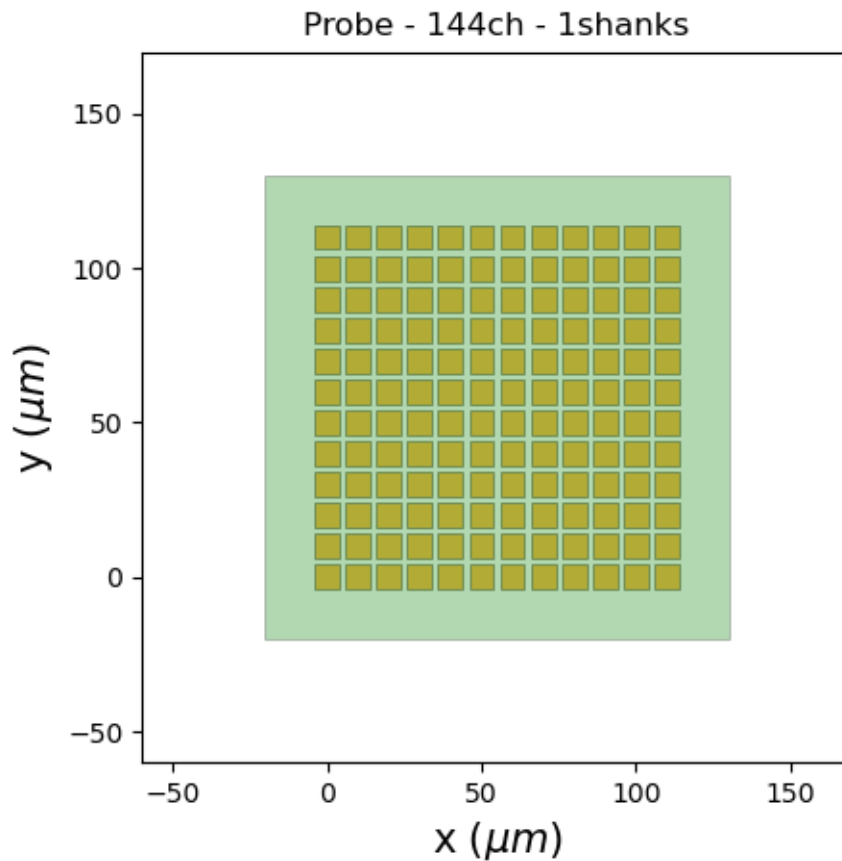


```
(<matplotlib.collections.PolyCollection object at 0xffff77ff4890>, <matplotlib.
collections.PolyCollection object at 0xffff77ff5af0>)
```

Generate a square probe:

```
square_probe = generate_multi_columns_probe(num_columns=12,
                                             num_contact_per_column=12,
                                             xpitch=10, ypitch=10,
                                             contact_shapes='square', contact_shape_
↳ params={'width': 8})
square_probe.create_auto_shape('rect')
plot_probe(square_probe)

plt.show()
```



Total running time of the script: (0 minutes 0.235 seconds)

## 1.8 More plotting examples

Here are some examples to showcase several plotting scenarios.

Import

```
import numpy as np
import matplotlib.pyplot as plt

from probeinterface import Probe, ProbeGroup
from probeinterface.plotting import plot_probe, plot_probe_group
from probeinterface import generate_multi_columns_probe, generate_linear_probe
```

Some examples in 2d

```
fig, ax = plt.subplots()

probe0 = generate_multi_columns_probe()
plot_probe(probe0, ax=ax)

# give each probe a different color
```

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```

probe1 = generate_linear_probe(num_elec=9)
probe1.rotate(theta=15)
probe1.move([200, 0])
plot_probe(probe1, ax=ax,
            contacts_colors=['red', 'cyan', 'yellow'] * 3)

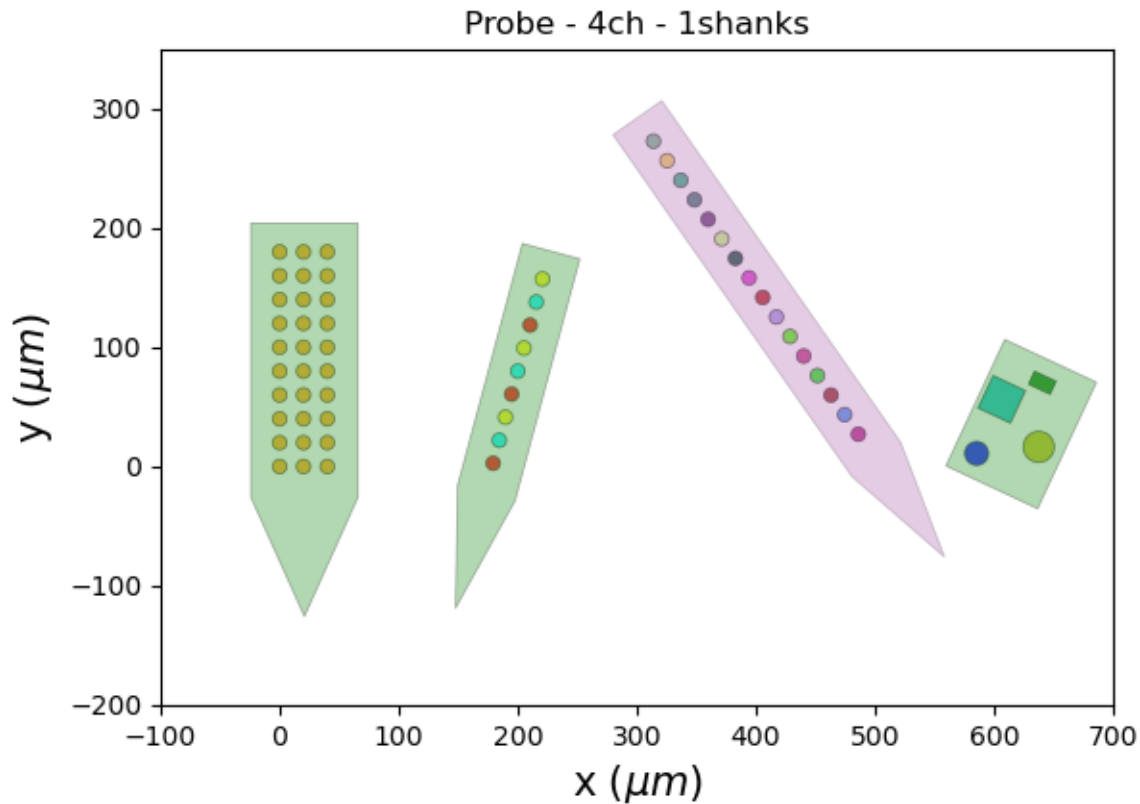
# prepare yourself for carnival!
probe2 = generate_linear_probe()
probe2.rotate(theta=-35)
probe2.move([400, 0])
n = probe2.get_contact_count()
rand_colors = np.random.rand(n, 3)
plot_probe(probe2, ax=ax, contacts_colors=rand_colors,
            probe_shape_kwargs={'facecolor': 'purple', 'edgecolor': 'k', 'lw': 0.5, 'alpha'
                                ↪ ': 0.2'})

# and make some alien probes
probe3 = Probe()
positions = [[0, 0], [0, 50], [25, 77], [45, 27]]
shapes = ['circle', 'square', 'rect', 'circle']
params = [{'radius': 10}, {'width': 30}, {'width': 20, 'height': 12}, {'radius': 13}]
probe3.set_contacts(positions=positions, shapes=shapes,
                    shape_params=params)
probe3.create_auto_shape(probe_type='rect')
probe3.rotate(theta=25)
probe3.move([600, 0])
plot_probe(probe3, ax=ax, contacts_colors=['b', 'c', 'g', 'y'])

ax.set_xlim(-100, 700)
ax.set_ylim(-200, 350)

ax.set_aspect('equal')

```



Some examples in 3d for the romantic who likes flowers...

