

# Project 2024

## BINF-F401

Vincent Detours

# Overview of course evaluation

## Written exam

- Questions assess your understanding of the theory
- It's an open book exam or 2 hours (but don't expect to study the course during these two hours!)
- You've got a personal grade

## Project

- You apply ideas and tools of the course on real data
- It's a mini research project evaluated from a written report
- It's done by groups of three students, so grade is collective

Final grade is the harmonic mean of exam and project (see [https://en.wikipedia.org/wiki/Harmonic\\_mean](https://en.wikipedia.org/wiki/Harmonic_mean)). Thus, you need reasonable scores for both exam and project to pass.

Scientific background

# Quantitative morphology



- Tissue morphology is the topic of a branch of medicine called pathology
- The diagnostic of many diseases, including cancer, rests of morphological analysis
- The main instrument of pathologists is the **microscope**



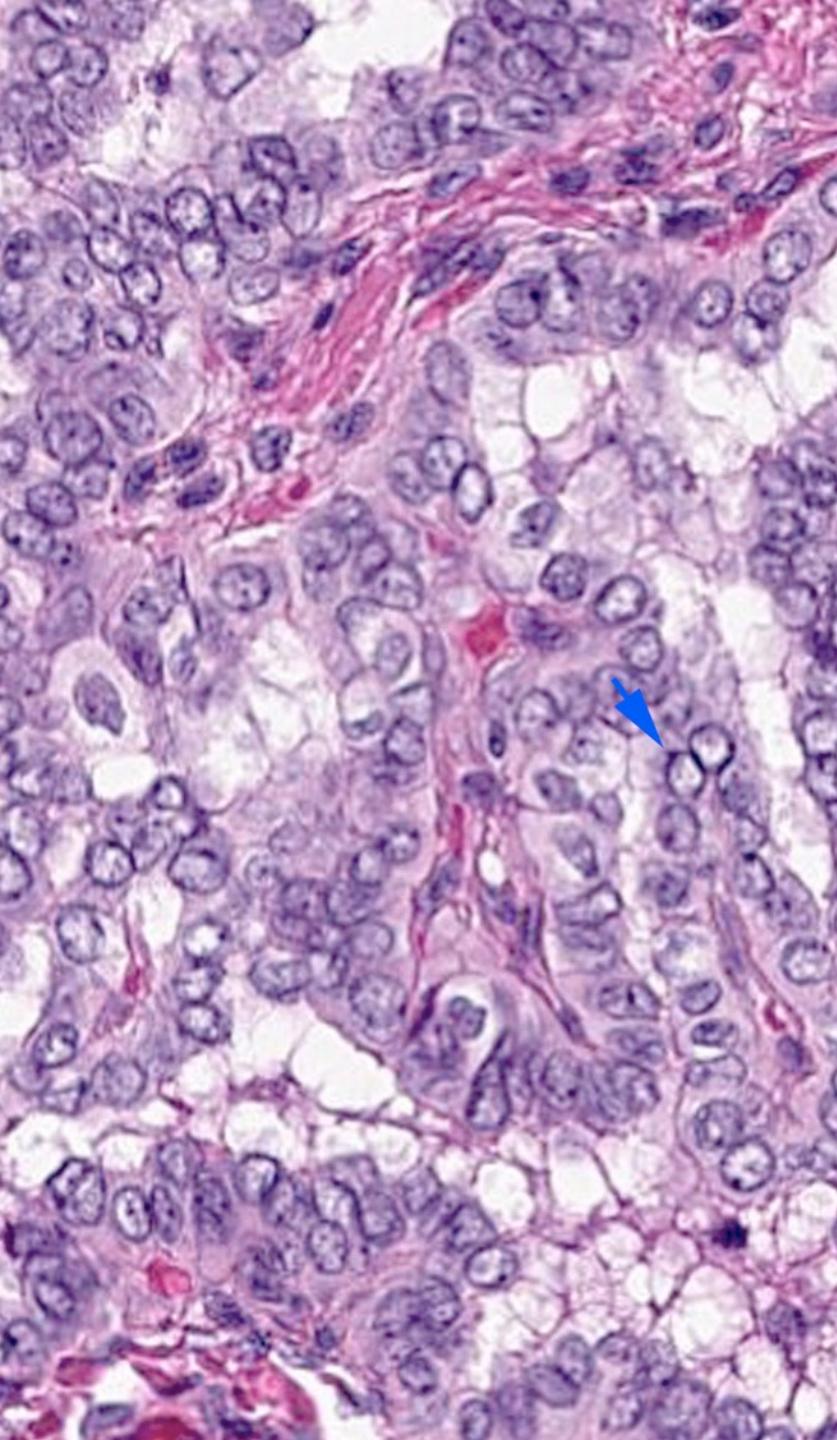
Microscope of  
van Leeuwenhoek  
(replica, 1670)

- The extraordinary progress of microscope technology paved the way of many conceptual advances in biology and medicine



Leica confocal  
microscope,  
2017

- But the description of morphology has barely evolved over centuries: it remains qualitative and somewhat subjective



## Example (thyroid cancer)

- Nuclei of cancer cells are large, irregular, light, have the aspect of ground glass. Some look like coffee beans.

This verbal description is

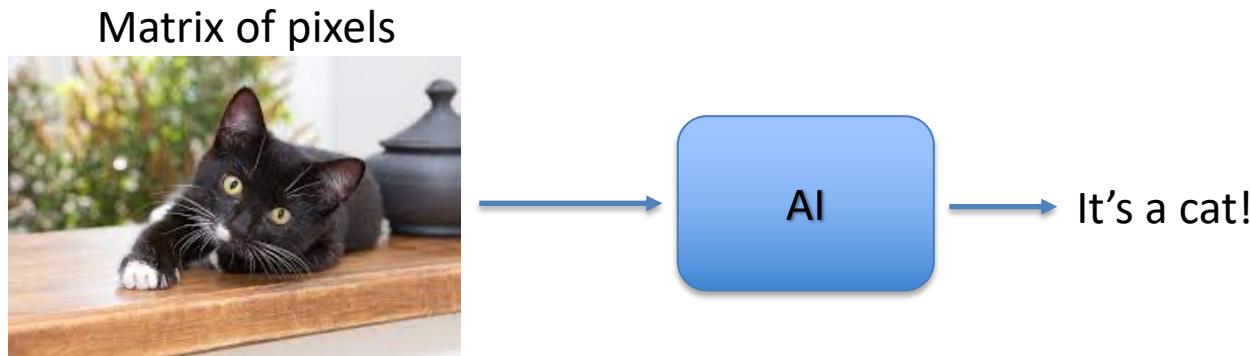
- **Qualitative:** what is the limit between normal and 'big' nuclei?
- **Subjective:** do two pathologists have the same idea of 'big', 'irregular' and 'coffee bean-like'?

These shortcomings are obstacles to

- the quality of diagnostic
- our understanding of morphology

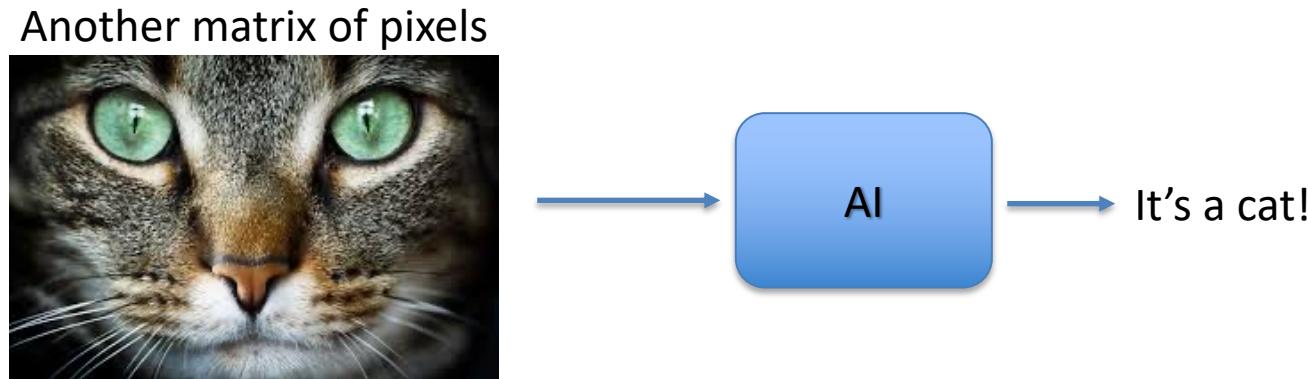
# Artificial intelligence may set morphology on a quantitative basis

- Photos is a matrices of pixels reflecting the activation of an optical sensor
- AI extract high-level **semantic information** from raw images:



