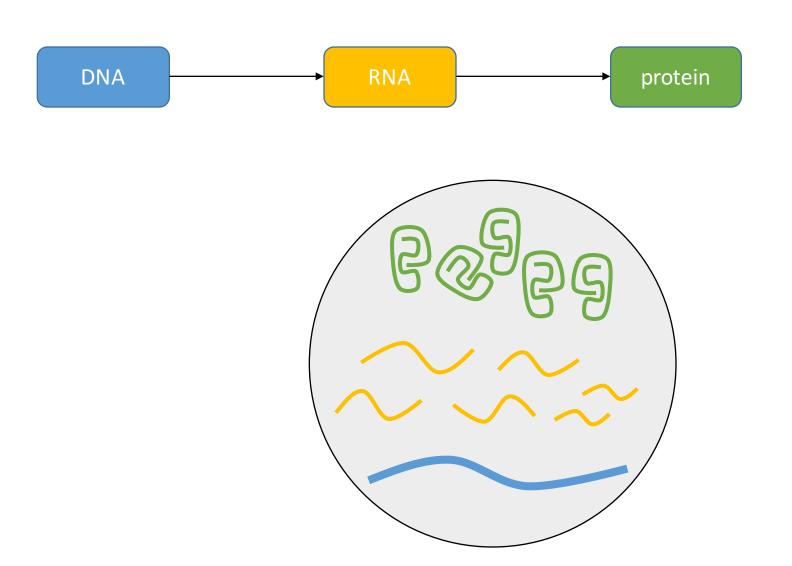
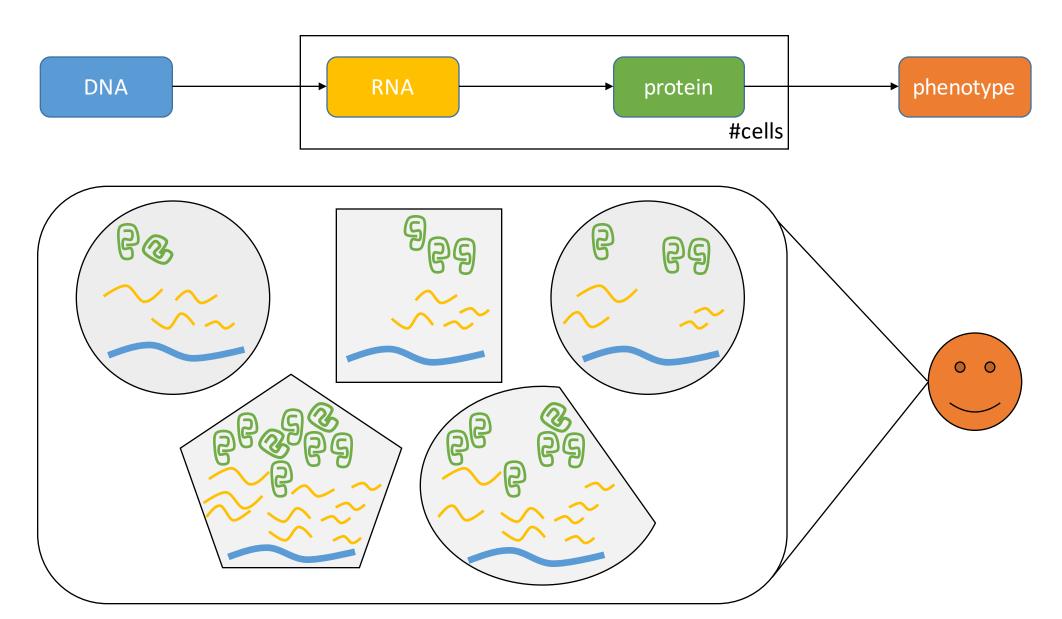
# Biological data: a crash course