```
fig = plt.figure()
ax = fig.add_subplot(1, 1, 1, projection='3d')

n = 8
for i in range(n):
    probe = generate_multi_columns_probe(num_columns=3,
                                         num_contact_per_column=[8, 9, 8],
                                         xpitch=20, ypitch=20,
                                         y_shift_per_column=[0, -10, 0]).to_3d()
    probe.rotate(theta=35, center=[0, 0, 0], axis=[0, 1, 0])
    probe.move([100, 50, 0])
    probe.rotate(theta=i * 360 / n, center=[0, 0, 0], axis=[0, 0, 1])
    plot_probe(probe, ax=ax,
               probe_shape_kwargs={'facecolor': ['purple', 'cyan'][i % 2], 'edgecolor':
    ↪ 'k', 'lw': 0.5, 'alpha': 0.2})

probe = generate_linear_probe(num_elec=24, ypitch=20).to_3d()

probe.move([0, 0, -450])
plot_probe(probe, ax=ax)

lims = -450, 450
```

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```
ax.set_xlim(*lims)
ax.set_ylim(*lims)
ax.set_zlim(*lims)

plt.show()
```

Probe - 24ch - 1shanks



Total running time of the script: (0 minutes 0.193 seconds)

## 1.9 More complicated probes

This example demonstrates how to generate a more complicated probe with hybrid contacts shape and contact rotations within the *contact\_plane\_axes* attribute.

```
import numpy as np
import matplotlib.pyplot as plt

from probeinterface import Probe
from probeinterface.plotting import plot_probe
```

Let's first set the positions of the contacts

```
n = 24
positions = np.zeros((n, 2))
for i in range(3):
    positions[i * 8: (i + 1) * 8, 0] = i * 30
    positions[i * 8: (i + 1) * 8, 1] = np.arange(0, 240, 30)
```

Electrode shapes can be arrays to handle hybrid shape contacts

```
shapes = np.array(['circle', 'square'] * 12)
shape_params = np.array([{'radius': 8}, {'width': 12}] * 12)
```

**The *plane\_axes* argument handles the axis for each contact.**

It can be used for contact-wise rotations.

*plane\_axes* has a shape of (num\_elec, 2, ndim)

```
plane_axes = [[[1 / np.sqrt(2), 1 / np.sqrt(2)], [-1 / np.sqrt(2), 1 / np.sqrt(2)]]] * n
plane_axes = np.array(plane_axes)
```

Create the probe

```
probe = Probe(ndim=2, si_units='um')
probe.set_contacts(positions=positions, plane_axes=plane_axes,
                  shapes=shapes, shape_params=shape_params)
probe.create_auto_shape()
```

```
plot_probe(probe)
```

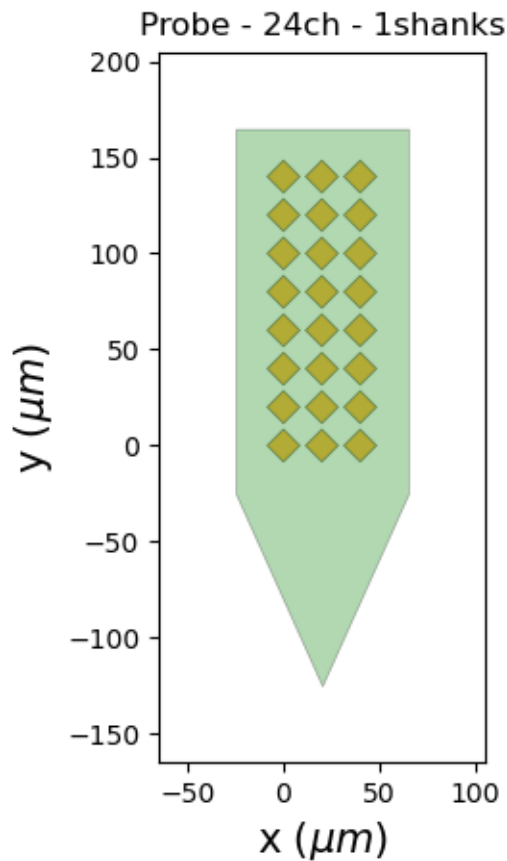


```
(<matplotlib.collections.PolyCollection object at 0xffff82437800>, <matplotlib.
collections.PolyCollection object at 0xffff82515e20>)
```

We can also use the *rotate\_contacts* to make contact-wise rotations:

```
from probeinterface import generate_multi_columns_probe

probe = generate_multi_columns_probe(num_columns=3,
                                     num_contact_per_column=8, xpitch=20, ypitch=20,
                                     contact_shapes='square', contact_shape_params={
↳ 'width': 12})
probe.rotate_contacts(45)
plot_probe(probe)
```



```
(<matplotlib.collections.PolyCollection object at 0xffff7a207560>, <matplotlib.
collections.PolyCollection object at 0xffff77e7cd40>)
```

```
probe = generate_multi_columns_probe(num_columns=5,
                                     num_contact_per_column=5, xpitch=20, ypitch=20,
                                     contact_shapes='square', contact_shape_params={
↳ 'width': 12})
thetas = np.arange(25) * 360 / 25
probe.rotate_contacts(thetas)
plot_probe(probe)

plt.show()
```



Total running time of the script: (0 minutes 0.159 seconds)

## 1.10 Get probe from library

*probeinterface* provides a library of probes from several manufacturers on the GitHub platform: [https://github.com/SpikeInterface/probeinterface\\_library](https://github.com/SpikeInterface/probeinterface_library)

Users and manufacturers are welcome to contribute to it.

The Python module provide a function to download and cache files locally in the *probeinterface* json-based format.

```
from pprint import pprint

import numpy as np
import matplotlib.pyplot as plt

from probeinterface import Probe, get_probe
from probeinterface.plotting import plot_probe
```

Download one probe:

```
manufacturer = 'neuronexus'
probe_name = 'A1x32-Poly3-10mm-50-177'
```

(continues on next page)

(continued from previous page)

```
probe = get_probe(manufacturer, probe_name)
print(probe)
```

```
A1x32-Poly3-10mm-50-177 - neuronexus - 32ch - 1shanks
```

Files from the library also contain annotations specific to manufacturers. We can see here that Neuronexus probes have contact indices starting at “1” (one-based)

```
pprint(probe.annotations)
```

```
{'first_index': 1,
 'manufacturer': 'neuronexus',
 'name': 'A1x32-Poly3-10mm-50-177'}
```

When plotting, the channel indices are automatically displayed with one-based notation (even if internally everything is still zero based):

```
plot_probe(probe, with_contact_id=True)
```

A1x32-Poly3-10mm-50-177 - neuronexus - 32ch - 1shanks



```
(<matplotlib.collections.PolyCollection object at 0xffff7ac4dc70>, <matplotlib.
collections.PolyCollection object at 0xffff77e17500>)
```

```
plt.show()
```

Total running time of the script: (0 minutes 0.060 seconds)

## 1.11 Automatic wiring

Here is an example on how to handle the wiring automatically and to get the `device_channel_indices`.

```
from pprint import pprint

import numpy as np
import matplotlib.pyplot as plt

from probeinterface import Probe, get_probe
from probeinterface.plotting import plot_probe
```

Download one probe:

```
manufacturer = 'neuronexus'
probe_name = 'A1x32-Poly3-10mm-50-177'

probe = get_probe(manufacturer, probe_name)
print(probe)
```

```
A1x32-Poly3-10mm-50-177 - neuronexus - 32ch - 1shanks
```

We can “wire” this probe to a recording device. Imagine we connect this Neuronexus probe with an Omnetic to an Intan RHD headstage.

