# Using the density sorter chip simulation software density\_sorter.py

as described in "Sorting cells by their density" by Nazila Norouzi, Heran C. Bhakta, and William H. Grover *PLOS ONE* 10.1371/journal.pone.0180520 Department of Bioengineering, University of California, Riverside

A custom Python program, density\_sorter.py, was written to simulate the behavior of particles in density sorter chips. The current version of the software is available as online Supplementary Information, and the latest version of the software is available for download from https://groverlab.org. The software depends on three additional free Python packages that must be installed first: numpy (http://numpy.org), scipy (http://scipy.org), and matplotlib (http://matplotlib.org). These dependencies can be downloaded and installed individually, or they also come bundled with science-focused free Python distributions like Anaconda (http://www.continuum.io).

# Importing the density\_sorter.py package

To use density\_sorter.py, first create an empty Python file in the same directory as density\_sorter.py. In the blank file, add the following line to import the density\_sorter.py package:

```
import density_sorter as ds
```

Next, add lines that define the density sorter chip, the particles to be sorted in the chip, and the fluid densities in the chip.

#### Specifying the density sorter chip

The density sorter chip is created as an instance of the ds.Chip object. For example, this code,

creates a density sorter chip called **chip** which contains a channel with a height of  $1 \times 10^{-3}$  m (1 mm), a depth of  $1 \times 10^{-3}$  m (1 mm), and a length of 0.022 m (22 mm). Channel height is in the dimension parallel to Earth's gravity (*i.e.*, the distance from the floor to the ceiling of the channel). Channel depth is the width of the channel perpendicular to gravity. Channel length is the distance from the beginning of the horizontal channel (where two or more fluids with different densities merge together) to the end of the channel (where the fluids split into two or more outlets).

### Specifying the particles to be sorted

Particles are instances of the ds.Particle object. For example, this code,

creates a particle called red\_blood\_cells with a radius of  $4.5 \times 10^{-6}$  m (4.5  $\mu$ m) and a density of 1110.0 kg/m³ (1.110 g/mL). The starting location of the particle in the channel is x=0 (meaning that the particle originates at the point along the channel where the two or more fluids of different densities merge together) and  $y=\text{chip.channel\_height} \times 0.86$  (meaning that the particle originates at a point that is 86% of the way to the top or ceiling of the channel; this represents a location that is in the middle of the topmost fluid density layer in this experiment). The remaining arguments for the particle, marker\_size=10 and marker\_color="r", specify the size (10 units) and color (red) to use when plotting the trajectory of this particle in the simulation results. Refer to the documentation for the Python plotting package matplotlib for details on these arguments.

For a second example of a particle object, here is the code that creates another particle, this one called white\_blood\_cells:

This particle has a different radius and density but starts in the same location as the red\_blood\_cells particle. It will be plotted using a larger marker colored green.

#### Specifying the fluids in the chip

Fluids are instances of the ds.Fluid object. For example, this code,

creates three different fluids. The first one, named f1, has a density of 1110.0 kg/m<sup>3</sup> (1.110 g/mL), a viscosity of 0.001 kg m<sup>-1</sup> s<sup>-1</sup>, and a flow rate into the chip of  $1.66 \times 10^{-11}$  m<sup>3</sup>/s (1.00  $\mu$ L/min). Note that in the current version of density\_sorter.py, the viscosity of the fluid is used when calculating the velocity of a particle in that fluid (solving Equation 2 in the main text), but not when calculating the horizontal flow profile in the channel (Equation 1 in the main text). Therefore, for accurate results, currently the viscosity of all fluids in a simulation should be equal. Finally, the argument color='#6666ff' specifies the color of the fluid to use when plotting the simulation results; this color is the hexadecimal representation of a dark blue color. Similarly, fluid f2 has a unique density (1.085 g/mL) and color (medium blue), and f3 has a unique density (1.070 g/mL) and color (light blue).

# Running the simulation

Once the chip, the particles to be sorted, and the fluids inside the chip are defined, the simulation is run using the ds.simulate() function. For example, the code

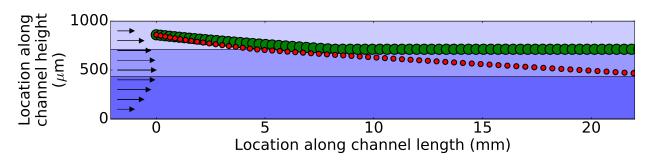
runs a simulation of the chip named chip containing the fluids f1, f2, and f3. The fluids are specified in the order in which the flow into the chip, from lowest (closest to Earth) to highest. To form a conventional density-gradient-like stack of densities in the horizontal channel (with the most-dense fluid on the bottom and the least-dense fluid on the top), this means that the most-dense fluid should be specified first (f1 in this example) and the least-dense fluid should be specified last (f3). Note that if fluids are pumped into a chip in an order that places a more-dense fluid *above* a less-dense fluid, the layers may automatically reorient themselves to place the less-dense layer on the bottom [1]. The density\_sorter.py software supports any number of different fluids with different densities. The argument particles=(white\_blood\_cells, red\_blood\_cells) specifies which particles to simulate in the chip; again, any number of different particle types are supported. The argument delta\_t=5 specifies the time resolution of the simulation; in this example, Equations 1 and 2 from the main text will be solved for each particle at five second increments, and a marker specifying the location of each particle will be plotted every five seconds. Finally, the argument yticks=[0, 500, 1000] specifies where to place tick marks on the y axis of the simulation results (in units of  $\mu$ m), and the argument xlim=[-2.1, 22] specifies the range of the x axis of the simulation results (the length of the plot in the direction of the channel length, in units of mm); the documentation for the Python plotting package matplotlib has more details on these arguments.

# Obtaining the simulation results

Combining the preceding lines of code into a single file creates the code needed to generate Fig 5d in the main text:

```
import density_sorter as ds
chip = ds.Chip(channel_height=1e-3, channel_depth=1e-3,
               channel_length=0.022)
red_blood_cells = ds.Particle(radius=9e-6/2.0, density=1110.0,
                              location=(0, chip.channel_height*0.86),
                              marker_size=10, marker_color="r")
white_blood_cells = ds.Particle(radius=13.5e-6/2.0, density=1080.0,
                                location=(0, chip.channel_height*0.86),
                                marker_size=20, marker_color="g")
f1 = ds.Fluid(density=1110.0, viscosity=0.001, flow_rate=1.66e-11,
              color='#6666ff')
f2 = ds.Fluid(density=1085.0, viscosity=0.001, flow_rate=1.66e-11,
              color='#9999ff')
f3 = ds.Fluid(density=1070.0, viscosity=0.001, flow_rate=8.33e-12,
              color='#ccccff')
ds.simulate(chip, fluids=(f1, f2, f3),
            particles=(white_blood_cells, red_blood_cells), delta_t=5,
            yticks=[0, 500, 1000], xlim=[-2.1, 22])
```

This code generates the following plot, also shown as Fig 5D in the main text:



The Python file for this and all other simulations shown in the manuscript are available for download as online *Supplementary Information*:

- fig2a.py: Code for generating the simulation in Fig 2A
- fig2b.py: Code for generating the simulation in Fig 2B
- fig3b.py: Code for generating the simulation in Fig 3B

- fig4b.py: Code for generating the simulation in Fig 4B
- fig5d.py: Code for generating the simulation in Fig 5D

# References

[1] Nazila Norouzi, Heran C Bhakta, and William H Grover. Orientation-based control of microfluidics. *PLOS ONE*, 11(3):e0149259, 2016.