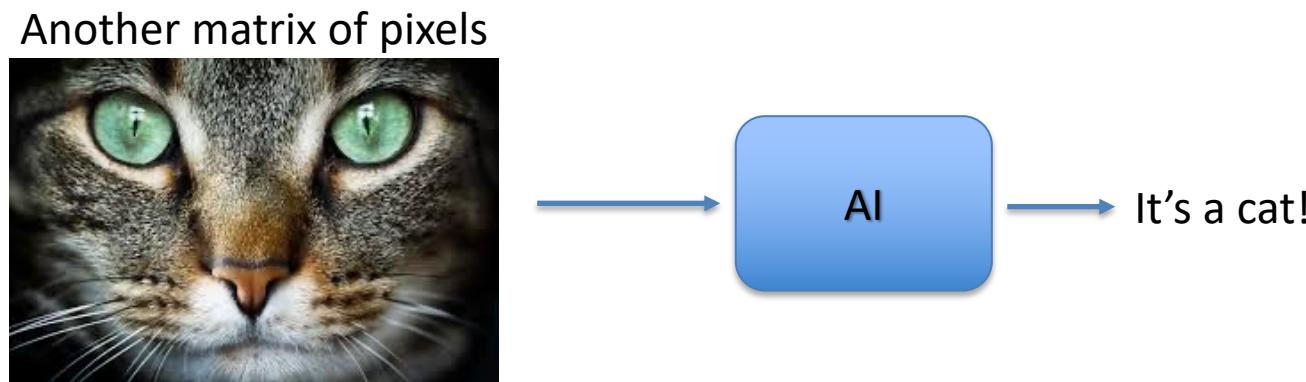
# Artificial intelligence may set morphology on a quantitative basis

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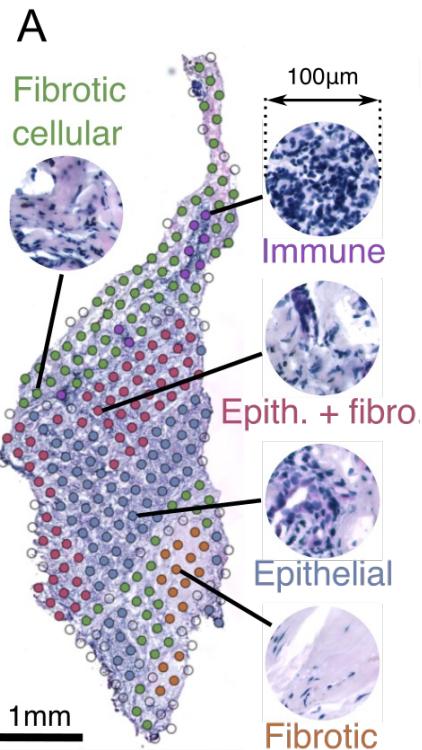
# Artificial intelligence may set morphology on a quantitative basis

- Photos is a matrices of pixels reflecting the activation of an optical sensor
- AI extract high-level **semantic information** from raw images:



- Intermediate representations of images computed by inner layers of deep neural network can be exploited to turn images into numerical semantic representations and group them by (semantic) similarity.

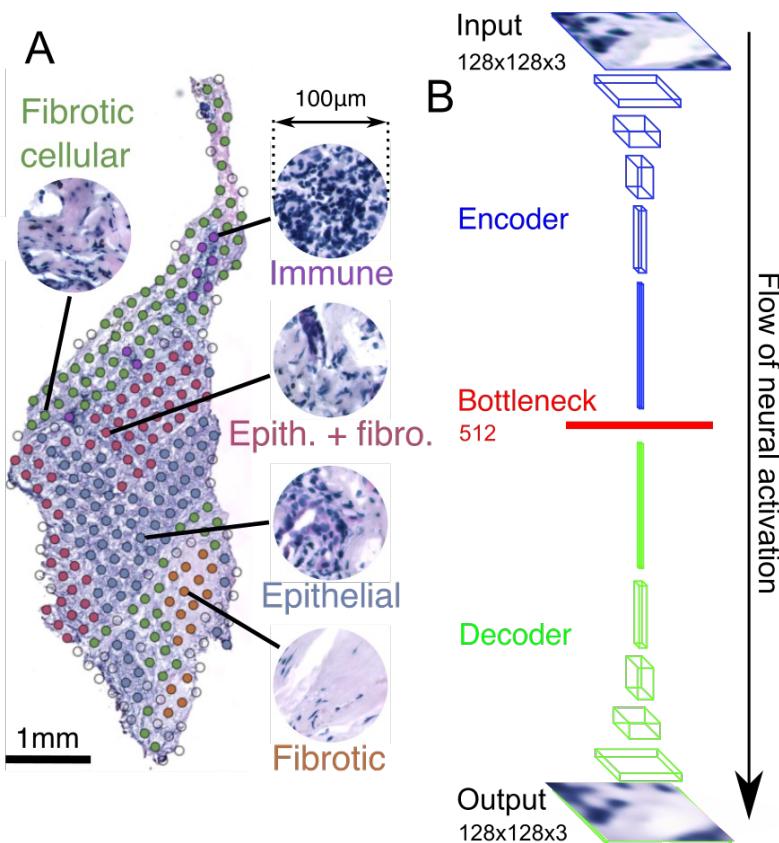
# An example of unsupervised AI



A papillary thyroid cancer slice was scanned at 40X

Morphology is heterogeneous across space

# An example of unsupervised AI



The slice was split into small tiles

Tiles were used to train an autoencoder

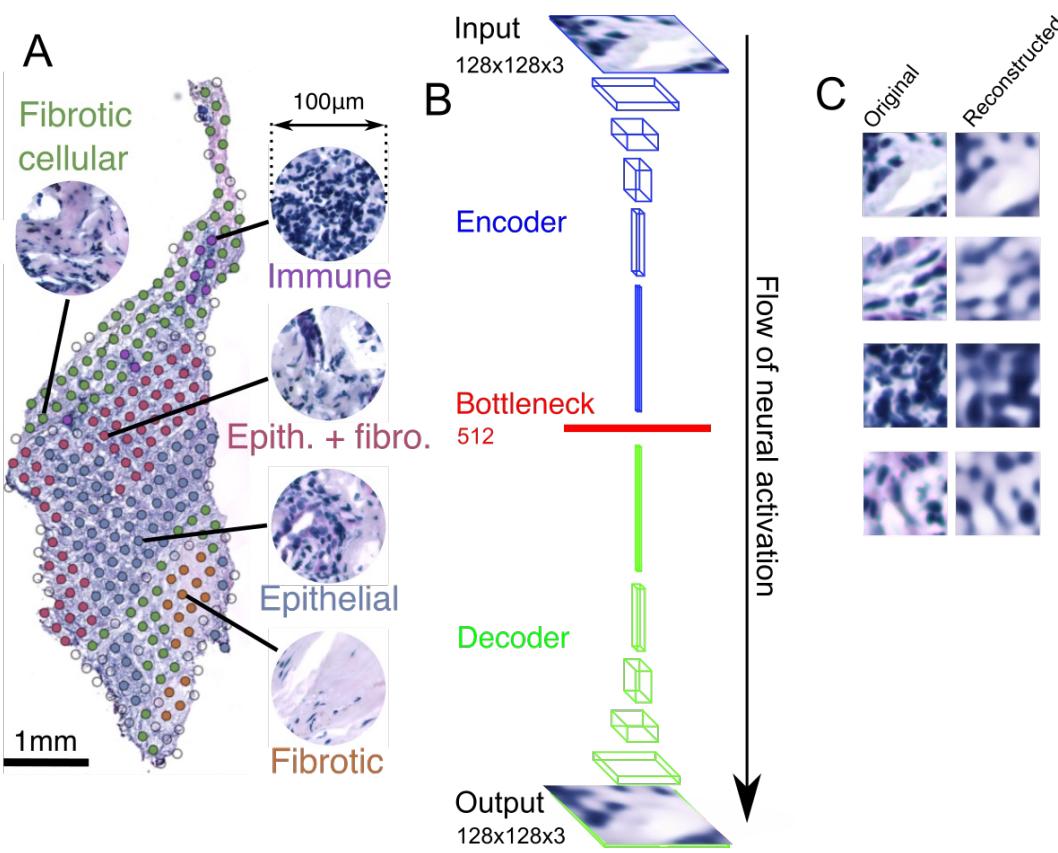
An autoencoder is a deep neural network trained to generate in its output the image it is presented as input

The trick is that the information flows through an informational bottleneck

Here the size of the bottleneck is 1% of the input image, thus the encoder must abstract out details and ignore noise

The numerical vector defining bottleneck neurons activations elicited by an image is called its ***latent representation***, it sits in a 512 dimensions space, that we also refer to as the ***morphological space***

# An example of unsupervised AI



Our autoencoder does generate the input images, these are blurry versions of the original

