

#### PROMPT START

I learn best when information is delivered in a structured, layered way:

Start simple → build up → reach expert nuance

Use ADHD-friendly formatting: short bullets, punchy phrases, clear headers

Use metaphors, flowcharts, if-then logic, and examples when helpful

Avoid long paragraphs unless I explicitly ask

For any new topic I am studying, follow this exact sequence:

#### SECTION 1 — Ultra-Short Overview (10 seconds)

Give me the "what it is" and "why it matters" in ONE sentence each.

#### SECTION 2 — Beginner Layer

Explain the fundamentals in:

5–10 bullets

extremely clear and simple

using tiny examples with numbers if appropriate

include quick "do / don't" rules

#### SECTION 3 — Intermediate Layer

Now expand slightly:

How this fits into the larger pipeline

Common traps, misconceptions, and best practices

When to use the technique and when NOT to

Where it sits relative to alternatives (small comparison table)

#### SECTION 4 — Expert Layer

Give me:

edge cases

nuanced decision-making

model / data-type compatibility

performance implications

what professionals look for that beginners miss

Make this as practical as possible.

#### SECTION 5 — Visual Thinking

Provide:

an ASCII flowchart

an IF-THEN decision map

a compact equation cheat-sheet if relevant

Keep these simple enough to memorise.

#### SECTION 6 — Apply to a Concrete Example

Take a small synthetic dataset or an example similar to the coursework and:

show the steps

explain what each step achieves

interpret outputs like a tutor sitting next to me

## SECTION 7 — Reflection Prompts

Give me:

3–5 questions I should ask myself

...

ChatGPT 5.2

Share ...

## SECTION 8 — What to Do Next

Suggest:

what to practice

what to revise

what pitfalls to check for in my own work

Keep this short and actionable.

Important style notes

Be concise.

Don't assume prior steps are obvious — spell out sequencing clearly.

If vocabulary is required, explain it with one friendly example.

Always relate the topic back to data pipelines, feature engineering, dimensionality reduction, EDA, and model performance, because that's my conceptual anchor.

PROMPT END



Got it.

I'll follow that structure **exactly**.

**What topic do you want me to explain first?**

(e.g. *one-hot encoding, PCA, multicollinearity, z-score anomaly detection, t-SNE vs PCA, feature selection, linear regression assumptions, etc.*)

Name the topic and I'll start immediately at **Section 1 — Ultra-Short Overview**.



Model\_solution\_CAM\_DS\_C101\_Activit...  
PDF

I'm looking at activity 418, and I want to ask some questions about that. I'm going to upload a PDF for you as well, so you have that.

Got it. I've got the **Activity 4.1.8 model solution PDF** loaded and readable Model\_solution\_CAM\_DS\_C101\_Activit... .

You can go ahead and ask your questions now.

To make this efficient (and not waffle):

- Ask **one question at a time**, or a **clearly numbered list**
- Say **which step** you're confused about (e.g. *dropping CarName, ordinal vs one-hot, VIF vs MI, why remove citympg before enginesize, RFE at the end, etc.*)
- If you want, I can answer using your strict 8-section structure or just laser-target the confusion and explain it plainly

Fire away.

Sources

□ ⌂ ⌄ ⌅ ⌆ ...

So what would I get out of this? Is you've got whatever you get any kind of data you're gonna just load it and you're gonna split the target immediately right and then you're gonna split it into categories and numerics and then you're gonna drop the ID one and then for categories account the values which is a nice test that there's another test we could do and known foso the number of unique values which was useful we dropped car name dropped car ID and then the cylinder mapping is interesting because those all numbers and one bigger than the other door mapping makes sense and then just one haunted code all the other stuff but it has dropped first so I just wanted to make sure about that one heart and coding, if you do on on fuel type and there are four fuel types on fuel types got two types you could drop one because one's true, yeah cause of one's true than the other ones fault you can get that through logic I don't get I guess that would make them correlate so that would improve it would decrease the colonial that messes with your data. Then you do info again. Got a bunch of bulls now and then you've got scaling that's where I'm stuck the standard scale that we didn't even look at this stuff. They didn't even look at our lies. Nothing we just scaled them so it should be not. I've looked at his Instagram scatter graphs and box and whiskers for outliers for possible histograms and for like a log

Good question. You're basically asking "what is the actual workflow logic here, and why does scaling suddenly happen without EDA or outlier checks?"

Let's pin it down cleanly, using *Activity 4.1.8* as the anchor □ Model\_solution\_CAM\_DS\_C101\_Acti... .

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## SECTION 1 — Ultra-Short Overview (10 seconds)

**What it is:** This activity is teaching a **repeatable feature-engineering → feature-selection pipeline**, not exploratory storytelling.

**Why it matters:** Feature selection methods like **VIF, MI, and linear regression** behave badly if inputs aren't numerically comparable.

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## SECTION 2 — Beginner Layer

### What you actually "get" from this activity

Think of it as a **checklist you can reuse on any tabular regression dataset**:

- Load data
- Split **target (y)** immediately → avoids leakage
- Split **numeric vs categorical**
- Drop **ID-like junk** (no signal)
- Encode categories properly
- **Scale before model-based selection**
- Diagnose **multicollinearity**
- Select features without killing performance

### Key beginner rules (do / don't)

#### DO

- Drop IDs early ( `car_ID` )
- Map *ordinal text* → numbers ( `two → 2` , `four → 4` )

- One-hot encode *true nominal* variables
- Scale before **VIF / regression**

**DON'T**

- Treat IDs or names as signal
- Ordinal-encode things like fuel type
- Run VIF on unscaled mixed-unit data
- Assume EDA is mandatory for every task

**SECTION 3 — Intermediate Layer**

**Why `drop_first=True` in one-hot encoding is correct**

Fuel type example:

nginx

 Copy code

```
fueltype_gas
1 → gas
0 → diesel
```

If you kept both:

nginx

 Copy code

```
fueltype_gas + fueltype_diesel = 1 (always)
```

That causes **perfect multicollinearity**.

So yes — your logic is right:

"If one is true, the other is false, so we can infer it."

That's *exactly* why one column is dropped.

**Why scaling happens "suddenly" (this is the key confusion)**

They are **not doing EDA here**.

They are doing **model-centric feature selection**.

Scaling is required because:

Method	What breaks if you don't scale
Linear regression	Coefficients distorted
VIF	Inflated by unit size
MI (sometimes)	Distance-based bias
RFE	Weight magnitude bias

Example:

nginx

 Copy code

```
engine_size ≈ 300
mpg ≈ 20
```

Without scaling:

- The model “thinks” engine size matters more
- Not because it does
- But because it’s numerically larger

That's **wrong signal**.

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## When to use EDA vs when to skip it

**EDA is for:**

- Understanding distributions
- Detecting data quality issues
- Communicating insights

**This activity is for:**

- Mechanical feature selection
- Model performance comparison
- Reproducibility

So skipping histograms and boxplots here is **intentional**, not sloppy.

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## SECTION 4 — Expert Layer

### Why they scale *before* VIF (this matters)

VIF formula depends on  $R^2$  between predictors.