Yakir Reshef

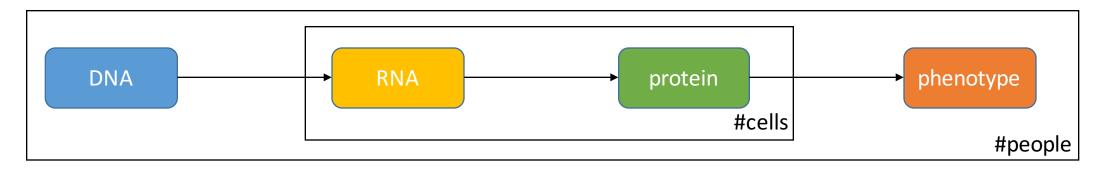
# The central dogma

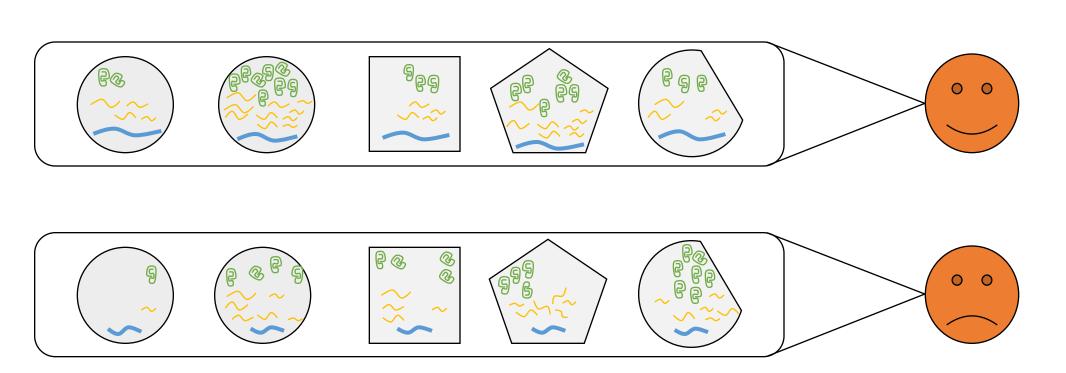


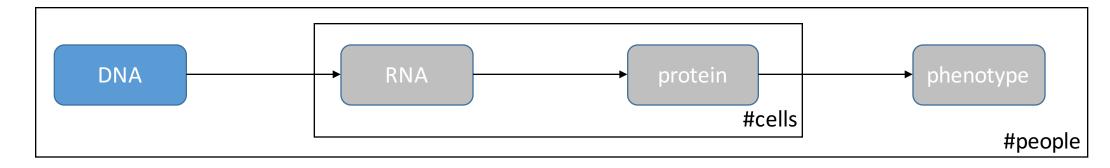
# The central dogma



# The central dogma







human genome (~109 base pairs)

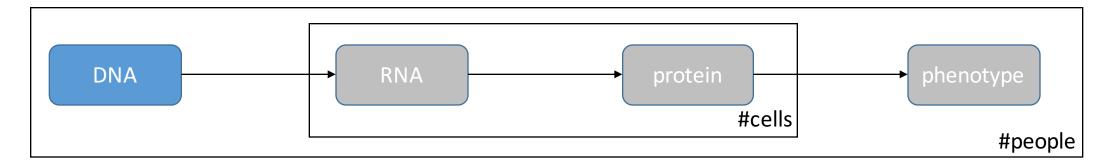
```
A/A C/C A/A C/C G/G G/G T/T C/C A/A

A/A C/C A/A G/C G/G G/G T/T C/C T/A

A/A C/C A/A G/G G/G G/G T/T C/C A/A

A/A C/C A/A G/G G/G G/G G/T C/C A/A

A/A C/C A/A C/C G/G G/G T/T C/C A/A
```



human genome (~109 base pairs)

Two alleles at each spot

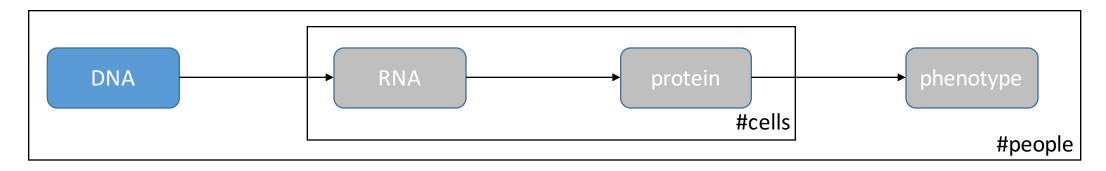
```
A/A C/C A/A C/C G/G G/G T/T C/C A/A

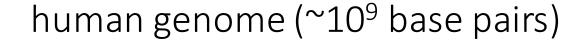
A/A C/C A/A G/C G/G G/G T/T C/C T/A

A/A C/C A/A G/G G/G G/G G/T C/C A/A

A/A C/C A/A C/C G/G G/G T/T C/C A/A
```