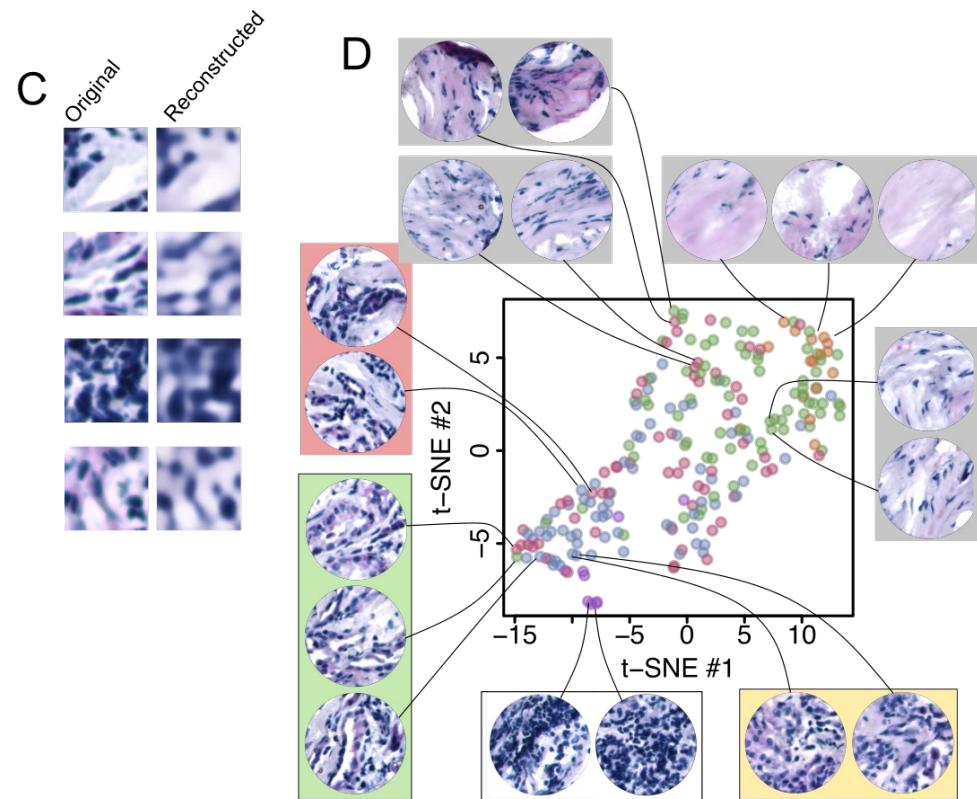
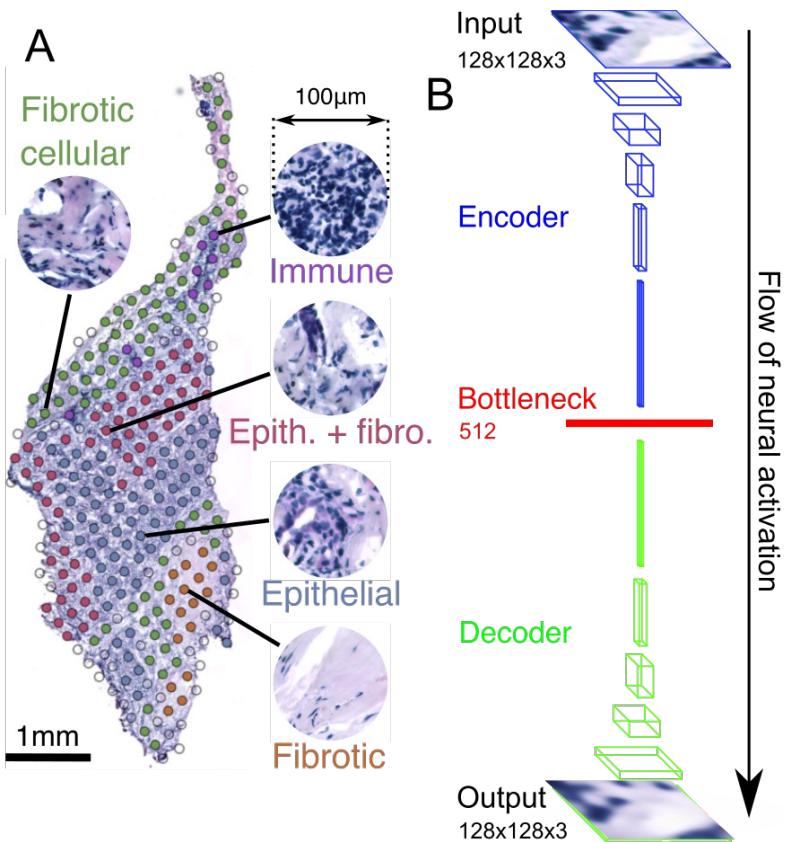
We are not interested in these reconstructed images, but in their latent representations

These are points in a 512 dimensions space, our poor brains can't cope!

So we collapse this space in 2D using the dimension reduction methods we routinely used in single cell transcriptomes analysis, e.g. t-SNE, UMAP, etc.

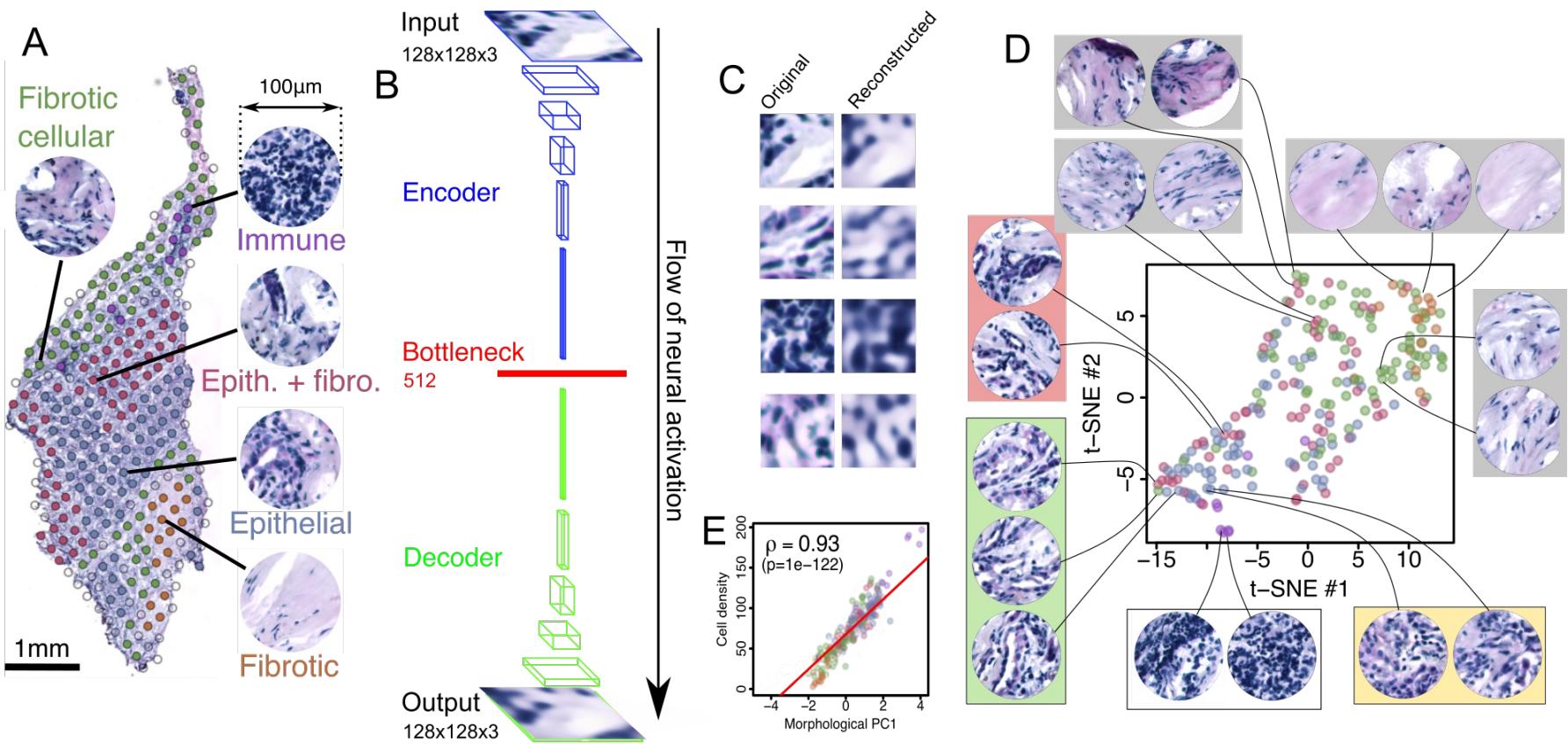
Now we can see the latent space...

# An example of unsupervised AI



... and it turns out to make histological sense, grouping together images that are morphologically similar.