Using the wiring documentation from these two sites: [https://neuronexus.com/wp-content/uploads/2018/09/Wiring\\_H32.pdf](https://neuronexus.com/wp-content/uploads/2018/09/Wiring_H32.pdf) [http://intantech.com/RHD\\_headstages.html?tabSelect=RHD32ch&yPos=0](http://intantech.com/RHD_headstages.html?tabSelect=RHD32ch&yPos=0)

After a long headache we can figure out the wiring to the device manually and set it using the `probe.set_device_channel_indices()` function:

```
device_channel_indices = [
    16, 17, 18, 20, 21, 22, 31, 30, 29, 27, 26, 25, 24, 28, 23, 19,
    12, 8, 3, 7, 6, 5, 4, 2, 1, 0, 9, 10, 11, 13, 14, 15]
probe.set_device_channel_indices(device_channel_indices)
```

In order to ease this process, *probeinterface* also includes some commonly used wirings based on standard connectors. In our case, we can simply use:

```
probe.wiring_to_device('H32>RHD2132')
print(probe.device_channel_indices)
```

```
[16 17 18 20 21 22 31 30 29 27 26 25 24 28 23 19 12  8  3  7  6  5  4  2
  1  0  9 10 11 13 14 15]
```

In this figure we have 2 numbers for each contact:

- the upper number “prbXX” is the Neuronexus index (one-based)
- the lower “devXX” is the channel on the Intan device (zero-based)

```
fig, ax = plt.subplots(figsize=(5, 15))
plot_probe(probe, with_contact_id=True, with_device_index=True, ax=ax)

plt.show()

"""
Available wiring "pathways"
-----

The available pathways can be found in the `probeinterface.wiring <>`_ module.

The following pathways are available:
"""

from probeinterface import get_available_pathways
print(get_available_pathways())
```



A1x32-Poly3-10mm-50-177 - neuronexus - 32ch - 1shanks



```
['H32>RHD2132', 'ASSY-156>RHD2164', 'ASSY-116>RHD2132', 'ASSY-77>Adpt.A64-0m32_2x-sm-NN>
↪RHD2164', 'ASSY-77>Adpt.A64-0m32_2x-sm-NN>two_RHD2132', 'cambridgeneurotech_mini-amp-64
↪']
```

Total running time of the script: (0 minutes 0.095 seconds)

## 1.12 Plot values

Here is an example of how to plot values with color scales. And also to plot an interpolated image.

```
from pprint import pprint

import numpy as np
import matplotlib.pyplot as plt

from probeinterface import Probe, get_probe
from probeinterface.plotting import plot_probe
```

Download one probe:

```
manufacturer = 'neuronexus'
probe_name = 'A1x32-Poly3-10mm-50-177'

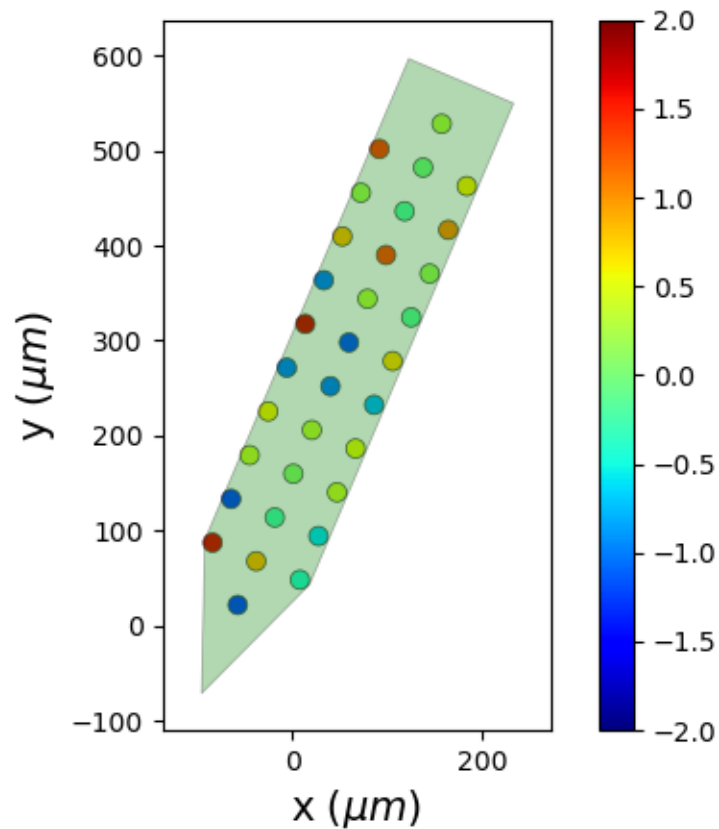
probe = get_probe(manufacturer, probe_name)
probe.rotate(23)
```

fake values

```
values = np.random.randn(32)
```

plot with values

```
fig, ax = plt.subplots()
poly, poly_contour = plot_probe(probe, contacts_values=values,
                                cmap='jet', ax=ax, contacts_kargs={'alpha' : 1}, title=False)
poly.set_clim(-2, 2)
fig.colorbar(poly)
```



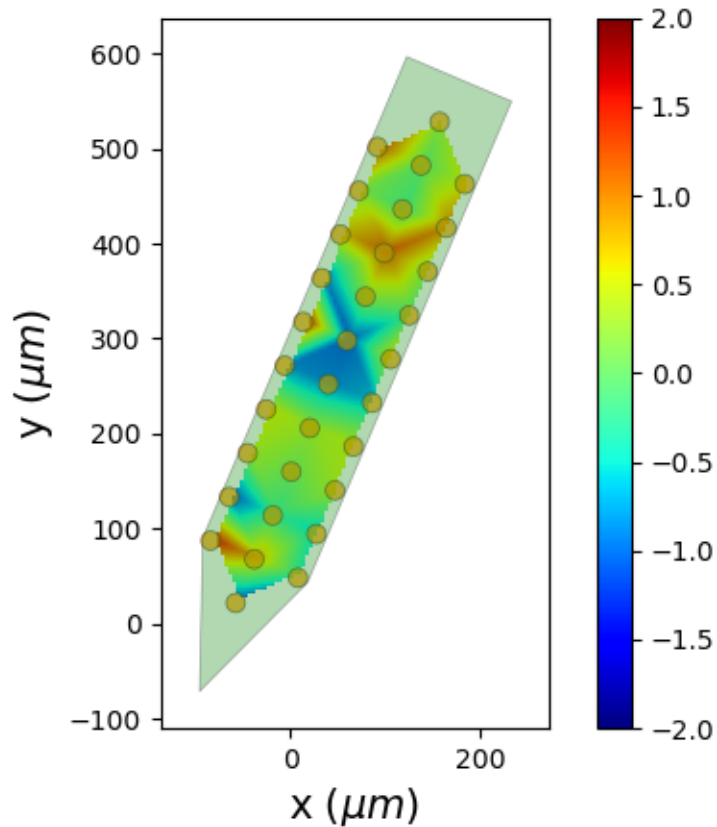
```
<matplotlib.colorbar.Colorbar object at 0xffff7a1bfd10>
```

generated an interpolated image and plot it on top

```
image, xlims, ylims = probe.to_image(values, pixel_size=4, method='linear')

print(image.shape)

fig, ax = plt.subplots()
plot_probe(probe, ax=ax, title=False)
im = ax.imshow(image, extent=xlims+ylims, origin='lower', cmap='jet')
im.set_clim(-2,2)
fig.colorbar(im)
```



```
(127, 67)
```