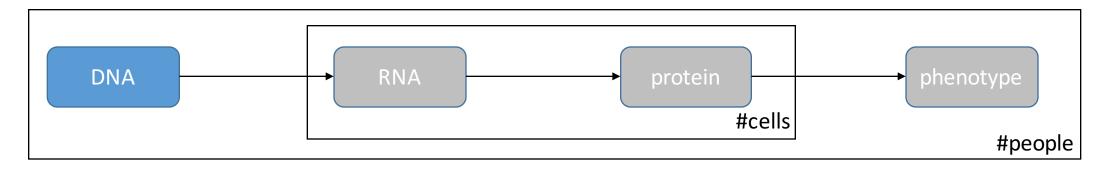
people





Two alleles at each spot

Most spots: no variation observed



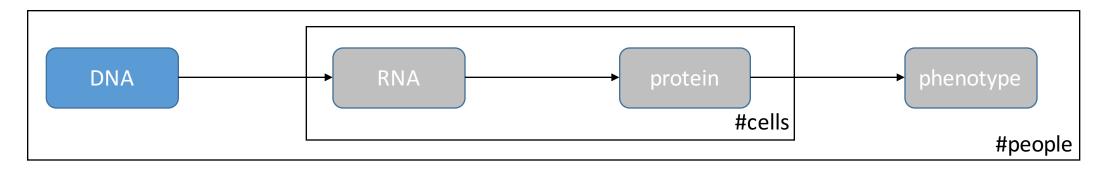
human genome (~10<sup>9</sup> base pairs)