# An example of unsupervised AI



In this example, the autoencoder has ‘discovered’ that cell density is an important organizing quantity of tissue analysis

# An example of unsupervised AI

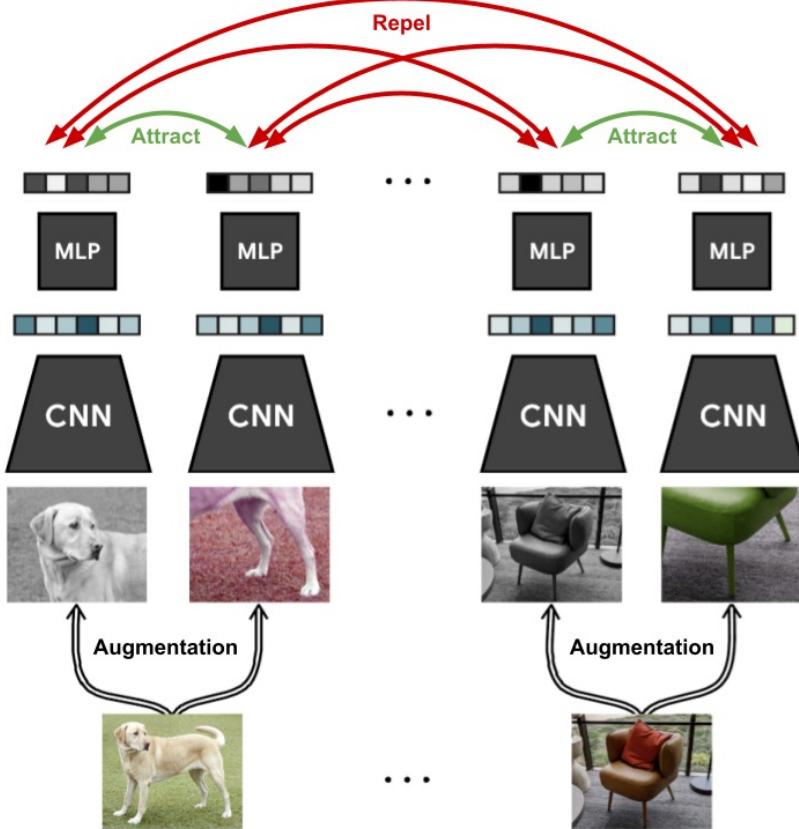
Overall,

- No human supervision/annotation and no a priori knowledge was needed to train the AI. It is truly free of cognitive biases and scientific a priori
- The AI turns the images into numerical vectors that represent tissue shape that are suitable to define similarity metrics
- The grouping of tissues in the morphological space makes histological sense
- We now have in our hands quantitative and reproducible computations in place of loose verbal statements like “these two morphologies are [similar/akin/related/share features]”
- The AI has an unlimited attention span. Large collections of high-resolution slides can be exhaustively examined

# Contrastive learning

- The reconstruction objective of the autoencoder is an overkill: the exact positions of cells is morphologically irrelevant
- It is even detrimental: we need latent representations that are insensitive to technical color variations, to the orientation of the slide under the microscope, etc.
- Contrastive learning does not use a reconstruction objective and it makes it possible to train AIs invariant to specific image features

# Contrastive learning



- We used the smCLR framework (Chen *et al.*, arxiv 2020)
- The AI is presented pairs of transformed images
- It is trained to guess if the two images are transformations of the same images or not
- The transformations define the invariance
- In this example, zoom/resize and color shift transformation makes the latent representations invariant to zoom level and color
- Learning is completely self-supervised because the transformations can be computed automatically

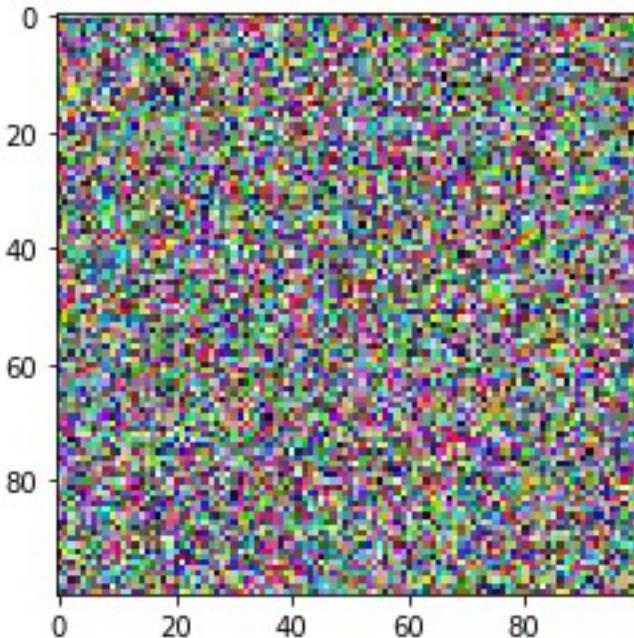
From <https://simclrgithub.io/>

# Pretext tasks

- Autoencoders and contrastive learning are instances of self-supervised AI, i.e. AI that are supervised, but with a supervision not requiring human intervention
- Another way to pretrain an AI is to supervise it with pretext task, i.e. a tasks loosely related to the final application
- For example, *the AI underlying your project was trained to classify images from the Internet into 1000 categories of everyday life* (e.g. cat, banana, train, table, ball, etc.).
- *This AI, has not seen any histological images during training*, yet this is the best we got so far for our exploration of histology.
- This is not completely unexpected after all: the fundamentals of pathologists' vision were not learned in medical school, but in their cradle while they were babies randomly gazing at their environment

# The core idea of AI

Most random pixel configurations looks like this



By comparison, real world images are very special. For example, nearby pixels are typically correlated.

- Images sit in a very high dimensional space (here, 100x100x3 variables)
- The vast majority of pixels configurations do not exist in the real world
- Images of the real world are embedded in a small part of the image space
- This is even more true of image in sub-domains, like cats, dogs, human faces, etc.
- AI algorithms are statistical machines that learn these embeddings from data

Scientific background

# The Canguilhem study



## Canguilhem and normal organs

- Essay "*Le normal et le pathologique*" by Georges Canguilhem, 1943
  - criticized the definition of disease states as mere deviations from a norm
- This is very relevant to the thyroid cancer overtreatment problem
- My lab proposes:
  - to survey **the diversity of normal organ morphologies**
  - to achieve this we will develop a novel **unbiased** and **quantitative** approach to morphology

# How normal are ‘normal’ organs? Asymptomatic population vs. textbook

For example, thyroid nodules are found in examinations *not* related to thyroid disease:

- neck palpation: 21% of patients
- ultrasonography: 67% of patients

Autopsy series suggest that:

- undiagnosed microcarcinomas in 22-36% of cases
- autoimmune thyroiditis in
  - 27% of women
  - 7% of men

# Overall goal of the study **(your project and beyond)**

- A. Survey the morphologies present in a large collection of asymptomatic thyroid histological slices
- B. Survey the correlation of morphological variations with
  1. genotypes
  2. **Gene expression**
  3. **Clinical data**
- In your project you will explore B2 and B3!
- Don't worry, we have computed morphological variations across all slices from GTEx (see 1<sup>st</sup> lecture)
- I'll provide nice pre-formatted matrices for morphological variations, clinical data and gene expression

Technical aspects

# GTEX samples

# Overview of GTEx

- 54 organs from 948 donors, most with
  - High-throughput genotypes
  - Genome-wide gene expression (RNA-seq)
  - Histology images (20X scans)
  - donor level clinical annotations
- GTEx samples were collected postmortem
- For an overview of the GTEx v8 release, see <https://www.gtexportal.org/home/tissueSummaryPage>

# Overview of GTEx

Each project group will be provided a data from a specific organ:

1. Clinical data
2. A morphological count matrix
3. A RNA read count matrix
4. Miscellaneous resources

for about 250-600 samples

Let me know if data is too big to run the analysis on your computer. We can decide to subsample the population.

# Clinical data: demographics/health

The clinical data matrix (clinical-data.tsv) includes,

**AGE:** age at death

**SEX:** 1-male, 2=female

**HGHT:** height of donor

**WGHT:** weight of donor

**BMI:** general indicator of the body fat an individual is carrying based upon the ratio of weight to height

# Clinical data: technical

The clinical data matrix (clinical-data.tsv) also includes,

**COHORT:** two types of donors, ‘Organ donor’ or ‘Postmortem’

**TRISCHD:** Ischemic Time (minutes). It’s the time elapsed between the presumed donor death and tissue collection.

**DTHHRDY:** Hardy scale. A number from 0 to 4 summarizing the circumstances of death

0=Ventilator Case

1=Violent and fast death

2=Fast death of natural causes

3=Intermediate death

4=Slow death

Details about clinical annotations here:

[https://ftp.ncbi.nlm.nih.gov/dbgap/studies/phs000424/phs000424.v8.p2/pheno\\_variable\\_summaries/phs000424.v8.pht002742.v8.GTEx\\_Subject\\_Phenotypes.data\\_dict.xml](https://ftp.ncbi.nlm.nih.gov/dbgap/studies/phs000424/phs000424.v8.p2/pheno_variable_summaries/phs000424.v8.pht002742.v8.GTEx_Subject_Phenotypes.data_dict.xml)

# Clinical data: miscellaneous

The clinical data matrix (clinical-data.tsv) also includes,

**SUBJID:** the GTEx ID of the subject, e.g. GTEX-111CU

**SMPLID:** the GTEx ID of the organ, e.g. GTEX-111CU-0226

**SMPTHNTS:** the sample's pathology notes taken by GTEx pathologists who examined the histological slices (possibly useful if you want to dive deeper into the project, they found quite few incidental diseases, failed dissection, etc.)