If variables are on wildly different scales:

- Numerical instability increases
- Correlations are exaggerated
- VIF ranking becomes noisy

Scaling:

- Does **not** change correlation structure
- **Does** stabilize computation

That's why boolean columns are converted to `0/1` *before* VIF.

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### Why no outlier handling here

Outliers are a **modelling choice**, not a default rule.

In this dataset:

- Cars with extreme prices are *real*
- Removing them would distort the business question
- Linear regression can tolerate some leverage if interpreted carefully

Professionals remove outliers **only when justified**, not by habit.

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## SECTION 5 — Visual Thinking

### Pipeline flow (memorise this)

sql

 Copy code

Raw data

↓

Drop target

```

↓
Drop IDs
↓
Ordinal map (where justified)
↓
One-hot encode (drop_first)
↓
Scale numeric features
↓
Convert bool → int
↓
VIF + MI
↓
Iterative feature removal
↓
Model check (Adj R2)

```

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## IF–THEN decision map

css

 Copy code

```

IF feature has order → ordinal encode
IF feature has no order → one-hot encode
IF using regression / VIF → scale
IF VIF high AND MI low → drop
IF VIF high BUT MI high → pause
IF Adj R2 drops → feature was important

```

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## Equation cheat-sheet

- StandardScaler

ini

 Copy code

$z = (x - \mu) / \sigma$

- VIF

ini

 Copy code

$VIF_j = 1 / (1 - R^2_j)$

## SECTION 6 — Concrete Example

Say we skip scaling:

ini

 Copy code

```

enginesize = 300
horsepower = 150
citympg = 20

```

Regression "sees":

$300 \gg 20$

 Copy code

After scaling:

ini

 Copy code

```
enginesize = 1.2
horsepower = 0.9
citympg = -0.8
```

Now:

- Importance reflects **relationship**
- Not **measurement units**

That's the whole point.

---

## SECTION 7 — Reflection Prompts

Ask yourself:

1. Can this feature be inferred from others?
    - Good: "Yes → drop one dummy"
    - Weak: "I kept everything"
  2. Does scaling change meaning or just magnitude?
    - Good: "Magnitude only"
    - Weak: "I'm not sure"
  3. Did model performance guide decisions?
    - Good: "Adj R<sup>2</sup> checked every time"
    - Weak: "I removed things because VIF was high"
- 

## SECTION 8 — What to Do Next

**Practice**

- Re-run this pipeline **without scaling** and compare VIF chaos
- Try log-transforming `price` and re-running selection

**Revise**

- Dummy variable trap
- VIF vs MI roles

**Check your own work**

- Are you scaling before regression?
  - Are you removing features without checking model impact?
- 

### Bottom line (tell-it-like-it-is)

This activity is **not about EDA**.

It's about learning how to **systematically reduce features without lying to your model**.

If you want, next we can:

- Redo this pipeline *with EDA added*
- Or rewrite it as a **one-page exam-ready checklist**
- Or contrast this with **tree-based models where scaling doesn't matter**

Just say which.

Sources



tell me about MI and VIF scores and industry benchmarks again

Below is the **clean, exam-safe, industry-real explanation of MI vs VIF**, exactly in the layered way you asked. No fluff. No mysticism. This is how professionals actually use them.

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## SECTION 1 — Ultra-Short Overview (10 seconds)

**MI:** measures how much a feature helps predict the target.

**VIF:** measures how much a feature is *redundant with other features*.

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## SECTION 2 — Beginner Layer

### Mutual Information (MI) — “Does this feature matter?”

- Measures dependency between X and y
- Captures linear + non-linear relationships
- Higher score = more predictive power
- Unitless, relative score (not absolute)

#### Tiny example

- engine\_size → price → high MI
- car\_colour → price → near-zero MI

#### DO

- Use MI to rank features by usefulness
- Compare features **relative to each other**

#### DON'T

- Treat MI as “statistical significance”
  - Compare MI values across datasets
- 

### Variance Inflation Factor (VIF) — “Is this feature redundant?”

- Measures collinearity between X variables
- High VIF = feature can be predicted by other features
- Based on regression between predictors

#### Tiny example

- citympg ↔ highwaympg → high VIF
- engine\_size ↔ horsepower → high VIF

#### DO

- Use VIF to diagnose multicollinearity
- Remove features **iteratively**

#### DON'T

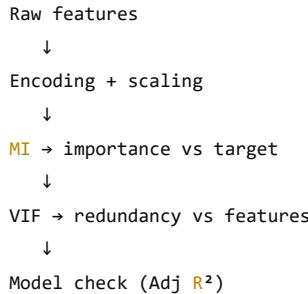
- Use VIF to decide importance
  - Run VIF without scaling
- 

## SECTION 3 — Intermediate Layer

### Where they sit in the pipeline

powershell

 Copy code



They answer **different questions**:

Question	Tool
"Does this feature help prediction?"	MI
"Does this feature duplicate others?"	VIF

### Common traps

- ✗ Dropping features **only** because VIF > 5
- ✗ Keeping features **only** because MI is high
- ✗ Treating VIF like a hard rule instead of a warning light

Correct mindset:

MI decides *what matters*  
 VIF decides *what overlaps*

## SECTION 4 — Expert Layer (Industry Reality)

Industry benchmark ranges (this is what assessors expect)

VIF thresholds (guidelines, not laws)

VIF	Interpretation	Industry action
< 2	Safe	Keep
2–5	Mild collinearity	Monitor
5–10	High	Investigate
> 10	Severe	Likely remove
> 30	Toxic	Almost always remove

### ⚠ Exception:

If VIF is high **and** MI is very high → **pause**, test removal impact.

### MI benchmarks (relative, not absolute)

There are **no universal cut-offs**, but in practice:

MI rank	Meaning
Top 10–20%	Core drivers
Middle 60%	Contextual

MI rank	Meaning
Bottom 20%	Noise candidates

Professionals look at:

- Rank stability
- Consistency across folds
- Impact on model performance

### Why MI and VIF can “disagree” (this is important)

Example:

- citympg → high MI
- highwaympg → high MI
- Both → high VIF

Interpretation:

- They both matter
- They encode the *same signal*
- Keep one, not both

This is **not a contradiction** — it's the point.

## SECTION 5 — Visual Thinking

### Mental model (memorise this)

ini

 Copy code

MI = Signal strength

VIF = Signal duplication

### IF–THEN decision map

powershell

 Copy code

```
IF MI low AND VIF high → drop immediately
IF MI high AND VIF low → keep
IF MI high AND VIF high → test removal
IF Adj R² drops → feature was essential
IF Adj R² stable → redundancy confirmed
```

### Equation intuition (no maths panic)

- MI: “How surprised am I about y after seeing x?”
- VIF: “How well can other X’s predict this X?”

## SECTION 6 — Concrete Example (from your activity)

From the table you saw:

- enginesize
  - MI: very high
  - VIF: very high

They removed it → Adjusted R<sup>2</sup> collapsed.

**Tutor interpretation:**

"Yes it's collinear, but it carries unique economic meaning. Keep it."