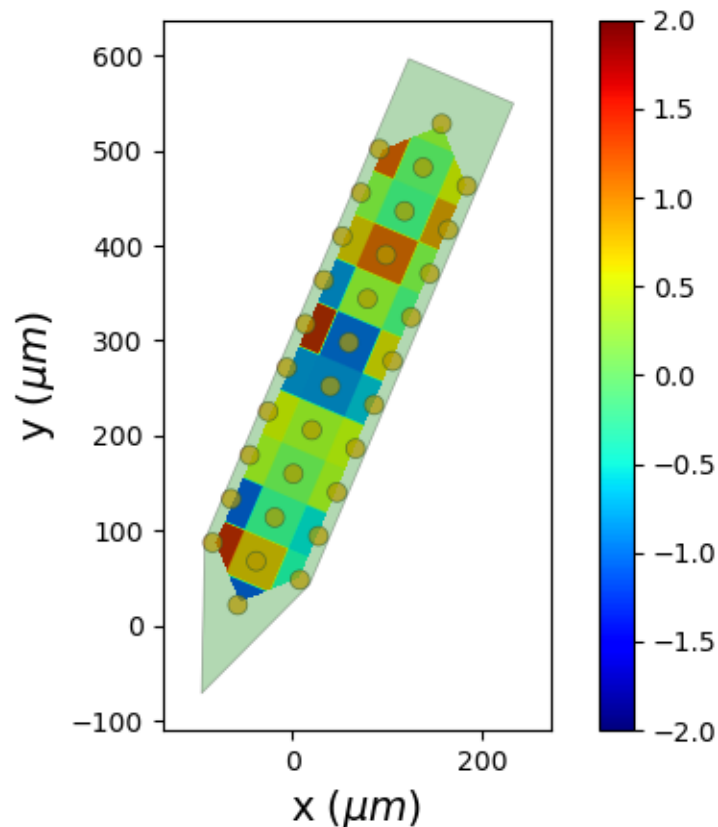
```
<matplotlib.colorbar.Colorbar object at 0xffff77e0f800>
```

works with several interpolation methods

```
image, xlims, ylims = probe.to_image(values, num_pixel=1000, method='nearest')

fig, ax = plt.subplots()
plot_probe(probe, ax=ax, title=False)
im = ax.imshow(image, extent=xlims+ylims, origin='lower', cmap='jet')
im.set_clim(-2,2)
fig.colorbar(im)

plt.show()
```



Total running time of the script: (0 minutes 1.026 seconds)

## 1.13 Overview

### 1.13.1 Introduction

To record neural electrical signals, extracellular neural probes are inserted into nervous tissues (e.g. brain, spinal cord). Neural probes are (usually) multi-channel arrays able to record from multiple contacts simultaneously, spanning from a few channels (e.g. tetrodes) to high-density silicon probes (e.g. Neuropixels - with up to 384 recording channels).

These probes (especially silicon probes) generally have a complex layout (or geometry) and can be connected to the recording system in multiple ways (wiring). To connect a neural probe to a recording device (e.g. Open Ephys, Blackrock, Ripple, Plexon, Intan, Multi-channel System) a headstage is used that is connected to the main recording device.

The complexity of the probe wiring and device wiring leads to the difficult task of directly linking the **physical contacts on the probe** and the **logical channel indices on the device**.

Recent *spike sorting* (i.e. methods to extract single neurons' activity from the extracellular recordings) algorithms strongly rely on the probe geometry to exploit the spatial distribution of the contacts and improve their performance.

Therefore, there is a need to correctly handle probe geometry and the wiring to the recording device in an easy-to-use and standardized way.

As an example, imagine you have:

- a **Neuronexus A1x32-Poly2** probe
- with the **intan RHD2132** headstage using the **omnetics 1315** connector
- connected on the **port B of an Open Ephys board**

What would be your final channel mapping be?

Of course one can sit down in the lab and try to figure it out... The goal of **probeinterface** is to make this time-consuming and error-prone process easier and standardized.

### 1.13.2 Scope

The scope of this project is to handle one (or several) Probe with three simple python classes:

- **Shank**
- *Probe*
- *ProbeGroup*.

**These classes handle:**

- probe geometry (2D or 3D contact layout)
- probe planar contours (polygon)
- shape and size of the contacts
- probe wiring to the recording device
- combination of several probes: global geometry + global wiring

**This package also provide:**

- read/write to a common format (JSON based)
- read/write function to other existing formats (PRB, NWB, CSV, MEArec, SpikeGLX, ...)
- plotting routines
- generator functions to create user-defined probes

### 1.13.3 Goal 1

This common interface could be used by several projects for spike sorting and electrophysiology analysis:

- **SpikeInterface**: integrate this into spikeextractors to handle channel location and wiring
- **NEO**: handle array\_annotations for AnalogSignal
- **SpikeForest**: use this package for plotting probe activity
- **Phy**: integrate for probe display
- **SpyKING Circus**: handle probe with this package
- **Kilosort**: handle probe with this package
- ...and more

### 1.13.4 Goal 2

Implement and maintain a collection of widely used probes in Neuroscience, for example:

- [Neuronexus](#)
- [Cambridge Neurotech](#)

We have started a work-in-progress repo with a [probe library](#)

### 1.13.5 Existing projects

probeinterface is not the first attempt to build a library of available probes. Here is a list of available resources:

- [JRClust probe library](#) - Matlab format
- [Klusta probe library](#) - PRB format
- [SpyKING Circus probe library](#) - PRB format
- [Justin Kiggins did some script for neuronexus mapping](#)

All of these projects only describe the contact positions. Furthermore there is a strong ambiguity for users between the **contact index on the probe** and the **channel index on device**. This could lead to a wrong interpretation of the wiring.

With probeinterface we try to provide a unified framework for probe description, handling, and a comprehensive probe library.

### 1.13.6 Acknowledgements

The probeinterface is inspired on the [MEAutility](#) package, written by [Alessio Buccino](#).

While the general idea of having an enhanced probe description is present, the MEAutility package mainly focuses on handling probes for modeling purposes, hence missing the wiring concept, and it can only handle a single probe at a time.

With probeinterface the focus is also to combine several Probes and to handle complex wiring for experimental description.

## 1.14 Examples

Start here with a tutorial showing probeinterface.

### 1.15 Format specifications

With probeinterface we introduce a simple format based on the JSON format. The format is a trivial json-serialisation of a Python dictionary. The dictionary maps every attribute of the Probe class.

In fact, the format itself describes a ProbeGroup, so it can include several probes. The format can describe a simple unique probe with its geometry and wiring, as well as a full experimental setup with several probes and their wiring to the recording device.

Here is a description of the fields in the json file.

**Let's imagine we want to describe a probe with:**

- 8 channels
- 2 shanks (one tetrode on each shank)



The first part contains fields about the `probeinterface` version and a list of probes:

```
{
  "specification": "probeinterface",
  "version": "0.1.0",
  "probes": [
    {
      ...
    }
  ]
}
```



Then each probe will be a sub-dictionary in the probes list:

```
{
  "ndim": 2,
  "si_units": "um",
  "annotations": {
    "name": "2 shank tetrodes",
    "manufacturer": "homemade"
  },
  "contact_positions": [
    ...
```

The probe dictionary contains all necessary fields and optional fields.

**Necessary:**

- ndim
- si\_units
- annotations
- contact\_positions
- contact\_shapes
- contact\_shape\_params

**Optional:**

- contact\_plane\_axes
- probe\_planar\_contour
- device\_channel\_indices
- shank\_ids

An example of a full json file:

```
{
  "specification": "probeinterface",
  "version": "0.1.0",
  "probes": [
    {
      "ndim": 2,
      "si_units": "um",
      "annotations": {
        "name": "2 shank tetrodes",
        "manufacturer": "homemade"
      },
      "contact_positions": [
        [
          25.0,
          0.0
        ],
        [
          0.0,
          25.0
        ]
      ],
```

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```

        [
            -25.0,
            0.0
        ],
        [
            0.0,
            -25.0
        ],
        [
            175.0,
            0.0
        ],
        [
            150.0,
            25.0
        ],
        [
            125.0,
            0.0
        ],
        [
            150.0,
            -25.0
        ]
    ],
    "contact_plane_axes": [
        [
            [
                1.0,
                0.0
            ],
            [
                0.0,
                1.0
            ]
        ],
        [
            [
                1.0,
                0.0
            ],
            [
                0.0,
                1.0
            ]
        ],
        [
            [
                1.0,
                0.0
            ],
            [

```

(continues on next page)

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```
    ]
  ],
  "contact_shapes": [
    "circle",
    "circle",
    "circle",
    "circle",
    "circle",
    "circle",
    "circle",
    "circle"
  ],
  "contact_shape_params": [
    {
      "radius": 6
    },
    {
      "radius": 6
    },
    {
      "radius": 6
    },
    {
      "radius": 6
    },
    {
      "radius": 6
    },
    {
      "radius": 6
    },
    {
      "radius": 6
    },
    {
      "radius": 6
    }
  ],
  "probe_planar_contour": [
    [
      -45.0,
      85.0
    ],
    [
      -45.0,
      45.0
    ],
    [
      -45.0,
      -45.0
    ],
  ],
```