**IMGURL:** link to the interactively zoomable high-resolution scan of the histological slice, e.g.  
<https://brd.nci.nih.gov/brd/specimen/GTEX-111CU-0226>

# Gene expression matrix

I'll also provide expression data (RNA-read-counts.tsv):

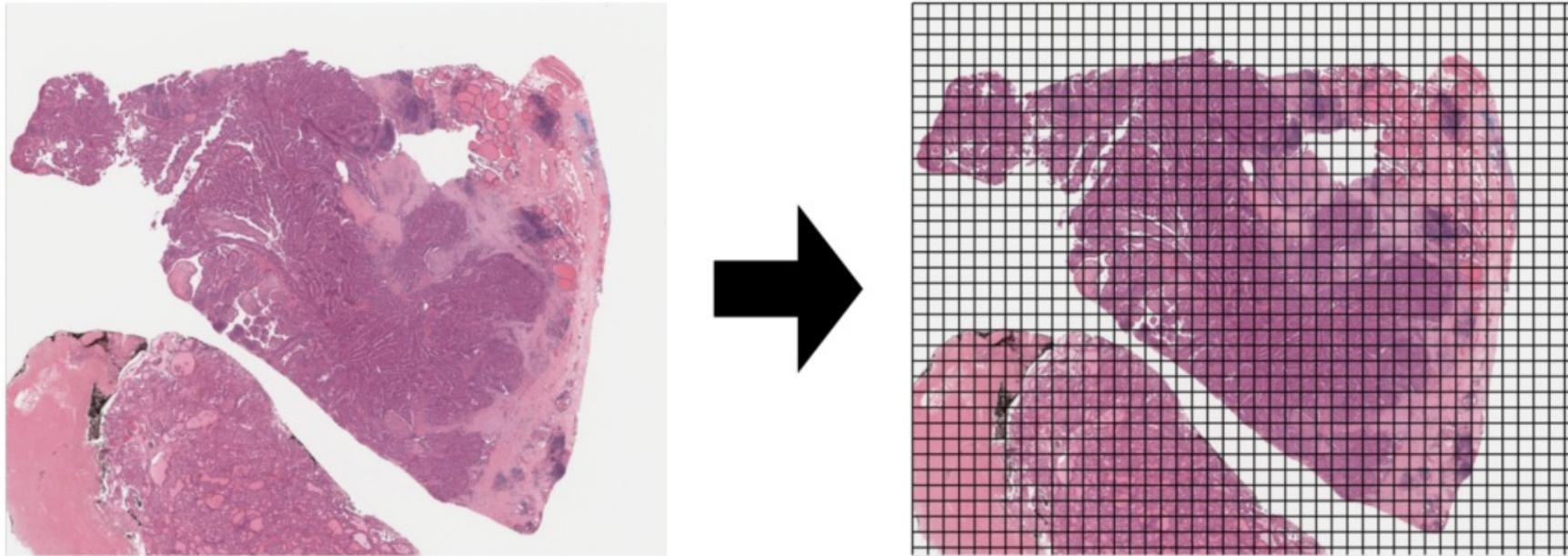
- There is one row per transcripts (56200 in total)
- Transcript ENSEMBL IDs and gene symbols are in the first and second columns
- Beside these, each column stands for a sample
- Expression was recorded as raw, unnormalized, read counts, i.e. a read count of 11 for gene G means that 11 reads align on G
- Raw read counts are suitable inputs for differential gene expression software such as DESeq2 or edgeR
- Column names of the expression matrix are indexed with **SMPLID**

# Morphological count matrix

I'll provide a count matrix of the morphologies identified by AI (morphological-counts.tsv)

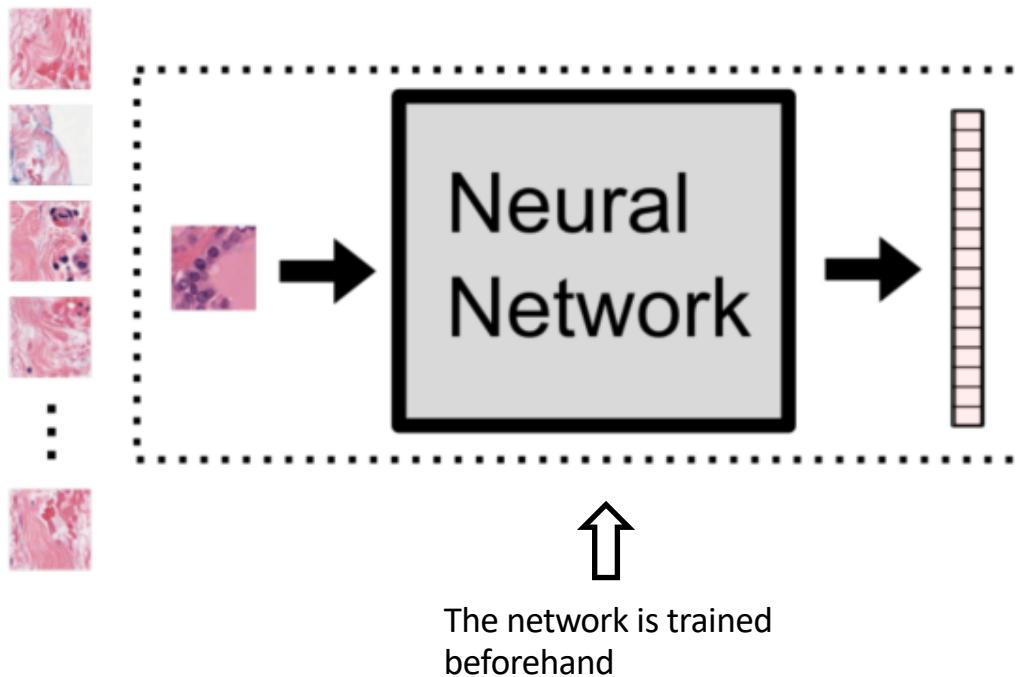
Here is how it was computed...