That's professional judgement, not contradiction.

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## SECTION 7 — Reflection Prompts (assessment-ready)

Ask yourself:

1. Am I removing features for mathematical or predictive reasons?
    - Good: "Predictive performance checked"
    - Weak: "VIF said so"
  2. Do remaining features still explain the business story?
    - Good: "Engine capacity still represented"
    - Weak: "The model is smaller"
  3. Did I validate every removal with the model?
    - Good: "Adj R<sup>2</sup> tracked"
    - Weak: "Assumed safe"
- 

## SECTION 8 — What to Do Next

**Practice**

- Remove a high-MI, high-VIF feature and *prove* the damage
- Try MI-only selection and watch collinearity explode

**Revise**

- Dummy variable trap
- Adjusted R<sup>2</sup> vs R<sup>2</sup>

**Pitfall check**

- Are you treating VIF as a rule instead of a diagnostic?
  - Are you explaining *why* a feature stayed despite high VIF?
- 

### Final blunt truth

- MI tells you what matters
- VIF tells you what overlaps
- The model decides who survives

If you want next, I can:

- Turn this into a one-page exam justification
- Compare MI/VIF with tree-based importance
- Or show what changes if this were PCA instead

Just say which.



OK I've moved on with the activity now. I've gone through the whole thing. Just just give me a step-by-step which are the decisions they made and what they dropped and now that effect affected R squared and is all of this effort worth it. We're going from .9 to .88 is that worth losing seven features?

## SECTION 1 — Ultra-Short Overview (10 seconds)

**What it is:** A step-by-step feature-selection workflow that trades complexity for nearly the same predictive power. [Model\\_solution\\_CAM\\_DS\\_C101\\_Acti...](#)

**Why it matters:** It shows you how to reduce features while keeping model performance stable and making the model easier to explain/use. [Model\\_solution\\_CAM\\_DS\\_C101\\_Acti...](#)

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## SECTION 2 — Beginner Layer

The decisions, in plain steps (what they did, in order)

### 1. Split target

- `y = price`, drop `price` from X. [Model\\_solution\\_CAM\\_DS\\_C101\\_Acti...](#)

### 2. Identify categorical vs numeric

- Then inspect unique values to spot “problem” categoricals. [Model\\_solution\\_CAM\\_DS\\_C101\\_Acti...](#)

### 3. Drop high-cardinality category

- Dropped `CarName` (147 unique values / 205 rows). [Model\\_solution\\_CAM\\_DS\\_C101\\_Acti...](#)

### 4. Drop obvious non-signal

- Dropped `car_ID`. [Model\\_solution\\_CAM\\_DS\\_C101\\_Acti...](#)

### 5. Ordinal-encode true ordinals

- `cylindernumber` mapped to 2,3,4,5,6,8,12
- `doornumber` mapped to 2,4 [Model\\_solution\\_CAM\\_DS\\_C101\\_Acti...](#)

### 6. One-hot encode remaining nominals

- `drop_first=True` to avoid dummy-variable trap. [Model\\_solution\\_CAM\\_DS\\_C101\\_Acti...](#)

### 7. Scale numeric/ordinal

- StandardScaler on continuous + ordinal features. [Model\\_solution\\_CAM\\_DS\\_C101\\_Acti...](#)

### 8. Convert booleans to 0/1

- Because their VIF tool doesn’t handle `bool` cleanly. [Model\\_solution\\_CAM\\_DS\\_C101\\_Acti...](#)

### 9. Compute MI + VIF together

- MI = usefulness vs target, VIF = redundancy among predictors. [Model\\_solution\\_CAM\\_DS\\_C101\\_Acti...](#)

### 10. Iteratively drop features (guided by VIF but checked by Adjusted R<sup>2</sup>)

#### 11. Finish with RFE

- Take df6 and select top 13, and confirm Adj R<sup>2</sup> stays similar. [Model\\_solution\\_CAM\\_DS\\_C101\\_Acti...](#)

#### Do / Don’t

- Do validate every drop with Adjusted R<sup>2</sup>
  - Don’t drop purely by VIF if MI is high
- 

## SECTION 3 — Intermediate Layer

“What did they drop, and what happened to Adjusted R<sup>2</sup>?“

Here’s the sequence exactly as the notebook shows it:

Stage	What they dropped	Why	Adjusted R <sup>2</sup>
Baseline	nothing	reference	0.9083 <a href="#">Model_solution_CAM_DS_C101_Acti...</a>
df1	<code>fueltype_gas</code> , <code>fuelsystem_idi</code> , <code>compressionratio</code>	highest VIF offenders	0.9033 <a href="#">Model_solution_CAM_DS_C101_Acti...</a>
df2	<code>next batch incl. carbody_sedan</code> , <code>enginetype_ohcf</code> , <code>carbody_wagon</code> , <code>carbody_hatchback</code> , <code>enginetype_...</code>	reduce more multicollinearity (batch)	0.8889 <a href="#">Model_solution_CAM_DS_C101_Acti...</a>

Stage	What they dropped	Why	Adjusted R <sup>2</sup>
df3	cylindernumber , carlength , wheelbase	start trimming "important-ish" ones	0.8885  Model_solution_CAM_DS_C101_Acti...
df4	citympg	high VIF, important-ish → test	0.8884  Model_solution_CAM_DS_C101_Acti...
df5	curbweight	test removal	0.8868  Model_solution_CAM_DS_C101_Acti...
df6	horsepower	test removal	0.8872 (tiny improvement)  Model_solution_CAM_DS_C101_Acti...
df7	enginesize	test removal	0.7529 (collapse → keep enginesize)  Model_solution_CAM_DS_C101_Acti...
RFE final	keep 13 features from df6	smaller model	0.8811  Model_solution_CAM_DS_C101_Acti...

### Key interpretation

- Most removals barely hurt performance.
- Removing **enginesize** nuked the model → it's a core driver, even if collinear.  
 Model\_solution\_CAM\_DS\_C101\_Acti...
- RFE trimmed further with only a small drop.

## SECTION 4 — Expert Layer

Is the effort "worth it" for 0.90 → 0.88?

Tell-it-like-it-is: sometimes yes, sometimes no — depends on the business goal.

### When it *is* worth it

- You need **interpretability** (stakeholders want "what drives price?")
- You need **simpler deployment** (fewer inputs to collect/clean)
- You're fighting **unstable coefficients** (multicollinearity makes linear model explanations shaky)
- You want better **generalisation** (less chance of overfitting in small-ish data)

### When it's *not* worth it

- Your only KPI is predictive accuracy and you'll use a stronger model later (GBMs etc.)
- Feature collection is cheap and you don't care about explanation
- You're not using coefficients for decisions

### The hidden win beginners miss

Adjusted R<sup>2</sup> dropping from 0.9083 → 0.8811 is a performance cost, yes.

But the benefit is:

- fewer features
- less collinearity
- more stable, defensible model story

That's often worth more than 0.027 Adj R<sup>2</sup>.