(continues on next page)

(continued from previous page)

```
[
    [
        0.0,
        -125.0
    ],
    [
        45.0,
        -45.0
    ],
    [
        45.0,
        45.0
    ],
    [
        105.0,
        45.0
    ],
    [
        105.0,
        -45.0
    ],
    [
        150.0,
        -125.0
    ],
    [
        195.0,
        -45.0
    ],
    [
        195.0,
        45.0
    ],
    [
        195.0,
        85.0
    ]
],
"shank_ids": [
    0,
    0,
    0,
    0,
    1,
    1,
    1,
    1
]
}
]
```

## 1.16 Probeinterface public library

Probeinterface also handles a collection of probe descriptions on the [GitHub platform](#)

The python module has a simple function to download and cache locally by using `get_probe(...)`

```
from probeinterface import get_probe
probe = get_probe(manufacturer='neuronexus',
                  probe_name='A1x32-Poly3-10mm-50-177')
```

We expect to build rapidly commonly used probes in this public repository.

### 1.16.1 How to contribute

TODO: explain with more details

1. **Generate the JSON file with probeinterface (or directly with another language)**
2. Generate an image of the probe with the `plot_probe` function in probeinterface
3. Clone the [probeinterface\\_library](#) repo
4. Put the JSON file and image into the correct folder or make a new folder (following the format of the repo)
5. Push to one of your branches with a git client
6. Make a pull request to the main repo

## 1.17 API

### 1.17.1 Probe

```
class probeinterface.Probe(ndim: int = 2, si_units: str = 'um', name: str | None = None, serial_number: str | None = None, model_name: str | None = None, manufacturer: str | None = None)
```

Class to handle the geometry of one probe.

This class mainly handles contact positions, in 2D or 3D. Optionally, it can also handle the shape of the contacts and the shape of the probe.

```
add_probe_to_zarr_group(group: zarr.Group) → None
```

Serialize the probe's data and structure to a specified Zarr group.

This method is used to save the probe's attributes, annotations, and other related data into a Zarr group, facilitating integration into larger Zarr structures.

## Parameters

### group

[zarr.Group] The target Zarr group where the probe's data will be stored.

### annotate(\*\*kwargs)

Annotates the probe object.

## Parameters

**\*\*kwargs** : list of keyword arguments to add to the annotations (e.g., brain\_area="CA1")

### annotate\_contacts(\*\*kwargs)

Annotates the contacts of the probe.

## Parameters

**\*\*kwargs** : list of keyword arguments to add to the annotations (e.g., quality=["good", "bad", ...])

### property contact\_positions

The position of the center for each contact

### copy()

Copy to another Probe instance.

Note: device\_channel\_indices are not copied and contact\_ids are not copied

### create\_auto\_shape(probe\_type: 'tip' | 'rect' = 'tip', margin: float = 20.0)

Create planar contour automatically based on probe contact positions.

## Parameters

### probe\_type

["tip" | "rect", default: "tip"] The probe type ('tip' or 'rect')

### margin

[float, default: 20.0] The margin to add to the contact positions

### static from\_dataframe(df: pandas.DataFrame) → Probe

Create Probe from a pandas.DataFrame see Probe.to\_dataframe()

## Parameters

### df

[pandas.DataFrame] The dataframe representation of the probe

### Returns

**probe**

[Probe] The instantiated Probe object

**static from\_dict**(*d: dict*) → *Probe*

Instantiate a Probe from a dictionary

### Parameters

**d**

[dict] The dictionary representation of the probe

### Returns

**probe**

[Probe] The instantiated Probe object

**static from\_numpy**(*arr: ndarray*) → *Probe*

Create Probe from a complex numpy array see Probe.to\_numpy()

### Parameters

**arr**

[np.array] The structured np.array representation of the probe

### Returns

**probe**

[Probe] The instantiated Probe object

**static from\_zarr**(*folder\_path: str | Path*) → *Probe*

Deserialize the Probe object from a Zarr file located at the given folder path.

### Parameters

**folder\_path**

[str | Path] The path to the folder where the Zarr file is located.

### Returns

**Probe**

An instance of the Probe class initialized with data from the Zarr file.

**static from\_zarr\_group**(*group: zarr.Group*) → *Probe*

Load a probe instance from a given Zarr group.



### Parameters

**group**

[zarr.Group] The Zarr group from which to load the probe.

### Returns

**Probe**

An instance of the Probe class initialized with data from the Zarr group.

**get\_contact\_count()** → int

Return the number of contacts on the probe.

**get\_contact\_vertices()** → list

Return a list of contact vertices.

**get\_shank\_count()** → int

Return the number of shanks for this probe.

**get\_shanks()**

Return the list of Shank objects for this Probe

**get\_slice(selection: ndarray[bool | int])**

Get a copy of the Probe with a sub selection of contacts.

Selection can be boolean or by index

### Parameters

**selection**

[np.array of bool or int (for index)] Either an np.array of bool or for desired selection of contacts or the indices of the desired contacts

### Returns

**sliced\_probe: Probe**

The sliced probe

**move(translation\_vector: np.array | list)**

Translate the probe in one direction.

### Parameters

**translation\_vector**

[list or array] The translation vector in shape 2D or 3D

**rotate(theta: float, center: list | np.ndarray | None = None, axis: 'xy' | 'yz' | 'xz' | None = None)**

Rotate the probe around a specified axis.

### Parameters

**theta**

[float] In degrees, anticlockwise/counterclockwise

**center**

[array | list | None, default: None] Center of rotation. If None, the center of probe is used

**axis**

["xy" | "yz" | "xz" | None, default: None] Axis of rotation. It must be None for 2D probes It must be given for 3D probes

**rotate\_contacts**(*thetas*: float | np.array[float] | list[float])

Rotate each contact of the probe. Internally, it modifies the `contact_plane_axes`.

### Parameters

**thetas**

[float | array[float] | list[float]] Rotation angle in degrees. If scalar, then it is applied to all contacts.

**set\_contact\_ids**(*contact\_ids*: np.array | list)

Set contact ids. Channel ids are converted to strings. Contact ids must be **unique** for the **Probe** and also for the **ProbeGroup**

### Parameters

**contact\_ids**

[list or array] Array with contact ids. If contact\_ids are int or float they are converted to str

**set\_contacts**(*positions*, *shapes*='circle', *shape\_params*={'radius': 10}, *plane\_axes*=None, *contact\_ids*=None, *shank\_ids*=None)

Sets contacts to a Probe.

**This sets four attributes of the probe:**

`contact_positions`, `contact_shapes`, `contact_shape_params`, `_contact_plane_axes`

### Parameters

**positions**

[array (num\_contacts, ndim)] Positions of contacts (2D or 3D depending on probe 'ndim').

**shapes**

["circle" | "square" | "rect" | array, default: "circle"] Shape of each contact ('circle'/'square'/'rect').

**shape\_params**

[dict or list of dict, default: {"radius": 10}] Contains kwargs for shapes: \* "radius" for circle \* "width" for square, \* "width/height" for rect

**plane\_axes**

[np.array (num\_contacts, 2, ndim) | None, default: None] Defines the two axes of the contact plane for each electrode. The third dimension corresponds to the probe *ndim* (2d or 3d).

**contact\_ids: array[str] | None, default: None**

Defines the contact ids for the contacts. If None, contact ids are not assigned.

**shank\_ids**

[array[str] | None, default: None] Defines the shank ids for the contacts. If None, then these are assigned to a unique Shank.

**set\_device\_channel\_indices**(*channel\_indices: np.array | list*)

Manually set the device channel indices.