# Step 1: tile the high-resolution image



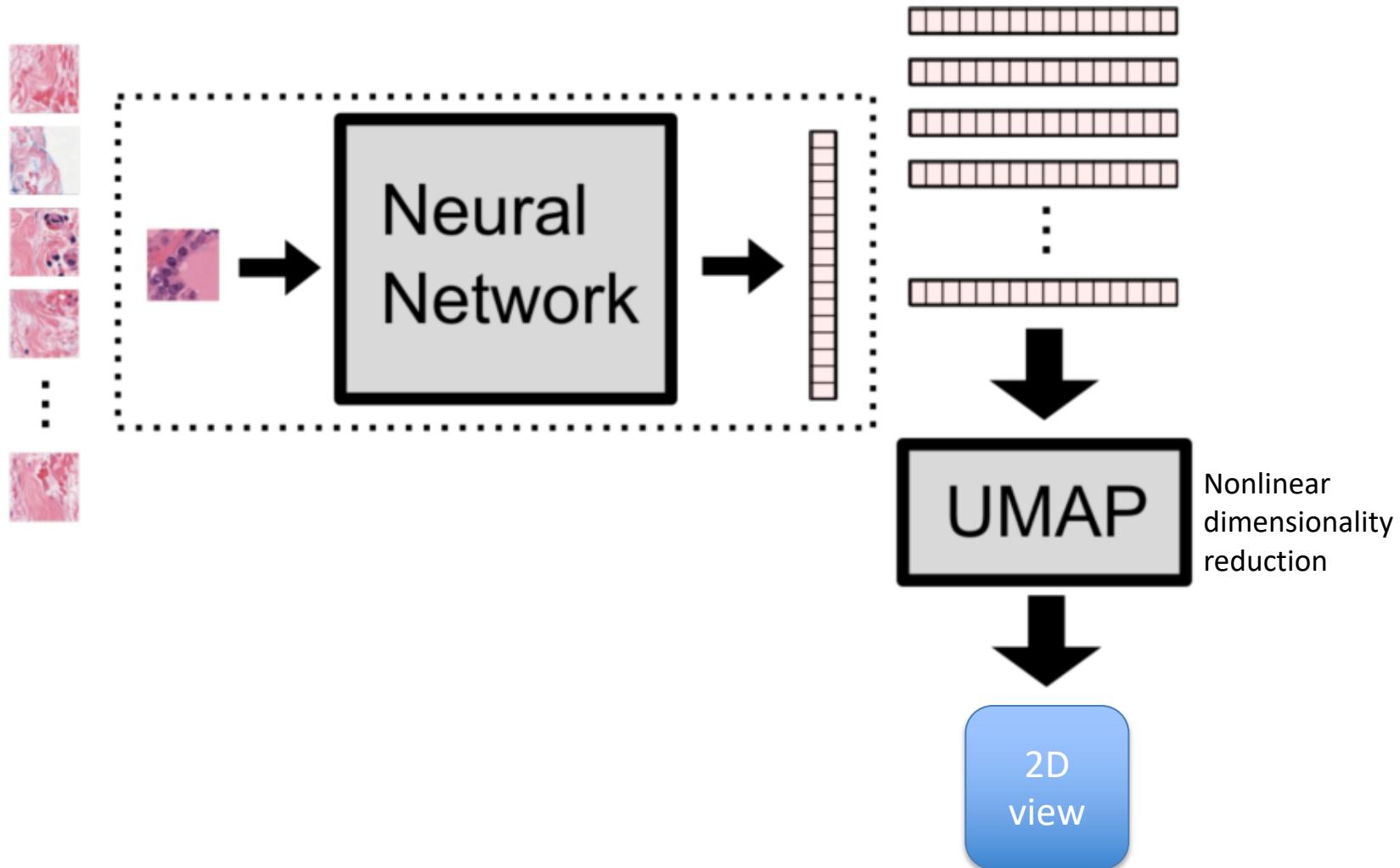
- Images were scanned at 20X magnification
- Each tile is  $224 \times 224 \text{ px}^2$  or  $110 \times 110 \text{ micron}^2$
- There are 5,000-10,000 tiles/image,
- And millions of tiles per organs, for example about 7,000,000 tiles in the 893 thyroid images

## Step 2: compute tiles' latent representations

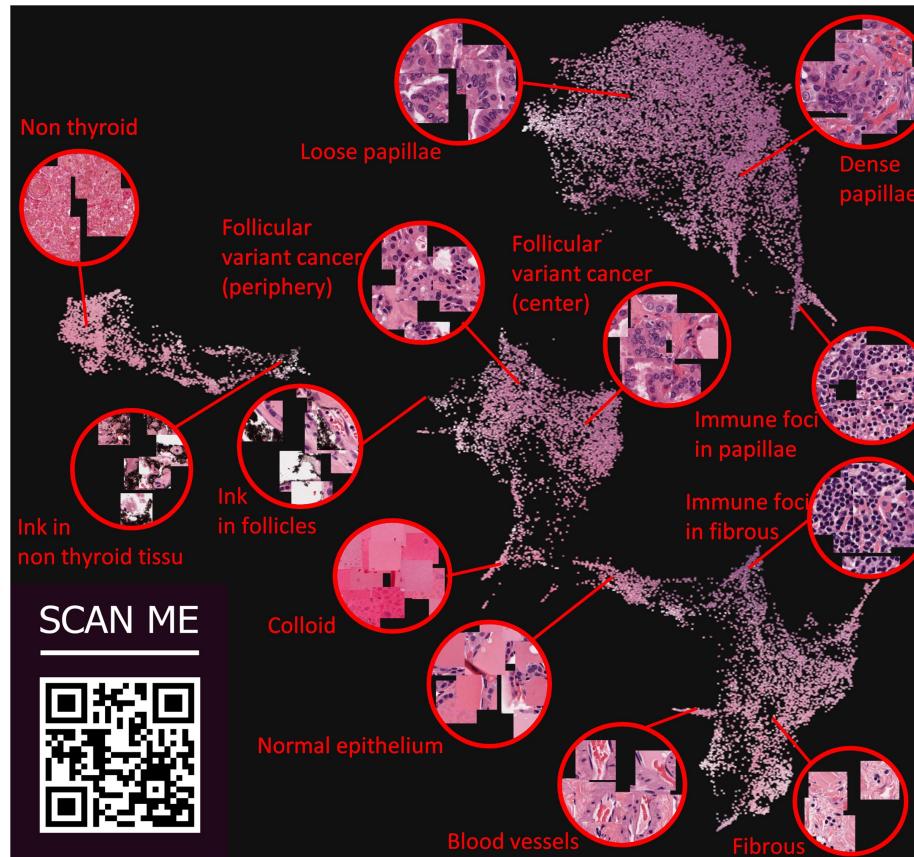


Now a tile is a point  
in a 384 dimensional  
space,  
 $384 << 224 \times 224 \times 3$

# Step 2: display tiles' latent representations (not part of project)

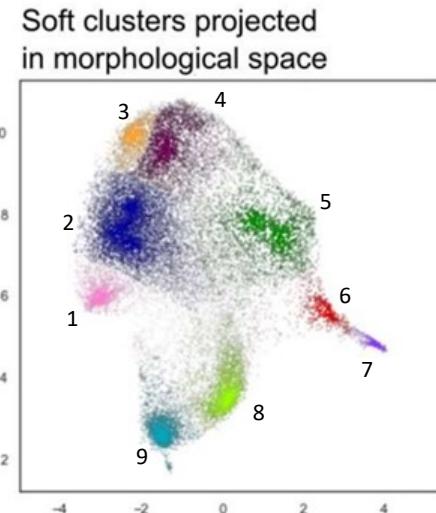


# Step 2: display tiles' latent representations (not part of project)



# Step 3: cluster tiles in latent space

HDBSCAN clustering



← This is a 1-slide toy example, we actually clustered the 5 to 10 millions of tiles from several 100s slices for each GTEx organ

We clustered the tiles based on the latent representations from step 2

For this project we defined 32 clusters, we call these 'morphological clusters'

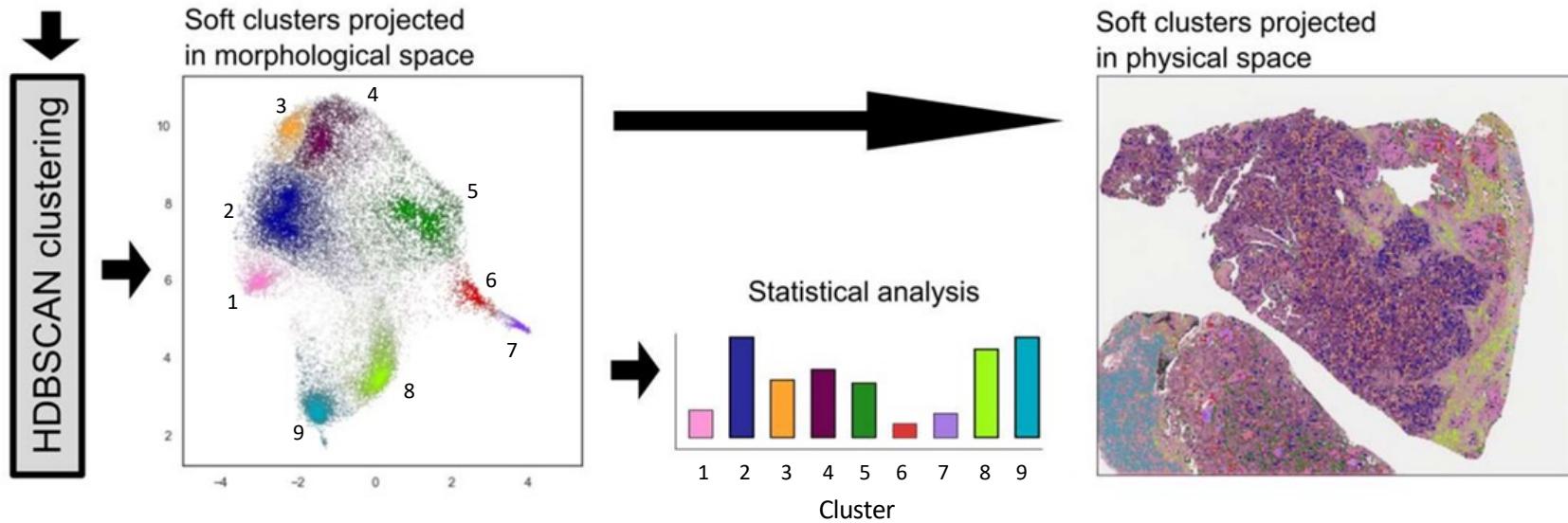
The clustering is done on all tiles available for each organs at once, so morphological clusters are representative all subjects for each organ in GTEx

An atlas of the morphological clusters is available at

[https://www-hpda.ulb.ac.be/iribhm/ai/atlasses/lunit\\_dino/YOUR\\_ORGAN/graphics/sankey.html](https://www-hpda.ulb.ac.be/iribhm/ai/atlasses/lunit_dino/YOUR_ORGAN/graphics/sankey.html)

Look at the G4 column (G4 = clustering granularity level 4, k=32 clusters)

# Step 4: cluster tiles in latent space



Once we have the morphological cluster identities of all tiles in a histology image, we can

- Compute the number of tiles in each cluster, that's a morphological summary, and use it in further calculation. That's what your project is about!
- Overlay morphological cluster IDs on the actual image
- Etc.