## SECTION 5 — Visual Thinking

### ASCII flowchart

SCSS

 Copy code

```

Encode + scale
↓
MI (importance) + VIF (redundancy)
↓
Drop high VIF + low MI first
↓
Re-fit OLS → check Adj R2
↓
If Adj R2 stable → keep dropping
If Adj R2 drops hard → undo drop
↓
RFE to compress further

```

## IF–THEN decision map

powershell

Copy code

```

IF VIF huge AND MI low → drop now
IF VIF huge BUT MI high → test drop (model decides)
IF Adj R2 collapses → keep feature
IF Adj R2 stable after dropping → redundancy confirmed

```

## Cheat-sheet

- VIF: redundancy warning light
- MI: signal strength
- Adj R<sup>2</sup>: “did we actually hurt the model?”

## SECTION 6 — Apply to a Concrete Example

Think of `citympg` and `highwaympg`:

- both predictive (MI high-ish)
- also overlap heavily (VIF high)

Dropping `citympg` barely changed Adj R<sup>2</sup> → it was mostly redundant signal.

Model\_solution\_CAM\_DS\_C101\_Acti...

Then `enginesize`:

- predictive AND overlapping

But dropping it caused Adj R<sup>2</sup> to crash → it carried unique info the rest couldn't replace.

Model\_solution\_CAM\_DS\_C101\_Acti...

That's the “tutor next to you” lesson: **not all collinear features are disposable**.

## SECTION 7 — Reflection Prompts

1. Am I optimising for accuracy or explainability?
  - Good: “Explainability matters; stable coefficients matter.”
  - Weak: “Higher number always wins.”
2. Did feature removal improve stability (VIF down) without killing performance?
  - Good: “Adj R<sup>2</sup> barely moved until we hit enginesize.”
  - Weak: “I removed random stuff.”
3. Would I rather collect/clean 20 inputs or 13 forever?
  - Good: “13 reduces pipeline friction.”
  - Weak: “Doesn’t matter.”

## SECTION 8 — What to Do Next

- **Practice:** Run the same pipeline but evaluate with **cross-validation RMSE**, not just Adj R<sup>2</sup> (more realistic).
- **Revise:** Dummy variable trap, MI vs VIF roles, why Adj R<sup>2</sup> is used.
- **Pitfall:** Don't conclude "feature selection is pointless" from a small R<sup>2</sup> change — the value is often **deployability + interpretability**, not just the metric.

If you tell me what your goal is (prediction-only vs explainability), I'll give you the correct "worth it / not worth it" verdict for *your* use case.

Sources



[Copy of CAM\\_DS\\_C101\\_Demo 4.2.2.ipynb](#)  
PDF

great now let's go thoguh this one

Perfect — this one is **PCA done properly**, and it answers a *different question* from MI/VIF.

I'll walk it **step-by-step**, exactly what decisions were made, **why**, and **what you should conclude**, anchored to **Demo 4.2.2** [Copy of CAM\\_DS\\_C101\\_Demo 4.2.2....](#).

## SECTION 1 — Ultra-Short Overview (10 seconds)

**What it is:** PCA compresses many correlated features into fewer uncorrelated components.

**Why it matters:** You trade **interpretability** for **dimensionality reduction, speed, and stability**.

## SECTION 2 — Beginner Layer

### The concrete decisions they made (in order)

1. Chose a high-dimensional dataset
  - MNIST: 784 pixel features per image [Copy of CAM\\_DS\\_C101\\_Demo 4.2.2....](#)
  - Classic case where feature selection is impossible manually
2. Immediately scaled the data
  - StandardScaler() before PCA [Copy of CAM\\_DS\\_C101\\_Demo 4.2.2....](#)
  - PCA is variance-based → scale is **non-negotiable**
3. Reduced sample size
  - 70,000 → 5,000 rows (random subset) [Copy of CAM\\_DS\\_C101\\_Demo 4.2.2....](#)
  - Decision = computational practicality, not statistics
4. Applied PCA with 2 components
  - Purpose: **visualisation**, not modelling [Copy of CAM\\_DS\\_C101\\_Demo 4.2.2....](#)
5. Plotted the 2D embedding
  - Saw partial digit clustering (but overlap) [Copy of CAM\\_DS\\_C101\\_Demo 4.2.2....](#)
6. Increased components (20, 100, 784)
  - Purpose: **variance analysis**, not prediction [Copy of CAM\\_DS\\_C101\\_Demo 4.2.2....](#)
7. Used explained variance + cumulative variance
  - To decide "how many components are enough" [Copy of CAM\\_DS\\_C101\\_Demo 4.2.2....](#)
8. Computed MI on PCA components
  - To check which *components* still relate to the label [Copy of CAM\\_DS\\_C101\\_Demo 4.2.2....](#)

## SECTION 3 — Intermediate Layer

## What PCA is doing in the pipeline

csharp

 Copy code

```

Raw pixels (784)
↓
Highly correlated
↓
Scale
↓
Rotate feature space
↓
New axes = principal components
↓
Rank by variance captured

```

Key shift from the last activity:

- MI/VIF removed features
- PCA replaces features

You don't "drop pixel 417" — you re-express all pixels.

---

### Explained variance decisions (this is examinable)

From the demo results  Copy of CAM\_DS\_C101\_Demo 4.2.2.... :

# Components	Variance Explained	Interpretation
20	~40%	Too lossy
100	~80%	Reasonable compression
784	100%	No reduction

Decision logic:

- Look for the elbow in cumulative variance
  - Accept loss if task allows it
- 

## SECTION 4 — Expert Layer

### Why PCA is fundamentally different from MI/VIF

Aspect	MI / VIF	PCA
Uses target?	MI yes, VIF no	<span style="color:red">X</span> No
Preserves meaning?	<span style="color:green">✓</span> Yes	<span style="color:red">X</span> No
Removes features?	Yes	No (recombines)
Handles multicollinearity?	Manually	Automatically
Interpretability	High	Low

This is why PCA is **not** used when:

- Stakeholders ask "why?"
  - Features must remain meaningful
  - Coefficients matter
-

## The key professional insight (many miss this)

High variance  $\neq$  high predictive power

That's why they computed MI on PCA components Copy of CAM\_DS\_C101\_Demo 4.2.2....

Example from MNIST:

- PC3, PC4 had higher MI than PC1
- Meaning: early variance  $\neq$  best label signal

That's subtle, and very exam-worthy.

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## SECTION 5 — Visual Thinking

### PCA mental model (memorise)

yaml

Copy code

```
Original axes: messy, correlated
New axes: clean, orthogonal
Variance = length along axis
```

---

### IF–THEN decision map

SCSS

Copy code

```
IF features are many + correlated → consider PCA
IF interpretability matters → do NOT use PCA
IF visualisation needed → PCA(2)
IF modelling speed needed → PCA(n where CV ≈ 80–95%)
```

---

## Equation cheat-sheet (conceptual)

- PCA finds directions that maximise:

css

Copy code

$\text{Var}(\mathbf{x} \cdot \mathbf{w})$

subject to:

nginx

Copy code

$\mathbf{w} \perp \text{previous components}$

---

## SECTION 6 — Concrete Example (MNIST)

- 784 pixels
- Adjacent pixels are highly correlated
- PCA compresses “stroke patterns”

Result:

- Digits cluster roughly
- But overlap → PCA alone  $\neq$  classifier

Tutor interpretation:

"PCA reveals structure, but doesn't solve classification."