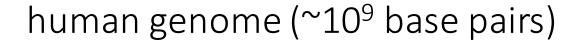
Two alleles at each spot

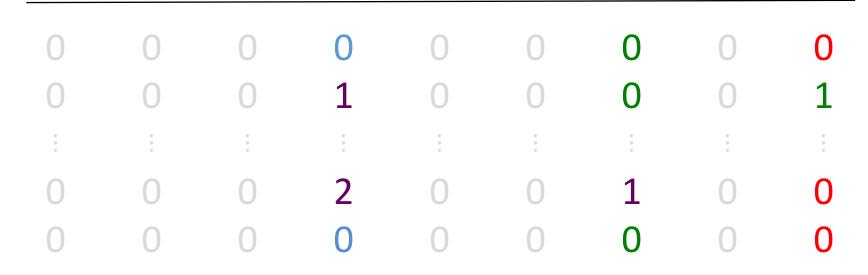
Most spots: no variation observed

Genetic variants can be coded as 0/1/2

people





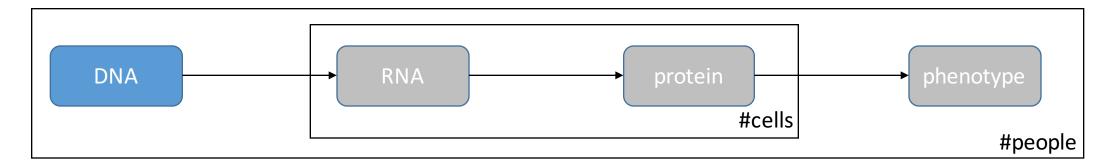


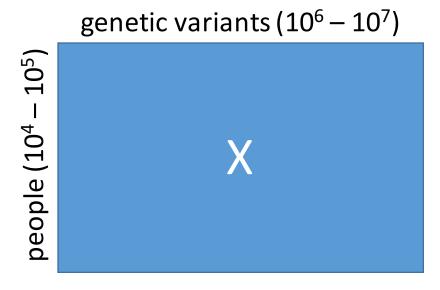
Two alleles at each spot

Most spots: no variation observed

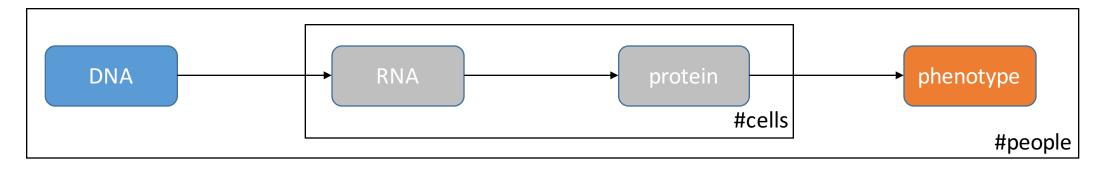
Genetic variants can be coded as 0/1/2

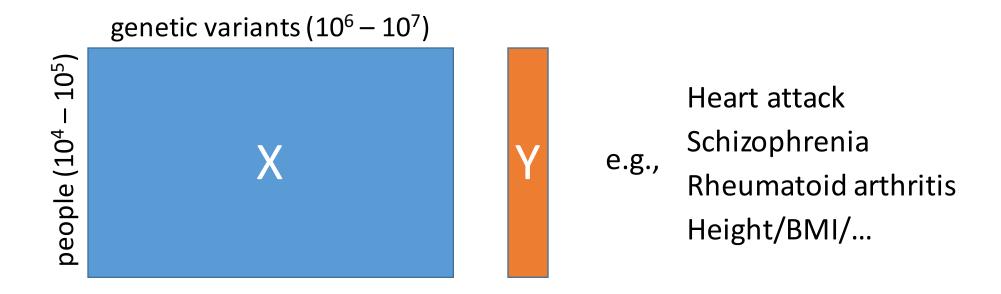
people



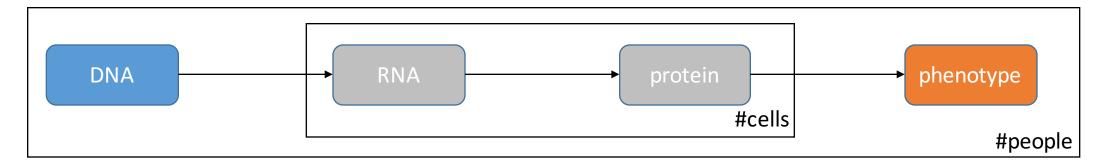


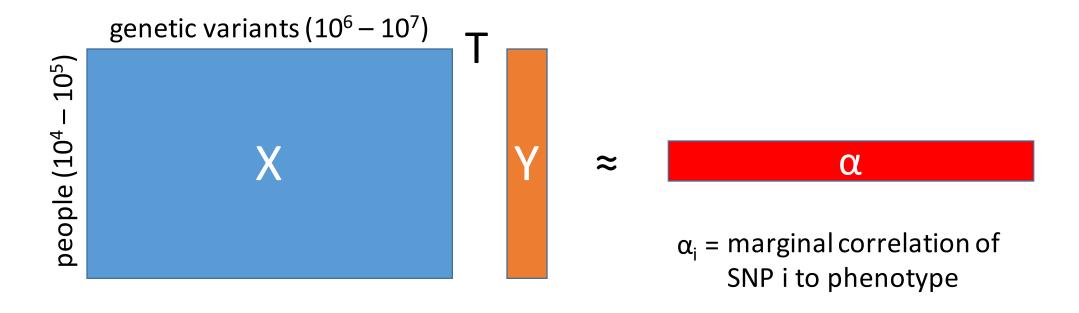
## Genome-wide association study (GWAS)