# Morphological count matrix

- I'll provide a matrix of the count of tiles in the morphological clusters (morphological-counts.tsv)
- The columns stand for morphological clusters (indexed from 0 to 31)
- The rows stand for samples (indexed by **SMPLID**)
- For example, if matrix entry (GTEX-111CU-0226, Mophological-cluster-15) = 286 :
  - It means thyroid GTEX-111CU-0226 has 286 tiles in Mophological-cluster-15.
  - Since tiles have a defined physical surface,  $110 \times 110 \text{ micron}^2 (0.11 \times 0.11 \text{ mm}^2)$  it also mean that Mophological-cluster-23 spans  $286 \times 0.11^2 = 3.5 \text{ mm}^2$  in histological image of thyroid GTEX-111CU-0226

# Morphological count matrix

- Thus, just as the RNA-seq read count matrix gives the expression of genes across the samples, the morphological count matrix gives the **expression of morphological clusters**
- Both are count data!
- Just as you will do with RNA-seq counts, I suggest you analyze morphological differential expression with DeSeq2 or edgeR

Your project step-by-step

# Questions to be addressed

# Overview of the project

In a nutshell,

The overall goal is to compare the morphological description of organs to their transcriptome

The morphological descriptions rests on unsupervised deep learning models

# Q1: explore clinical variables

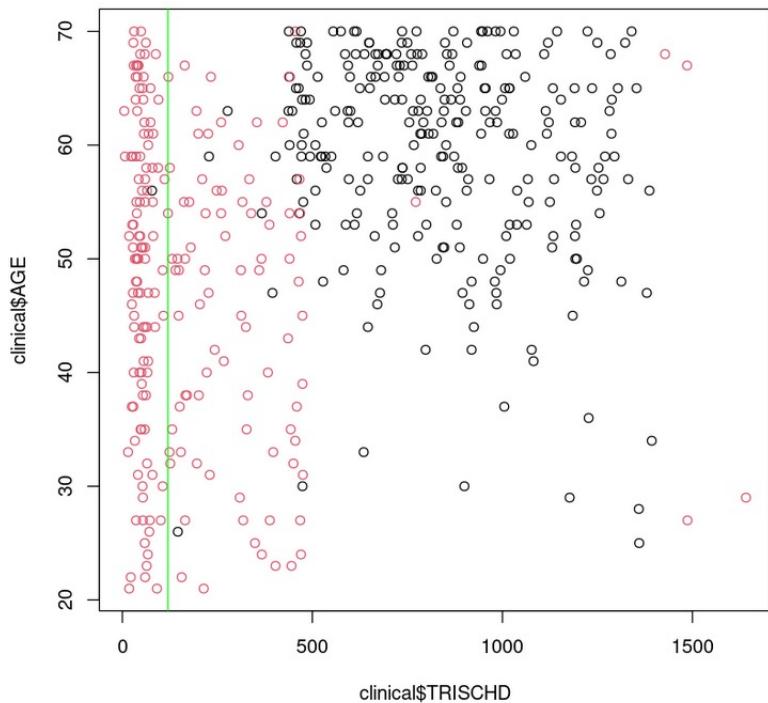
1. How are they distributed?
2. Are they correlated?
3. In particular, are some technical variables possibly confounding demographic/health variables?

**Hint:** Tools to address this may include PCA analysis, showing a variable's correlation matrix, specific plots,...

**Hint:** DTHHRDY is more akin to a categorical variable.

# Q1: explore clinical variables

**Hint:** Q1.3 is very important!



COHORT:  
**Organ donors**  
Postmortem

Here we see that AGE is confounded by TRISCHD and COHORT

Thus, any statistical analysis of AGE will need to be adjusted (i.e. normalized) for TRISCHD and COHORT

(Your data won't necessarily look like this...)

# Q2: Clinical data vs. morphology

1. Compute systematically associations between clinical variables and morphological cluster counts. The purpose is to compare the magnitude of the associations of the different variables with morphology.
2. Discuss the association with technical variables.
3. For non-technical variables, redo the analysis with adjustment for the confounding technical variables, if any is reported in Q2.2. Report and discuss significant associations.

# Q2: Clinical data vs. morphology

**Hint:** This is a differential expression analysis where we study ‘differential **morphological cluster** expression’ instead of differential **gene** expression. So, I suggest you use proven tool developed for transcript count data, like DESeq2, edgeR, etc.

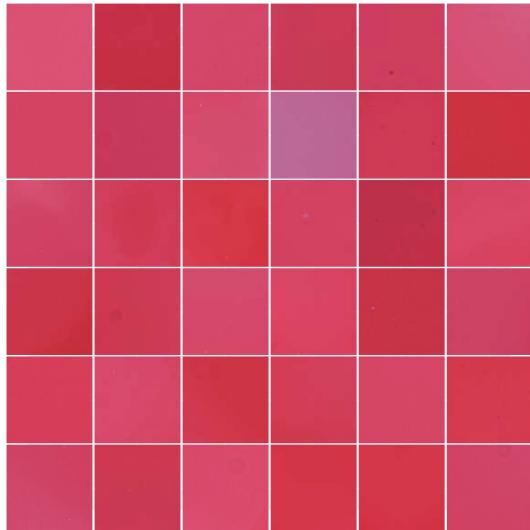
**Hint:** These tools implements multivariate model formulas that will enable the treatment of confounders in Q2.3. For example, formula ‘ $\sim \text{AGE} + \text{X} + \text{Y}$ ’ will compute the multivariate association of morphological clusters with variables AGE, X and Y. So, if you look at AGE from this model it will be adjusted for the variations of X and Y.

Thus, DESeq2 not only automatically handles normalization for total count and other intensity biases of count data, but it also enables you to cancel out your variables of choice in the analysis.

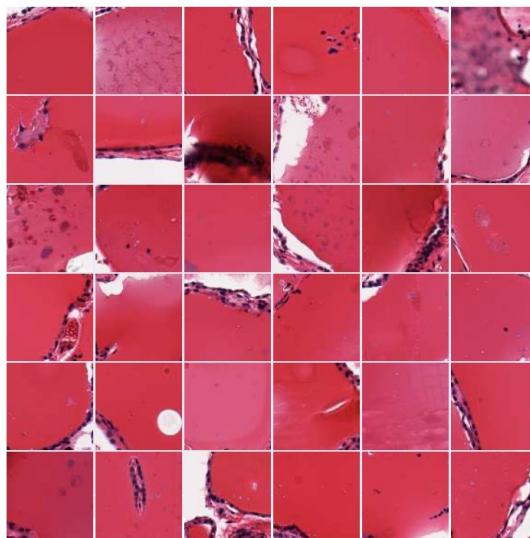
**Hint:** the function ‘as.formula’ (turns char string into a formula) could be useful to automate your analysis...

# Q2: Clinical data vs. morphology

36 tiles from  
A thyroid  
morphological  
cluster  
(colloid)



36 tiles from  
another thyroid  
morphological  
(edge of follicle)



**Hint:** Counts of different morphological clusters may be correlated with one another, as shown in the atlas. One reason is that patterns on a scale of  $110 \times 110$  micron $^2$  may be part of the same larger-scale morphological entity.

A trivial example: these two clusters are both part of follicles (center and edge), so they tend to co-occur in the same samples

Less trivial sources of correlation include disease states, e.g. autoimmunity

By the way, the order of the cluster in the atlas is based on a (meta-) clustering of the morphological cluster counts.

