A

morphology
cell area, volume, circularity, aspect ratio

stiffness
cell membrane Young's modulus

motility
cell speed, position in time

contractility
nuclear volume, traction force

proliferation
number of cells over time

culture substrates

cell lines

genomics
whole exome sequencing, annotated variant calls

proteomics
iBAQ, Phospho, TMT, protein descriptions

RNA
miRNA, mRNA, gene and differential expression

B

motility

id	measurement id
cl_id	unique cell line id
sub_id	unique substrate id
avg_speed	mean cell speed
avg_distance	mean distance travelled (by a cell)

cell line

id	unique cell line id
name	cell line catalog id
tissue	cell line source tissue

substrate

id	unique substrate id
name	substrate lab name
matrix	hydrogel matrix type

proteomics

id	assay measurement id
cl_id	unique cell line id
sub_id	unique substrate id
peptide	peptide sequence
protein	standard protein name
prob	Peptide Prophet score

motility

id	cl_id	sub_id	avg_speed	...
0	0	0	35.5	...
1	0	1	44.0	...
2	1	1	19.5	...
...	...	...	...	...

cell_line

id	name	tissue	...
0	A375	skin	...
1	22Rv1	prostate	...
...	...	...	...

substrate

id	name	matrix	...
0	glass	na	...
1	HaCol	HA	...
...	...	...	...

proteomics_iBAQ

id	cl_id	sub_id	peptide	...
0	0	0	R.LGLFYQLLHK.V	...
1	0	1	R.LGLFYQLLHK.V	...
...	...	...	...	...

R: library(dplyr); left_join(motility, proteomics_iBAQ, by = c('cl_id', 'sub_id'));

Python: import pandas; motility.merge(proteomics_iBAQ, how = 'left', on =['cl_id', 'sub_id'])

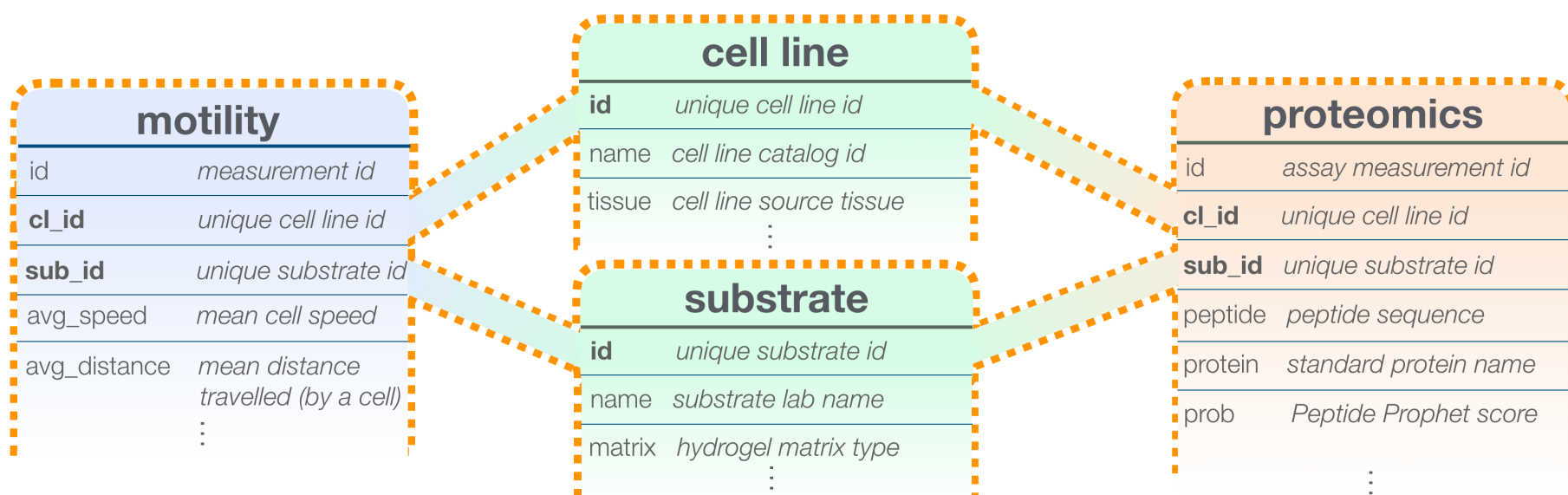**SQL:** SELECT * FROM motility LEFT JOIN proteomics_iBAQ
ON motility.cl_id = proteomics_iBAQ.cl_id AND motility.sub_id = proteomics_iBAQ.sub_id;

Result:

id	cl_id	sub_id	avg_speed	avg_distance	peptide	protein	prob	...
0	0	0	35.5	71.0	R.LGLFYQLLHK.	sp|A1L0T0|ILVBL_HUMAN	0.92	...
...	...	...	...	...	...	...	...	...