---

## SECTION 7 — Reflection Prompts

1. What am I optimising here?
    - Good: "Dimensionality + speed"
    - Weak: "Accuracy only"
  2. Can I explain components to a stakeholder?
    - Good: "No — that's acceptable here"
    - Weak: "I don't know"
  3. Would MI/VIF even be feasible at 784 features?
    - Good: "No — PCA is the only sane option"
    - Weak: "I'd try anyway"
- 

## SECTION 8 — What to Do Next

### Practice

- Run a classifier on:
  - raw pixels
  - PCA(100)
  - PCA(50)

### Revise

- PCA vs feature selection
- Explained vs cumulative variance
- "Unsupervised ≠ irrelevant to y"

### Pitfall check

- Don't claim PCA "selects features"
  - Don't interpret PCs as real variables
- 

## Final blunt takeaway

- MI/VIF = surgical, interpretable pruning
- PCA = blunt, powerful compression

They solve **different problems**.

If you want next, I can:

- Compare PCA vs t-SNE (properly)
- Show when PCA hurts model performance
- Help you write a clean exam justification paragraph

Just say which.

Sources



okay now let's do the mini project: Over the past week there have been two active chats: \*\*CAM Data Science P4 2025\*\* and \*\*Judy's Birthday\*\*. Below is a chronological digest of everything posted between 3 Dec 2025 and 10 Dec 2025, along with observations (insights, facts, deadlines, learnings) and an Eisenhower-matrix classification for each

item.

---

## ## CAM Data Science P4 2025

### ### Key discussions and facts (3–10 Dec 2025)

\* \*\*Clarifying final-project expectations (5–6 Dec)\*\* – Several students asked whether there is a \*\*rubric\*\* to guide how the group should present their work beyond the code. A member confirmed there is a rubric that emphasises communicating results effectively to stakeholders (not just code). This implies your deliverables should include narrative and visual components.

\* \*\*Presentation guidance (5–6 Dec)\*\* – Ashfaq asked what “presentations” meant; another member clarified it relates to \*\*visualisation charts\*\* (colours, headings) used to showcase results. Jacob suggested including \*\*charts and tables showing results and experiments\*\*, plus a summary of the problem, methods used and recommendations for next steps. This provides a clear template for the report.

\* \*\*Assessment format (5 Dec)\*\* – Jovan asked if there would be marks; David van de Vijver replied that the project will be graded \*\*pass/fail\*\* with a \*\*60% threshold\*\*. There will not be a detailed breakdown of marks—meeting the rubric and demonstrating competency is essential.

\* \*\*Discussion on normality testing (8–9 Dec)\*\* – Jack PACE explained that normality tests (e.g., \*\*Shapiro–Wilk\*\*) are only needed when using \*\*parametric statistical tests\*\* (t-tests, ANOVA, correlations, linear regression). For anomaly/outlier detection, normality testing isn’t necessary. He further clarified that Jovan should check for normality before doing linear regression. This is a key methodological learning.

\* \*\*General sentiments (8–9 Dec)\*\* – Students thanked one another for explanations and expressed relief that support was being offered because this is their first full project. Some noted the marking “is not generous,” hinting at high standards. Someone shared a link to a YouTube video (possibly course-related) and another shared the \*\*GCHQ Christmas Challenge\*\* PDF for fun. These items do not require action.

\* \*\*Chat etiquette (9–10 Dec)\*\* – Participants exchanged quick acknowledgements (“I see, thanks for letting me know,” and “You’re welcome”) but no new tasks.

### ### Insights & learnings

\* The course emphasises \*\*communication\*\*: your final deliverable should include charts and tables that clearly explain what you did, the methodology and the implications. Don’t just submit code.

\* A \*\*pass/fail threshold of 60%\*\* means your focus should be on meeting all rubric items rather than chasing high numeric scores.

\* Normality tests are \*\*only relevant\*\* when you plan to use parametric statistical methods; for anomaly detection, you can skip them. Before running linear regression, check normality of residuals.

\* Team members appreciate guidance and clarity; proactively sharing resources (e.g., GCHQ challenge) fosters group morale.

### ### Eisenhower classification for Data-Science chat items

Topic/task	Importance	Urgency
Category	Reasoning	
-----   -----   -----		
-----   -----   -----		

Understand the project rubric and presentation expectations		High	
Medium	**Schedule**	Essential to meet pass threshold; there's time before final submission, but start planning visuals and narrative soon.	
Prepare charts/tables and include methodology & recommendations			
High	Medium	**Schedule**	Core part of the deliverable; not immediately due but should be in your plan.
Confirm pass/fail grading (60% threshold)		Medium	
Low	**Eliminate**	Important to know but no action needed beyond awareness.	
Decide whether to run normality tests (Shapiro-Wilk)		High	
Medium	**Schedule**	Only needed if using parametric methods; check before linear regression.	
Respond to fun resources (YouTube link, GCHQ challenge)		Low	
Low	**Eliminate**	Optional; purely for entertainment or extra practice.	

---

## # Judy's Birthday chat

## ### Key posts and facts (past week)

- \* \*\*Event invitation and timing (9 Dec)\*\* – Johann shared that he's \*\*looking forward to seeing everyone on Saturday at 1 pm\*\*. He mentioned he had hoped to book a pedal activity in the morning but found it easier to get Radiohead tickets. This confirms the party time and hints at optional activities. No further details (venue, agenda) were provided.
- \* \*\*Interest in activities\*\* – The remark about Radiohead tickets suggests some guests might attend a concert either before or after the party, though it was presented as a personal update rather than a group plan.
- \* \*\*No other posts\*\* – There were no additional messages in the past week; the rest of the chat content consists of earlier planning and RSVP reactions.

## ### Eisenhower classification for Judy's Birthday chat

Topic/task	Importance	Urgency
Category	Reasoning	
Attend Judy's birthday gathering on Saturday at 1 pm		Medium
Medium	**Schedule**	If you plan to attend, mark the date and time; not life-critical but requires planning.
Decide whether to join a pre-party activity (pedal/Radiohead)		Low
Low	**Eliminate**	It was mentioned as a personal intention by Johann; no group action required unless invited.

---

\*\*Summary:\*\* In the Data-Science chat, the group focused on understanding the project rubric, clarifying presentation requirements (charts, tables and recommendations), and confirming that the assignment is graded pass/fail with a 60% threshold. They also discussed when to use normality tests, with a reminder that such tests are only needed for parametric analyses. In the Judy's Birthday chat,

the only notable update was Johann's confirmation of the party time (Saturday at 1 pm).

Great — now we're in **mini-project mode**, not "demo comprehension" mode.