# Q3: Morphology vs. gene expression

1. Report:
  - The number of significant down-regulated and up-regulated genes associated with each morphological cluster
  - Report the the 10 most significant up-regulated genes
2. Same as Q3.1 with REACTOME gene sets (provided in the resource folder)
3. Discuss the results, technically and biologically

# Q3: Morphology vs. gene expression

**Hint:** Use dedicated RNA-seq tools that take count data as input (e.g. DESeq2, edgeR, etc.) for Q3.1

**Hint:** I highly recommend you filter transcripts beforehand. You don't need transcripts that are not/little expressed in your organ. It's also a good idea to focus on transcripts showing high variability (use the median average deviation, a.k.a. `mad()` in R). Don't hesitate to be drastic in your filtering (e.g. it's OK to remove >50% of all transcripts)

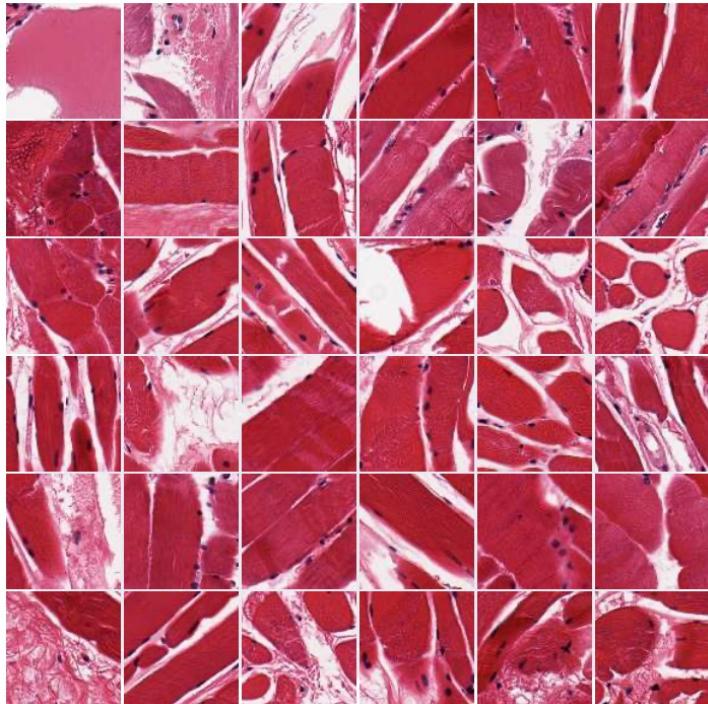
The filtering reduces the multiple testing problem, of course. But it also reduces the computational burden. After appropriate filtering, I could run DESeq2 analyses for all 32 morphological clusters on 465 samples in ~1 hour and a peak RAM usage < 4GB

**Hint:** Just as in Q2, you may need to adjust for technical confounders.

**Hint:** It might help to use the  $\log_{10}(x+1)$  of the morphological counts

**Hint:** DESeq2, edgeR handle multiple testing. But you'll have another layer of multiple testing since you will run these algorithms for the 32 morphological clusters.

# Q3: Morphology vs. gene expression



**Hint:** Surgeons sometime take muscle adjacent with the thyroid..

In other organs fat or connective tissue may contaminate the sample.

You may use it as an adjustment covariate in your analysis

# Q3: Morphology vs. gene expression

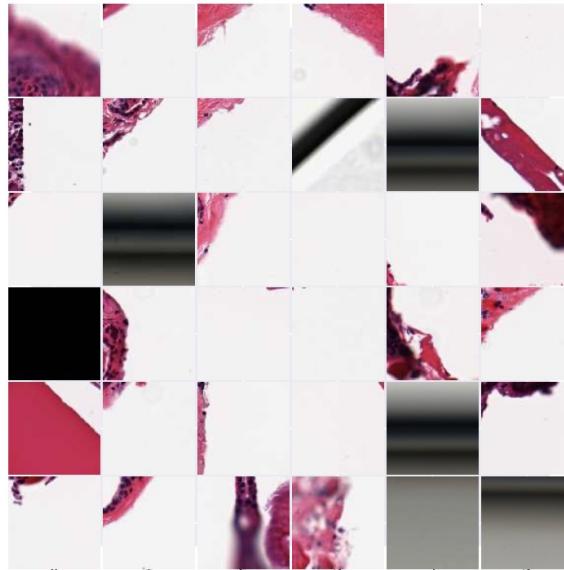
**Hint:** In Q3.2, running 32 times GSEA may not be computationally tractable. I suggest you use instead the fgsea package, which takes as input a gene ranking (i.e. provided by the differential analyses of Q3.1 output)

(Yes, I know, it's not using the gold standard sample permutation of GSEA. But I tried it for you and it's reasonable in this context where the transcriptional signal is quite massive)

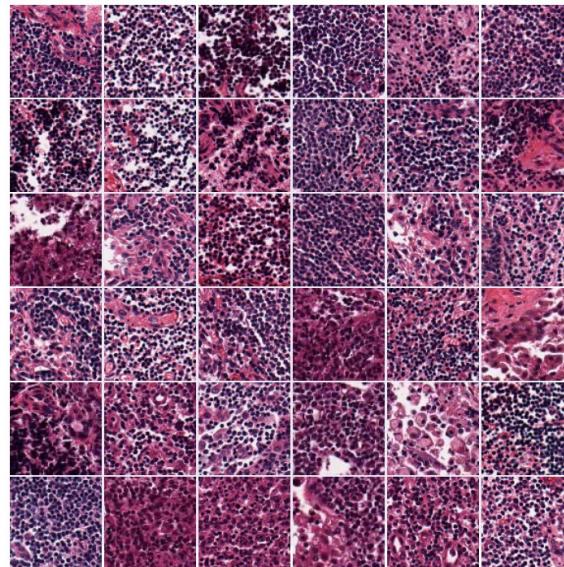
**Hint:** The REACTOME gene sets are provided in file c2.cp.reactome.v7.5.1.symbols.gmt in the resource folder. The fgsea package provides a function to read \*.gmt files

# Q3: Morphology vs. gene expression

tissue edges  
and various  
artifacts



Dense  
lymphocytes  
aggregates



You may have  
remarkable clusters...

**Hint:** Think of them as  
negative and positive  
controls.

**Hint:** Can you estimate  
the prevalence of  
inflammation ? (Not  
present in all organs)

Your project step-by-step

# Handing out your report

# Project report

You are asked to describe your work in a written report

It includes :

- An short introduction to the topic
- A careful description of methods and results
- A discussion of your results for each questions

Dumping code and results is *not* good enough, you must show me you understand what you are doing

# Project report

- The report is handed out as a **PDF** file or a **PDF-converted Jupyter notebook**
- Since I am asking quite a few results (e.g. series of genes differentially expressed in 32 analysis), you may put the larger outputs as appendices to the report, or hide them in your notebook, and discuss the most salient findings in the main text
- I am not defining a specific report length. Good reports are neither too short, nor too long. 15-20 pages (appendix not included) seems reasonable.

# Project report

- This report is a good exercise for your master thesis and for scientific writing in general
- Try to be specific, precise and quantitatively accurate. For example, don't write '*many genes are associated with cluster Z*', but '*N genes are associated with cluster Z*', where N is the number you have computed

# Grading of your projects

- Questions Q1-Q3: **15pt**
- Quality of your PDF report (it needs to be concise, clear, precise, well presented), **3pt**
- Reproducibility: all your analyses must be reproducible, i.e. all the steps are carefully documented, including parameter settings and software versions, **2pt**
- ...and **2pt** to be gained beyond 20 for the motivated ones who go off the beaten track with original analyses, etc.

# Handing out your project report

- Deadline is **June 9th 23:59:59.**
- Send me the report by e-mail  
([Vincent.Detours@ulb.be](mailto:Vincent.Detours@ulb.be)), **including ‘BINF-F401’ in the subject line**
- Get back to me if I don’t acknowledge receipt of your report within 3 days.

Your project step-by-step

# Rules of the game

# Groups

- There will be 10 groups of 3 and 1 group of 4 students
- Each group is assigned a specific organ
- You will be informed by mail about which group you've been assigned to if you haven't chosen one by March 20<sup>th</sup>, when each group will be informed about where their data is

# Rules of the game

Choose your own weapons. I do advise R, but I'll accept alternatives.

You are encouraged to communicate with one another, but

- Remember, each group has its own unique dataset
- Beware of herd effects, the majority and/or the leading figures can be dead wrong
- Plagiarism is not acceptable
- ChatGPT and other AI text generators are unreliable for scientific facts, they easily spit-out falsehood with an impeccable style, including made-up citations of papers that don't exist! **It's up to you to use or not AI text generators as long as 1- you clearly insert AI generated text in quote marks and 2- say which AI wrote it and provide the prompt used to generate the text.** Of course you will be held responsible for all the text in your report.

# Rules of the game

I'll address your questions by e-mail, if

- You use your brain and do your home work before asking, e.g. I won't reply if the answer is in the R documentation or can be obtained from a basic web search. (I basically request the same etiquette as in any technical forum on the Internet.)
- The subject line of all your correspondance with me must start with '**BINF-F401:**'

# Some tips from past experience...

- This is a science project, your technical choices must be argumented and the calculations must be reproducible, i.e. all the information needed to rerun the analyses must be provided. *In science details do matter.*
- Dumping graphics and stats in a document is not enough. The students who got the best grades examined critically their results and demonstrated that they understood the limits and biological significance of what they did.
- Technical problems are hard to anticipate, so don't wait for the last minute to discover them, and then be left with no time to overcome them.