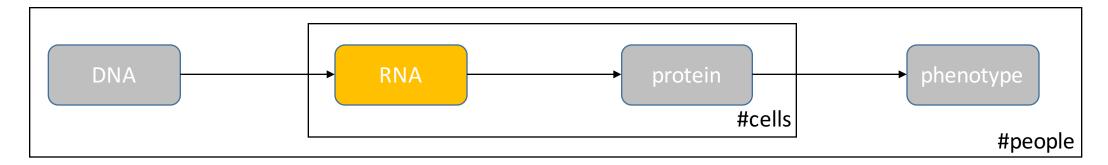


## Genome-wide association study (GWAS)



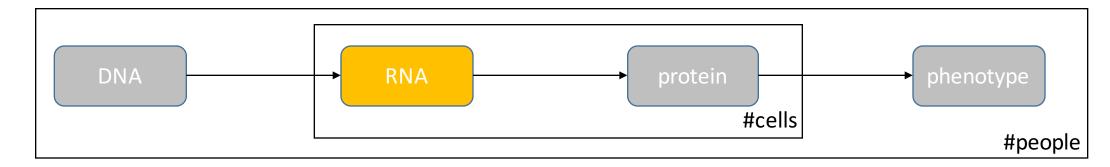


## Gene expression



human genome

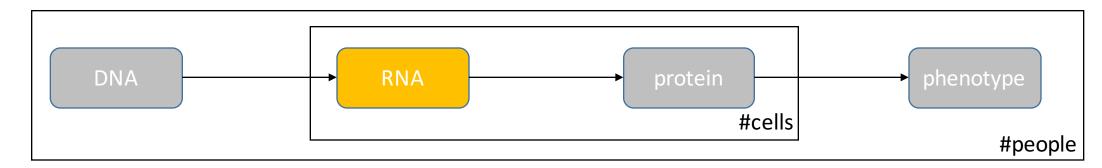
#### Gene expression

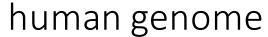






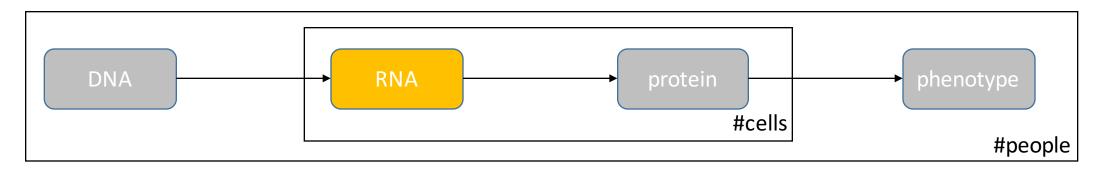
## Single-cell RNA sequencing



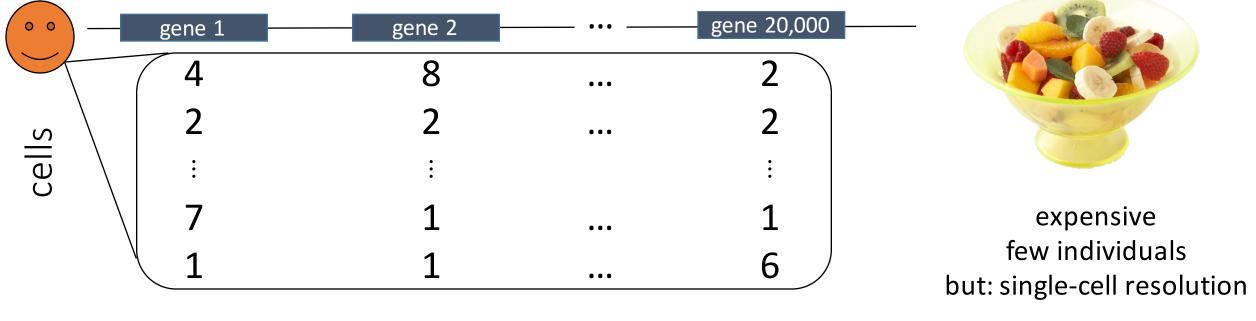




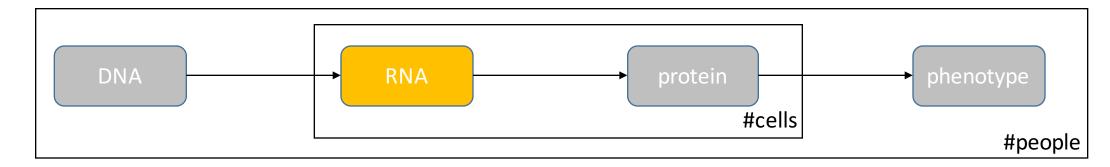