If some channels are not connected or not recorded then channel should be set to “-1”

**Parameters****channel\_indices**

[array[int] | list[int]] The device channel indices to set

**set\_planar\_contour**(*contour\_polygon: list*)

Set the planar contour (the shape) of the probe.

**Parameters****contour\_polygon**

[list] List of contour points (2D or 3D depending on ndim)

**set\_shank\_ids**(*shank\_ids: np.array | list*)

Set shank ids.

**Parameters****shank\_ids**

[list or array] Array with shank ids, if int or float converted to strings

**to\_2d**(*axes: xy' | 'yz' | 'xz = 'xy'*)

Transform 3d probe to 2d probe.

Note: device\_channel\_indices are not copied.

**Parameters****plane**

[“xy” | “yz” | “xz”, default: “xy”] The plane on which the 2D probe is defined.

**to\_3d**(*axes: xy' | 'yz' | 'xz = 'xz'*)

Transform 2d probe to 3d probe.

Note: device\_channel\_indices are not copied.

### Parameters

#### axes

["xy" | "yz" | "xz", default: "xz"] The axes that define the plane on which the 2D probe is defined.  
'xy', 'yz', 'xz'

**to\_dataframe**(*complete: bool = False*) → pandas.DataFrame

Export the probe to a pandas dataframe

### Parameters

#### complete

[bool, default: False] If True, export complete information about the probe, including the probe plane axis.

### Returns

#### df

[pandas.DataFrame] The dataframe representation of the probe

**to\_dict**(*array\_as\_list: bool = False*) → dict

Create a dictionary of all necessary attributes. Useful for dumping and saving to json.

### Parameters

#### array\_as\_list

[bool, default: False] If True, arrays are converted to lists

### Returns

#### d

[dict] The dictionary representation of the probe

**to\_image**(*values: np.array | list, pixel\_size: float = 0.5, num\_pixel: Optional[int] = None, method: linear' | 'nearest' | 'cubic' = 'linear', xlims: Optional[tuple] = None, ylims: Optional[tuple] = None*) → tuple[np.ndarray, tuple, tuple]

Generated a 2d (image) from a values vector with an interpolation into a grid mesh.

### Parameters

#### values

[np.ndarray | list] vector same size as contact number to be color plotted

#### pixel\_size

[float, default: 0.5] size of one pixel in micrometers

#### num\_pixel

[Optional[int] | None, default: None] alternative to pixel\_size give pixel number of the image width

#### method

["linear" | "nearest" | "cubic", default: "linear"] Method of interpolation to generate a grid mesh

**xlims**  
[Optional[tuple], default: None] Force image xlims

**ylims**  
[Optional[tuple], default: None] Force image ylims

## Returns

**image**  
[2d array] The generated image

**xlims**  
[tuple] The x limits

**ylims**  
[tuple] The y limits

**to\_numpy**(*complete: bool = False*) → array

Export to a numpy vector (structured array). This vector handles all contact attributes.

Equivalent to the ‘to\_dataframe()’ pandas function, but without pandas dependency.

Very useful to export/slice/attach to a recording.

## Parameters

**complete**  
[bool, default: False] If True, export complete information about the probe, including contact\_plane\_axes/si\_units/device\_channel\_indices

## returns

**arr**  
[numpy.array] With complex dtype

**to\_zarr**(*folder\_path: str | Path*) → None

Serialize the Probe object to a Zarr file located at the specified folder path.

This method initializes a new Zarr group at the given folder path and calls *add\_probe\_to\_zarr\_group* to serialize the Probe’s data into this group, effectively storing the entire Probe’s state in a Zarr archive.

## Parameters

**folder\_path**  
[str | Path] The path to the folder where the Zarr data structure will be created and where the serialized data will be stored. If the folder does not exist, it will be created.

**wiring\_to\_device**(*pathway: str, channel\_offset: int = 0*)

Automatically set device\_channel\_indices based on a pathway.

See probeinterface.get\_available\_pathways()

### Parameters

#### **pathway**

[str] The pathway. E.g. 'H32>RHD'

#### **channel\_offset: int, default: 0**

An optional offset to add to the device\_channel\_indices

## 1.17.2 ProbeGroup

### **class** probeinterface.ProbeGroup

Class to handle a group of Probe objects and the global wiring to a device.

Optionally, it can handle the location of different probes.

#### **add\_probe**(probe: [Probe](#))

Add an additional probe to the ProbeGroup

### Parameters

#### **probe: Probe**

The probe to add to the ProbeGroup

#### **auto\_generate\_contact\_ids**(\*args, \*\*kwargs)

Annotate all contacts with unique contact\_id values.

### Parameters

*\*args*: will be forwarded to *probeinterface.utils.generate\_unique\_ids* *\*\*kwargs*: will be forwarded to *probeinterface.utils.generate\_unique\_ids*

#### **auto\_generate\_probe\_ids**(\*args, \*\*kwargs)

Annotate all probes with unique probe\_id values.

### Parameters

*\*args*: will be forwarded to *probeinterface.utils.generate\_unique\_ids* *\*\*kwargs*: will be forwarded to *probeinterface.utils.generate\_unique\_ids*

#### **static from\_dict**(d: dict)

Instantiate a ProbeGroup from a dictionary

### Parameters

**d**  
[dict] The dictionary representation of the probegroup

### Returns

**probegroup**  
[ProbeGroup] The instantiated ProbeGroup object

**static from\_numpy**(arr: ndarray) → *ProbeGroup*  
Create ProbeGroup from a complex numpy array see ProbeGroup.to\_numpy()

### Parameters

**arr**  
[np.array] The structured np.array representation of the probe

### Returns

**probegroup**  
[ProbeGroup] The instantiated ProbeGroup object

**get\_contact\_count**() → int  
Total number of channels.

### Returns

**n: int**  
The total number of channels

**get\_global\_contact\_ids**() → ndarray  
Gets all contact ids concatenated across probes

### Returns

**contact\_ids: np.ndarray**  
An array of the contaact ids across all probes

**get\_global\_device\_channel\_indices**() → ndarray  
Gets the global device channels indices and returns as an array

### Returns

**channels: np.ndarray**

a numpy array vector with 2 columns (probe\_index, device\_channel\_indices)

### Notes

If a channel within channels has a value of -1 this indicates that that channel is disconnected

**set\_global\_device\_channel\_indices**(*channels: np.array | list*)

Set global indices for all probes

### Parameters

**channels: np.array | list**

The device channel indices to be set

**to\_dataframe**(*complete: bool = False*) → pandas.DataFrame

Export the probegroup to a pandas dataframe

### Parameters

**complete**

[bool, default: False] If True, export complete information about the probegroup, including the probe plane axis.

### Returns

**df**

[pandas.DataFrame] The dataframe representation of the probegroup

**to\_dict**(*array\_as\_list: bool = False*)

Create a dictionary of all necessary attributes.

### Parameters

**array\_as\_list**

[bool, default: False] If True, arrays are converted to lists, by default False

### Returns

**d**

[dict] The dictionary representation of the probegroup

**to\_numpy**(*complete: bool = False*) → ndarray

Export all probes into a numpy array.



## Parameters

**complete: bool, default: False**

If True, export complete information about the probegroup including contact\_plane\_axes/si\_units/device\_channel\_indices

### 1.17.3 Import/export to formats

**Read/write probe info using a variety of formats:**

- probeinterface (.json)
- PRB (.prb)
- CSV (.csv)
- mearec (.h5)
- spikeglx (.meta)
- ironclust/jrclust (.mat)
- Neurodata Without Borders (.nwb)

`probeinterface.io.read_probeinterface(file: str | Path) → ProbeGroup`

Read probeinterface JSON-based format.

## Parameters

**file: Path or str**

The file path

## Returns

probegroup : ProbeGroup object

`probeinterface.io.write_probeinterface(file: str | Path, probe_or_probegroup: Probe | ProbeGroup)`

Write a probeinterface JSON file.

The format handles several probes in one file.