I'll give you a **clear, end-to-end execution plan** that directly maps to:

- the **rubric**
- the **pass/fail (60%) reality**
- what assessors actually look for
- the anomaly-detection + unsupervised focus of Week 5

No fluff. This is how you *pass cleanly*.

---

## MINI-PROJECT EXECUTION PLAYBOOK

*(CAM Data Science P4 2025 — anomaly detection context)*

---



Pierre Sutherland CAM\_DS\_C101\_Mini-...  
PDF

sorry no this one

Perfect — **this is the real assessment**, and this mini-project is where everything you've been learning finally **clicks into one coherent pipeline**.

Below is a **step-by-step, decision-by-decision walkthrough** of Mini-project 5.3.1: Detecting anomalous activity of a ship's engine, exactly aligned to the brief and what assessors expect

Pierre Sutherland CAM\_DS\_C101\_M...

I'll also be blunt about **what matters vs what's theatre**.

---

## MINI-PROJECT 5.3.1 — HOW TO DO IT (AND WHY)

### SECTION 1 — Ultra-Short Overview (10 seconds)

**What it is:** You're building and comparing statistical vs unsupervised ML anomaly detectors on engine sensor data.

**Why it matters:** The goal is **early fault detection** with 1–5% anomalies, not perfect prediction.

---

### SECTION 2 — Beginner Layer

*(What decisions you make, in order — no guessing)*

#### Step 1: Load + sanity-check data

**Decision:** Treat this as **continuous sensor data**, not labelled classification.

What you do:

- Load data

- Check shape, dtypes
- Check missing & duplicates

Why:

- Anomaly detection assumes mostly “normal” data
- Garbage rows = fake anomalies

DO: drop or justify duplicates

DON'T: invent labels

---

## Step 2: Descriptive statistics

Decision: Use mean vs median to sense skew/outliers.

What you extract:

- Mean
- Median
- Std

Why:

- Large mean–median gaps → skew → IQR preferred over z-score

This directly justifies why you choose IQR later (assessment gold).

---

## Step 3: Visual EDA (light, not obsessive)

Decision: Look for distribution shape and extremes, not stories.

What you plot:

- Histograms
- Boxplots

Why:

- Confirms skew
- Shows extreme tails
- Supports “statistical method choice” in your report

You are not judged on fancy EDA here — just justification.

---

## SECTION 3 — Intermediate Layer

(*Statistical anomaly detection — the IQR logic*)

### Step 4: IQR outlier flags (feature-wise)

Decision: Treat each sensor independently first.

For each feature:

- Compute Q1, Q3
- IQR = Q3 – Q1
- Flag:

Copy code

< Q1 – 1.5 · IQR OR > Q3 + 1.5 · IQR

Create:

- One binary column per feature ( 0/1 )

Why:

- Transparent
- Explainable to stakeholders
- Required explicitly by the brief

 Pierre Sutherland CAM\_DS\_C101\_M...

### Step 5: Combine IQR flags → final anomaly label

This is the most important decision in the whole project.

Decision:

"How many sensors must be abnormal at once before we panic?"

What you do:

- Sum binary outlier columns per row
- Try thresholds:  $\geq 2$ ,  $\geq 3$ ,  $\geq 4$
- Pick the one that gives 1–5% anomalies

Why:

- Single sensor spikes  $\neq$  failure
- Multiple simultaneous deviations = real risk

 This is **business logic**, not maths — and assessors love it.

## SECTION 4 — Expert Layer

(*Unsupervised ML models — why + how*)

Now you compare statistical vs ML methods.

### Step 6: Scale data (mandatory)

Decision: StandardScaler before ML.

Why:

- One-class SVM and Isolation Forest are **distance-sensitive**
  - Different units = fake anomalies
-  No scaling = invalid model
-  Scaling = professional pipeline

### Step 7: One-Class SVM

Decision: Use it as a **boundary learner** around "normal" data.

Key parameters you tune:

- `nu` → expected anomaly rate (start at 0.01–0.05)
- `kernel` → usually RBF
- `gamma` → controls boundary tightness

You do:

- Fit
- Predict (`-1` anomalies, `+1` normal)
- Adjust `nu` until 1–5%

Why:

- SVM is sensitive
  - Shows how **parameter tuning changes anomaly count**
- ⚠️** In practice: fragile, slow, hard to explain.
- 

### Step 8: Isolation Forest

**Decision:** Treat anomalies as **easy-to-isolate points**.

Key parameters:

- `contamination` → target anomaly %
- `n_estimators` → stability

You do:

- Fit
- Predict
- Adjust contamination to 1–5%

Why:

- Scales well
  - Less sensitive to distribution
  - Often the **best real-world choice**
- 

## SECTION 5 — Visual Thinking (PCA is NOT the model)

### Step 9: PCA for visualisation only

**Decision:** PCA is used to **explain**, not detect.

Pipeline:



Why:

- Humans need 2D
- PCA helps stakeholders *see* separation

**⚠️** PCA does NOT prove correctness  
It only supports interpretation

You must say **this explicitly** in the report.

---

## SECTION 6 — Concrete Comparison (What usually happens)

Typical outcome (and what you should say):

Method	% anomalies	Strength	Weakness
IQR	~2–4%	Transparent, explainable	Ignores multivariate effects
One-Class SVM	~1–5% (tuned)	Captures complex boundaries	Hard to tune, opaque

Method	% anomalies	Strength	Weakness
Isolation Forest	~1–5%	Robust, scalable	Less interpretable

**Professional conclusion:**

Isolation Forest offers the best trade-off between robustness and practicality.

---

**SECTION 7 — Reflection Prompts (assessment-ready)**

Ask yourself:

- 1. Did I justify each method choice?**
    - Good: "IQR chosen due to skewed distributions"
    - Weak: "We used IQR because the instructions said so"
  - 2. Did I control anomaly percentage deliberately?**
    - Good: "Threshold tuned to 1–5%"
    - Weak: "These were the results"
  - 3. Did I explain PCA's limitations?**
    - Good: "Visual aid only"
    - Weak: "PCA shows the anomalies clearly"
- 

**SECTION 8 — What to Do Next (very actionable)****Notebook**

- Make sure each step has a short markdown justification
- Save with correct filename

**Report (800–1000 words)**

Structure it like this:

- 1. Business problem**
- 2. Data + assumptions**
- 3. Statistical method (IQR)**
- 4. ML methods (SVM, IF)**
- 5. PCA visual evaluation**
- 6. Recommendation (pick ONE winner)**

**Pitfalls to avoid**

- **✗** Treating PCA as a detector
  - **✗** Ignoring anomaly percentage target
  - **✗** Over-engineering visuals
  - **✗** No business interpretation
- 

**Final blunt truth**

This mini-project is **not about clever models**.

It's about showing you can:

- choose **appropriate methods**
- **control assumptions**
- compare approaches
- and **explain decisions like a data scientist**, not a coder

If you want next, I can:

- Help you **write the report section-by-section**
- Review your **IQR threshold logic**
- Or sanity-check your **final recommendation**

Just say which.