## Single-cell RNA sequencing

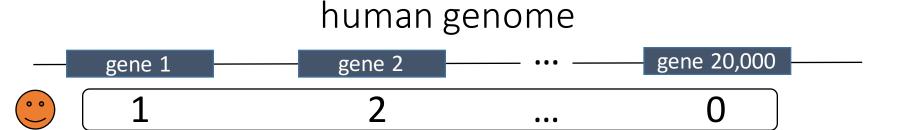






# Bulk RNA sequencing

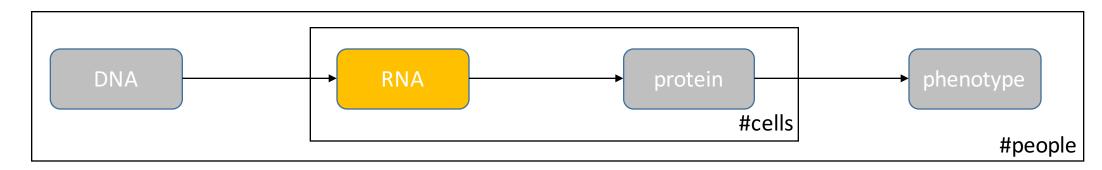


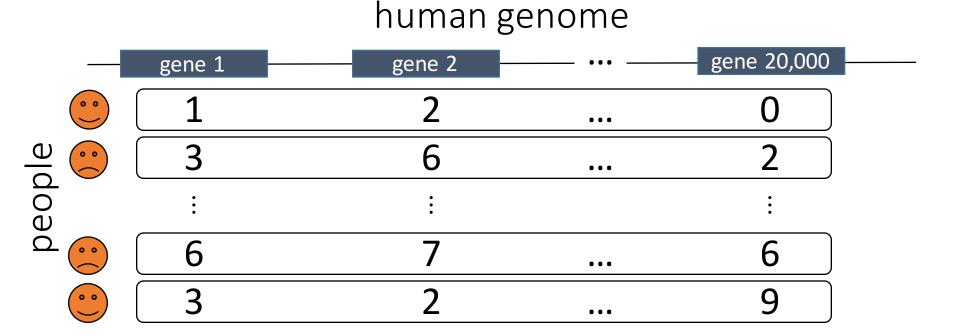




people

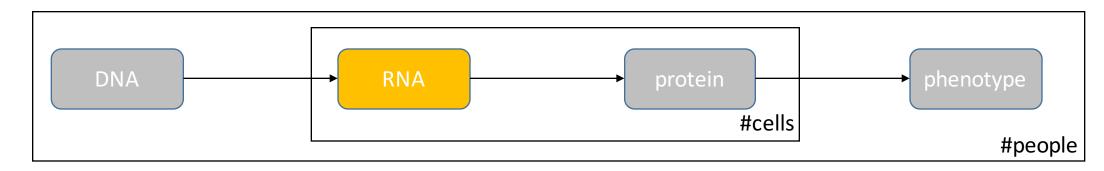
## Bulk RNA sequencing

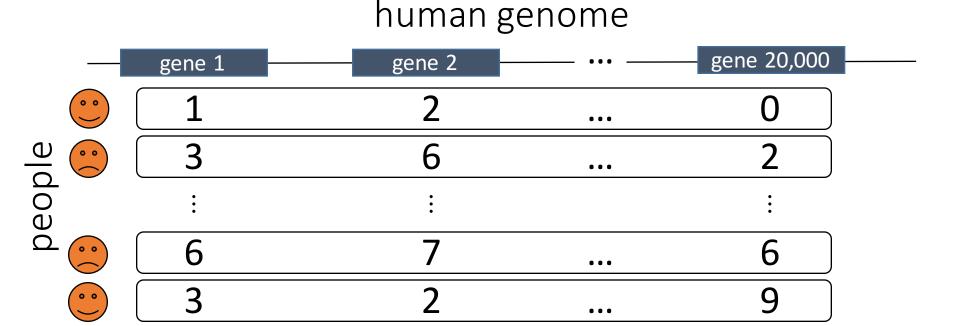






## Bulk RNA sequencing







cheap many individuals but: only averages

#### Summary