## Parameters

**file**

[Path or str] The file path

**probe\_or\_probegroup**

[Probe or ProbeGroup object] If probe is given a probegroup is created anyway

`probeinterface.io.read_prb(file: str | Path) → ProbeGroup`

Read a PRB file and return a ProbeGroup object.

Since PRB does not handle contact shapes, contacts are set to be circle of 5um radius. Same for the probe shape, where an auto shape is created.

PRB format does not contain any information about the channel of the probe Only the channel index on device is given.

## Parameters

### file

[Path or str] The file path

## Returns

probegroup : ProbeGroup object

probeinterface.io.**write\_prb**(*file: str, probegroup: ProbeGroup, total\_nb\_channels: int | None = None, radius: float | None = None, group\_mode: str = 'by\_probe'*)

Write ProbeGroup into a prb file.

### This format handles:

- multi Probe with channel group index key
- channel positions with “geometry”
- device\_channel\_indices with “channels” key

### Note: much information is lost in the PRB format:

- contact shape
- shape
- channel index

### Note:

- “total\_nb\_channels” is needed by spyking-circus
- “radius” is needed by spyking-circus
- “graph” is not handled

## Parameters

### file: str

The name of the file to be written

### probegroup: ProbeGroup

The Probegroup to be used for writing

### total\_nb\_channels: Optional[int], default None

\*\*\*to do

### radius: Optional[float], default None

\*\*\* to do

### group\_mode: str

One of “by\_probe” or “by\_shank

probeinterface.io.**read\_csv**(*file: str | Path*)

Return a 2 or 3 columns csv file with contact positions

probeinterface.io.**write\_csv**(*file, probe*)

Write contact postions into a 2 or 3 columns csv file

`probeinterface.io.read_spikeglx(file: str | Path) → Probe`

Read probe position for the meta file generated by SpikeGLX

See <http://billkarsh.github.io/SpikeGLX/#metadata-guides> for implementation. The x\_pitch/y\_pitch/width are set automatically depending the NP version.

The shape is auto generated as a shank.

**Now reads:**

- NP0.0 (=phase3A)
- NP1.0 (=phase3B2)
- NP2.0 with 4 shank
- NP1.0-NHP

### Parameters

**file**

[Path or str] The .meta file path

### Returns

probe : Probe object

`probeinterface.io.read_mearec(file: str | Path) → Probe`

Read probe position, and contact shape from a MEArec file.

See <https://mearec.readthedocs.io/en/latest/> and <https://doi.org/10.1007/s12021-020-09467-7> for implementation.

### Parameters

**file**

[Path or str] The file path

### Returns

probe : Probe object

`probeinterface.io.read_nwb(file)`

Read probe position from an NWB file

## 1.17.4 Probe generators

This module contains useful helper functions for generating probes.

`probeinterface.generator.generate_dummy_probe(elec_shapes: circle | 'square' | 'rect = 'circle') → Probe`

Generate a dummy probe with 3 columns and 32 contacts. Mainly used for testing and examples.

### Parameters

#### **elec\_shapes**

["circle" | "square" | "rect", default: 'circle'] Shape of the electrodes

### Returns

#### **probe**

[Probe] The generated probe

`probeinterface.generator.generate_dummy_probe_group()` → *ProbeGroup*

Generate a ProbeGroup with 2 probes. Mainly used for testing and examples.

### Returns

#### **probe**

[Probe] The generated probe

`probeinterface.generator.generate_tetrode(r: float = 10.0)` → *Probe*

Generate a tetrode Probe.

### Parameters

#### **r: float, default: 10**

The distance multiplier for the positions

### Returns

#### **probe**

[Probe] The generated probe

`probeinterface.generator.generate_multi_columns_probe(num_columns: int = 3,  
num_contact_per_column: int = 10, xpitch:  
float = 20, ypitch: float = 20,  
y_shift_per_column: Optional[np.array | list]  
= None, contact_shapes: 'circle' | 'rect' |  
'square' = 'circle', contact_shape_params:  
dict = {'radius': 6})` → *Probe*

Generate a Probe with several columns.

### Parameters

#### **num\_columns**

[int, default: 3] Number of columns

#### **num\_contact\_per\_column**

[int, default: 10] Number of contacts per column

#### **xpitch**

[float, default: 20] Pitch in x direction

**ypitch**

[float, default: 20] Pitch in y direction

**y\_shift\_per\_column**

[Optional[array-like], default: None] Shift in y direction per column. It needs to have the same length as num\_columns, by default None

**contact\_shapes**

["circle" | "rect" | "square", default: "circle"] Shape of the contacts

**contact\_shape\_params**

[dict, default: {"radius": 6}] Parameters for the shape. For circle: {"radius": float} For square: {"width": float} For rectangle: {"width": float, "height": float}

**Returns****probe**

[Probe] The generated probe

```
probeinterface.generator.generate_linear_probe(num_elec: int = 16, ypitch: float = 20, contact_shapes:
circle' | 'rect' | 'square' = 'circle',
contact_shape_params: dict = {'radius': 6}) → Probe
```

Generate a one-column linear probe.

**Parameters****num\_elec**

[int, default: 16] Number of electrodes

**ypitch**

[float, default: 20] Pitch in y direction

**contact\_shapes**

["circle" | "rect" | "square", default: "circle"] Shape of the contacts

**contact\_shape\_params**

[dict, default: {"radius": 6}] Parameters for the shape. For circle: {"radius": float} For square: {"width": float} For rectangle: {"width": float, "height": float}

**Returns****probe**

[Probe] The generated probe

**1.17.5 Plotting**

A simple implementation for plotting a Probe or ProbeGroup using matplotlib.

Depending on Probe.ndim, the plotting is done in 2D or 3D

`probeinterface.plotting.plot_probe`(*probe*, *ax=None*, *contacts\_colors=None*, *with\_contact\_id: bool = False*, *with\_device\_index: bool = False*, *text\_on\_contact: list | ndarray | None = None*, *contacts\_values: ndarray | None = None*, *cmap: str = 'viridis'*, *title: bool = True*, *contacts\_kargs: dict = {}*, *probe\_shape\_kwargs: dict = {}*, *xlims: tuple | None = None*, *ylims: tuple | None = None*, *zlims: tuple | None = None*, *show\_channel\_on\_click: bool = False*)

Plot a Probe object. Generates a 2D or 3D axis, depending on `Probe.ndim`

## Parameters

### **probe**

[Probe] The probe object

### **ax**

[matplotlib.axis | None, default: None] The axis to plot the probe on. If None, an axis is created

### **contacts\_colors**

[matplotlib color | None, default: None] The color of the contacts

### **with\_contact\_id**

[bool, default: False] If True, channel ids are displayed on top of the channels

### **with\_device\_index**

[bool, default: False] If True, device channel indices are displayed on top of the channels

### **text\_on\_contact: None | list | numpy.array, default: None**

Addintional text to plot on each contact

### **contacts\_values**

[np.array, default: None] Values to color the contacts with

### **cmap**

[a colormap color, default: “viridis”] A colormap color

### **title**

[bool, default: True] If True, the axis title is set to the probe name

### **contacts\_kargs**

[dict, default: {}] Dict with kwargs for contacts (e.g. alpha, edgecolor, lw)

### **probe\_shape\_kwargs**

[dict, default: {}] Dict with kwargs for probe shape (e.g. alpha, edgecolor, lw)

### **xlims**

[tuple | None, default: None] Limits for x dimension

### **ylims**

[tuple | None, default: None] Limits for y dimension

### **zlims**

[tuple | None, default: None] Limits for z dimension

### **show\_channel\_on\_click**

[bool, default: False] If True, the channel information is shown upon click

### Returns

**poly**

[PolyCollection] The polygon collection for contacts

**poly\_contour**

[PolyCollection] The polygon collection for the probe shape

`probeinterface.plotting.plot_probe_group(probegroup, same_axes: bool = True, **kargs)`

Plot all probes from a ProbeGroup Can be in an existing set of axes or separate axes.