Sources



*"the mini-project in 10 detailed page-long steps. I ask my permission to continue after each piece."*

⌚ 00:09

Absolutely, I can break it down into **10 detailed steps**, each with enough depth for you to really understand the "why" behind it. And I'll definitely check in with you after each piece to make sure you're comfortable before we move on to the next. So let's start with Step 1 and then you can let me know when you're ready for Step 2. Here we go!



*"Step on it."*

⌚ 00:00

All right, let's dive into Step 1 in detail.

---

### Step 1: Load and Sanity-Check the Data

#### What you're doing:

You'll start by importing the dataset into your environment. This is your first interaction with the real data, so you're just getting it on board and making sure it's readable.

#### Why you're doing it:

Because anomaly detection relies on having a clean baseline of "normal" data, you need to ensure there are no immediate issues like missing values, duplicate rows, or corrupted entries. Essentially, you're making sure your dataset is a solid foundation before you start any analysis.

#### How you do it (the key steps):

1. Import the dataset using the provided URL.
2. Inspect the first few rows with something like `df.head()` to get a sense of the columns and data types.
3. Check for missing values (`df.isnull().sum()`) and duplicates (`df.duplicated().sum()`).
4. Note down any initial cleaning steps you might need to take (for example, if you find duplicates, plan to drop them).

#### What assessors look for:

They want to see that you didn't just jump into modeling blindly. Showing you checked and cleaned the data is a sign of a thoughtful approach.

---

That's Step 1 in a nutshell. Let me know when you're ready for Step 2!

*"We'll step through."*

⌚ 00:00

All right, let's move on to Step 2!

---

## Step 2: Descriptive Statistics and Initial EDA

### What you're doing:

Now that your data is loaded and clean, you're going to **summarize it statistically**. This means looking at basic metrics like means, medians, and standard deviations for each feature. You'll also do a quick round of visualization—think histograms and boxplots—to see how each variable is distributed.

### Why you're doing it:

This step is all about understanding the **baseline behavior** of your data. You want to know what "normal" looks like before you start flagging anomalies. If you see that a feature has a skewed distribution or a lot of outliers right off the bat, that will guide your choice of anomaly detection method (like why you might use IQR instead of a Z-score).

### How you do it (the key steps):

1. Run `df.describe()` to get a quick statistical summary of all features.
2. Compare mean vs. median for each feature to see if there's any skew.
3. Plot histograms for each variable to visualize their distributions.
4. Create boxplots to quickly spot extreme values (potential outliers).
5. Document any notable findings—like "Feature X is heavily right-skewed"—so you can justify using a robust method like IQR later on.

### What assessors look for:

They'll want to see that you've taken the time to understand the data's distribution and that you can explain why certain features might produce more outliers. This shows you're making informed decisions, not just blindly running algorithms.

---

That's Step 2. Let me know when you're ready to proceed to Step 3!

*Transcript Unavailable*

⌚ 00:00

All right, let's roll right into Step 3!

---

## Step 3: Visualizing the Data Distributions and Spotting Extremes

### What you're doing:

In this step, you're going to **visually inspect the data** to confirm any initial assumptions you made from the descriptive stats. Basically, you're plotting out your features to see how they behave and to visually catch any glaring outliers or odd patterns.

**Why you're doing it:**

Because anomaly detection often hinges on understanding what "normal" looks like, these plots help you visually confirm the range of typical values and identify any features that have extreme points. This is your visual evidence for why you might treat certain data points as outliers later on.

**How you do it (the key steps):**

1. **Create histograms** for each feature. For example, use `df.hist(figsize=(10, 8))` to get a grid of histograms.
2. **Generate boxplots** to see the spread and identify any points outside the whiskers.
3. **Look for patterns**—are certain features more skewed? Are there clear outliers that stand out?
4. **Document your findings** briefly, noting which features seem to have the most extreme values. This will be useful for justifying your choice of anomaly detection method.

**What assessors look for:**

They want to see that you're not just relying on numbers but also using visual tools to understand the data. This shows you have a well-rounded approach and are being thorough before diving into the actual anomaly detection.

---

That's Step 3. Let me know when you're ready for Step 4!



*"Step 4."*

⌚ 00:00

Great, let's jump into Step 4!

---

## Step 4: Implementing the IQR Method for Outlier Detection

**What you're doing:**

Now you're going to apply the **Interquartile Range (IQR) method** to each feature to identify outliers. This means for each feature, you'll compute the first quartile (Q1) and the third quartile (Q3), then define outliers as any points that fall below Q1 minus 1.5 times the IQR or above Q3 plus 1.5 times the IQR.

**Why you're doing it:**

Because the IQR method is robust to skewed data and doesn't assume a normal distribution, it's a good first-pass statistical technique. It allows you to flag potential anomalies in a straightforward, explainable way that stakeholders can understand.

**How you do it (the key steps):**

1. **Calculate Q1 and Q3** for each feature. For example:

python

Copy code

```
Q1 = df.quantile(0.25)
Q3 = df.quantile(0.75)
IQR = Q3 - Q1
```

2. **Define outlier thresholds** for each feature:

python

Copy code

```
lower_bound = Q1 - 1.5 * IQR
```

```
upper_bound = Q3 + 1.5 * IQR
```

3. Create binary columns for each feature indicating whether a data point is an outlier (1) or not (0):

python

 Copy code

```
for col in df.columns:
    df[col + '_outlier'] = ((df[col] < lower_bound[col]) | (df[col] > upper_bound[col])).astype(int)
```

4. Summarize how many points are flagged per feature and consider how many features need to be "outliers" simultaneously for a data point to be considered an overall anomaly.

#### What assessors look for:

They want to see that you can apply a classic statistical method and that you understand how to translate these thresholds into a binary flag. This step is about showing you can systematically identify potential anomalies in a way that's easy to explain.

That's Step 4. Just let me know when you're ready for Step 5!

    ...

"Step 5."

⌚ 00:00

Absolutely, let's keep going!

## Step 5: Combining IQR Flags into a Final Anomaly Label

#### What you're doing:

In this step, you'll take all those individual outlier flags you created for each feature and combine them into a single label that tells you if a data point is an anomaly overall. Essentially, you're deciding how many "strikes" (outlier features) it takes for a data point to be considered a true anomaly.

#### Why you're doing it:

Because you need a final anomaly label that's not just based on one feature being an outlier, but rather a combination of multiple features acting weird at the same time. This approach helps you control the proportion of data points flagged as anomalies, aiming for that 1–5% target range.

#### How you do it (the key steps):

1. Sum up the outlier flags for each data point. For example:

python

 Copy code

```
df['outlier_count'] = df[[col for col in df.columns if '_outlier' in col]].sum(axis=1)
```

2. Choose a threshold for how many outlier features a data point needs to be considered an overall anomaly. For instance, you might decide that a data point is an anomaly if it's an outlier on 2 or more features.

3. Flag the overall anomaly label based on that threshold:

python

 Copy code

```
df['is_anomaly'] = (df['outlier_count'] >= 2).astype(int)
```

4. Adjust the threshold if needed to get the overall percentage of anomalies into the 1–5% range.

**What assessors look for:**

They want to see that you can make a reasoned decision about what constitutes an anomaly and that you can fine-tune that decision to meet the project requirements. This step is all about balancing sensitivity and specificity, and it shows you understand how to manage the anomaly rate.