### Parameters

**probegroup**

[ProbeGroup] The ProbeGroup to plot

**same\_axes**

[bool, default: True] If True, the probes are plotted on the same axis

**kargs: dict**

see docstring for plot\_probe for possible kargs

## 1.17.6 Library

Provides functions to download and cache pre-existing probe files from some manufacturers.

The library is hosted here: [https://gin.g-node.org/spikeinterface/probeinterface\\_library](https://gin.g-node.org/spikeinterface/probeinterface_library)

The gin platform enables contributions from users.

`probeinterface.library.get_probe(manufacturer: str, probe_name: str, name: str | None = None) → Probe`

Get probe from ProbeInterface library

### Parameters

**manufacturer**

["cambridgeneurotech" | "neuronexus"] The probe manufacturer

**probe\_name**

[str (see probeinterface\_library for options)] The probe name

**name**

[str | None, default: None] Optional name for the probe

### Returns

probe : Probe object

## 1.18 Release notes

### 1.18.1 probeinterface 0.2.21

Feb, 1st 2024

#### Features

- Add equality dunder method and test to *Probe* object (#248)
- Add save to zarr method to *Probe* object (#250)
- Fix *Probe* special properties setters (skip empty strings) (#252, #253)

### 1.18.2 probeinterface 0.2.20

Dec, 11th 2023

#### Features

- Fix Open Ephys recording state options (#239)
- Make docstrings-style compliant and add assert messaging (#241)
- Add missing NP2.4 and NP-Ultra probe part number (#243)

### 1.18.3 probeinterface 0.2.19

Nov, 2nd 2023

#### Features

- Unify NP reading with probe part number (#232)

### 1.18.4 probeinterface 0.2.18

Oct, 30th 2023

#### Features

- Extend probe constructor (name, serial\_number, manufacturer, model\_name) (#206)
- Extend available NP2 probe types to commercial types (20\*\* series) (#217)
- Remove with\_channel\_index argument from plot\_probe (#229)
- Remove checker for unique contact ids in probe group (#229)
- Unify usage of “contact” and remove “channel” notation (except for “device\_channel\_index”) (#229)



## Bug fixes

- Fix shank\_pitch to NP-2.4 in SpikeGLX (#205)
- Fix y\_shift\_per\_column docs and add assertion (#212)
- Change np.in1d to np.isin as the former will be deprecated (#220)
- Fix contour of NP2.0 for Open Ephys Neuropixels (#224)

## Docs

- Add available pathways in 'Automatic wiring' docs (#213)
- Add Typing and Update Docstrings (#214)
- Add more details to how to contribute (#222)

### 1.18.5 probeinterface 0.2.17

Thanks a lot to Ramon Heberto Mayorquin, who did the most the changes for this release.

June, 26th 2023

## Packaging / Documentation / Testing

- Move probe libray from [GIN](#) to [GitHub](#) (#195)
- Restructure repo to follow `src/probeinterface` convention
- Black formatting anf pre-commit CI (#190-#191)
- Add safe import utils (#175)
- Add type hints in IO module (#173)
- Fix code coverage (#171)
- Cron job and manual trigger for CI tests (#170)
- Add badges and code coverage to actions (#168)
- Handle temporary files in the test suite (#164)
- Reorganize testing directory (#163)
- Update test workflow to use latest version of actions (#162)
- Add MEArec test data (#176)
- Add Maxwel and 3brain to tests (#172)
- Add test for shank (#181)
- Improve Documentation (#157 / 158)

### Features

- Extended support for Neuropixels probes: \* Fix CatGT parsin (#193) \* Map NP1010 probe to the usual NP1 geometry (#188) \* Open Ephys: Support subselection of channels in Record Node (#180) \* Add NP-ultra probe testing data for spikeglx (#177) \* Add IMRO tests (#179) \* Consolidate Neuropixels information in one place (#174) \* Refactor NP information (#166-#167) \* Add NHP probe support for SpikeGLX (#169-#165-#160-#156)

### Bug fixes

- Fix DeprecationWarning: invalid escape sequence m (#183)
- Mearec description to string (#159)

### Testing

- Add MEArec test data (#176)
- Add Maxwell and 3brain to tests (#172)
- Add test for shank (#181)

## 1.18.6 probeinterface 0.2.16

February, 9th 2023

- Fix for read\_spikeglx() when not all channels are saved

## 1.18.7 probeinterface 0.2.15

December, 12th 2022

- Bug fix when parsing Open Ephys version from XML file (<https://github.com/SpikeInterface/probeinterface/pull/146>)
- Add test files and tests for Open Ephys reader

## 1.18.8 probeinterface 0.2.14

October, 27th 2022

- Fix a **important bug** in read\_spikeglx() / read\_imro() that was leading to wrong contact locations when the Imec Readout Table (aka imRo) was set with complex multi-bank patterns. The bug was introduced with version **0.2.10**, released on September 1st 2022, and it is also present in these versions: **0.2.10**, **0.2.11**, **0.2.12**, and **0.2.13**.

**If you used spikeinterface/probeinterface with SpikeGLX data using one of these versions, we recommend you to check your contact positions (if they are non-standard - using the probe tip) and re-run your spike-sorting analysis if they are wrong.**

A big thanks to Tom Bugnon and Graham Findlay for [spotting the bug](#).

### 1.18.9 probeinterface 0.2.13

October, 20th 2022

- Fix install bug due to pyproject.toml
- Better handling of contact ids for unknown NP type in OpenEphy
- Including ability to read phase3A neuropixel arrays

### 1.18.10 probeinterface 0.2.12

October, 10th 2022

- New configuration files with pyproject.toml

### 1.18.11 probeinterface 0.2.11

September, 14th 2022

- do not rely on BASESTATION field to parse OpenEphys probe

### 1.18.12 probeinterface 0.2.10

September, 1st 2022

- fix read\_openephys()
- fix read\_spikeglx()
- regenerate cambridge neurotec
- implement read\_imro() / write\_imro()
- Add new wiring : 'ASSY-77>Adpt.A64-Om32\_2x-sm>two\_RHD2132'
- Handle OpenEphys NPIX with multiple probes
- Add cross-checked ASSY-116>RHD2132 mapping

### 1.18.13 probeinterface 0.2.9

April, 15th 2022

- openephys neuropixel
- fix examples

### 1.18.14 probeinterface 0.2.8

March, 23rd 2022

- wiring CambridgeNeurotec mini-amp-64
- expose function select\_dimensions (2d>3d and 3d>2d)
- add to\_dict/from\_dict in ProbeGroup
- Add “text\_on\_contact” in plot\_probe()
- Add read\_openephys function for Neuropux-PXI plugin

### 1.18.15 probeinterface 0.2.7

March, 1 2022

- add read\_3brain to io
- annotate spikeGLX with probe version

### 1.18.16 probeinterface 0.2.6

November, 26 2021

- documention improvement
- spikeglx neuropixel2 integration
- plotting improvement

### 1.18.17 probeinterface 0.2.5

September, 14 2021

- vector annotations added to numpy representation
- add “electrode” to annotations from read\_maxwell

### 1.18.18 probeinterface 0.2.4

July, 30 2021

- expose read\_maxwell function
- vector annotations
- changes to BIDS format

### 1.18.19 probeinterface 0.2.3

May, 21 2021

- add a pathway
- show\_channel\_on\_click
- debug read\_mearec()

### 1.18.20 probeinterface 0.2.2

April, 4 2021

- better plot\_probe with index
- write\_prb handle group\_mode
- add wiring RDH2164
- doc improvement

### 1.18.21 probeinterface 0.2.1

March, 24 2021

- read/write to BIDS proposal.
- to\_numpy()/from\_numpy()
- to\_dataframe()/from\_dataframe()
- read\_mearec

### 1.18.22 probeinterface 0.2.0

March, 2 2021

Format improvement with all ids in str.

### 1.18.23 probeinterface 0.1.0

11th jan 2021

Initial release.



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