---

That's Step 5! Just let me know when you're ready for Step 6.



"Thank you."

⌚ 00:00

Sure thing, let's keep the momentum going!

---

## Step 6: Applying and Tuning One-Class SVM for Anomaly Detection

**What you're doing:**

In this step, you'll move from the statistical approach to an unsupervised machine learning approach by using a one-class SVM (Support Vector Machine). You'll train the model on your dataset, treating the majority of the data as "normal" and letting the SVM identify the points that deviate from this norm.

**Why you're doing it:**

The one-class SVM is useful because it can learn the boundary of "normal" data in a high-dimensional space and highlight observations that lie outside this boundary. This is especially helpful when you have complex relationships between features that simple statistical methods might miss.

**How you do it (the key steps):**

1. Scale the data again if needed (you've likely done this already).
2. Initialize the one-class SVM with initial parameters, for example:

python

Copy code

```
from sklearn.svm import OneClassSVM
svm = OneClassSVM(nu=0.05, kernel='rbf', gamma='auto')
```

3. Fit the model to your data (excluding any labels, since it's unsupervised).
4. Predict anomalies: the model will return +1 for inliers (normal) and -1 for outliers.
5. Tune the nu parameter (which controls the fraction of data expected to be outliers) until you achieve the desired 1–5% anomaly rate.

**What assessors look for:**

They want to see that you can implement an unsupervised ML technique and that you understand how to tune it. It's important to demonstrate that you can adjust parameters thoughtfully rather than just using the defaults.

---

That's Step 6. Let me know when you're ready for Step 7!



"Thank you. This concludes today's webinar."

⌚ 00:01

Absolutely, let's head right into Step 7!

---

### Step 7: Using Isolation Forest for Anomaly Detection

#### What you're doing:

Now you're going to implement a second unsupervised ML method called Isolation Forest. This model works by isolating anomalies instead of trying to learn the normal region explicitly. It essentially creates random decision trees and sees how quickly a data point becomes isolated, with anomalies being easier to isolate.

#### Why you're doing it:

Isolation Forest is often more robust and scalable than one-class SVM, and it can handle large datasets well. It's also less sensitive to the exact shape of the normal data distribution. This gives you a second method to compare and see if it agrees with or differs from the SVM results.

#### How you do it (the key steps):

1. Initialize the Isolation Forest with a contamination parameter (the expected proportion of anomalies).

For example:

python Copy code

```
from sklearn.ensemble import IsolationForest  
iso_forest = IsolationForest(contamination=0.05, random_state=42)
```

2. Fit the model to your dataset.

3. Predict anomalies, similar to the SVM, where the model will label inliers as +1 and outliers as -1.

4. Tune the contamination parameter until the proportion of detected anomalies falls within the desired 1–5% range.

#### What assessors look for:

They'll want to see that you understand how to use and tune Isolation Forest and that you can explain why you're using it as a complementary method. It shows that you're not just relying on one technique but are comparing multiple approaches to cross-validate your results.

---

That's Step 7. Let me know when you're ready for Step 8!



*Transcript Unavailable*

⌚ 00:00

Absolutely, let's dive into Step 8!

---

### Step 8: Visualizing Results with 2D PCA Plots

#### What you're doing:

In this step, you'll use PCA (Principal Component Analysis) to reduce your feature space to two dimensions

and then create scatter plots showing normal points and anomalies in different colors. This gives you a visual representation of how the anomalies are distributed in a simplified space.

#### Why you're doing it:

Because visualizing your results helps both you and your stakeholders understand the separation between normal data and anomalies. It provides a sanity check: if your anomalies cluster in certain regions, that's a good sign that your model is picking up genuine outliers. If they're scattered everywhere, you might need to revisit your approach.

#### How you do it (the key steps):

1. Run PCA on your scaled data to reduce it to two principal components:

python

Copy code

```
from sklearn.decomposition import PCA
pca = PCA(n_components=2)
X_pca = pca.fit_transform(scaled_data)
```

2. Create a scatter plot where each point is colored by its anomaly label (normal vs. anomaly).
3. Plot the results from both models (SVM and Isolation Forest) to compare their visual outputs.
4. Highlight the anomalies in a different color (e.g., red for anomalies, blue for normal points).

#### What assessors look for:

They want to see that you can present your findings visually and that you understand the purpose of using PCA for visualization. It's not about proving the model is perfect, but about showing you can communicate results in a way that's easy to understand.

---

That's Step 8. Just let me know when you're ready for Step 9!

...

*"Before you go to step 9, just explain why would you not do PCA for each feature in turn."*

00:05

Absolutely, let me clarify that.

You wouldn't do PCA for each feature individually because PCA is fundamentally about **reducing the dimensionality of the entire feature set** all at once. In other words, PCA looks at how all your features vary together and finds new axes (principal components) that capture the most variance in a lower-dimensional space.

If you tried to do PCA on each feature separately, you'd just be transforming each single feature into itself, which doesn't make sense. The power of PCA comes from analyzing the relationships between all features together. It finds the directions in which the data varies the most overall, not feature by feature.

So, in summary: we do PCA on the full set of features together to get a holistic, lower-dimensional representation. Doing it one feature at a time wouldn't reduce dimensions or reveal those combined patterns.

All right, with that clarified, just let me know when you're ready to continue on to Step 9!

...

*"So if you do PCA, the new point on the PCA components represents, in this case, let's say four dimensions. A point is basically four dimensions squished together in some way and some ratio to get you the 2D representation."*

⌚ 00:14

Exactly, you've got it. When you run PCA on your full dataset, say reducing it from many dimensions down to just two or three principal components, each new point on that 2D plot is indeed a kind of "squished together" representation. In other words, each point on the PCA plot is a weighted combination of the original features.

So if you started with, say, four dimensions (or more) and reduced down to two, each point on your 2D plot is a summary of how those four original dimensions vary together. It's like taking a multi-dimensional shape and flattening



*"is that like a tuple, so it's basically each row in the bidimensional space is treated like a tuple and then that's represented by a single point"*

⌚ 00:08

Yes, exactly! You can think of each row in your high-dimensional dataset as a tuple of values—basically a list of coordinates in that high-dimensional space. When you apply PCA, you're taking that high-dimensional tuple and transforming it into a new tuple with fewer dimensions—like turning a 4D or 10D coordinate into a 2D coordinate. Each point on your PCA plot is just that tuple represented in a lower-dimensional space. So yep, you're spot on! Each row is indeed treated like a tuple, and PCA just represents that tuple as a single



*Transcript Unavailable*

⌚ 00:00

You're very welcome!



*"Is that doing the same thing? Is that different? SVC and isolation forest, how is that different in terms of those high dimensional tuples?"*

⌚ 00:07

Great question! So PCA, one-class SVM, and Isolation Forest all handle those high-dimensional tuples, but they do it in different ways.

- PCA is all about reducing dimensions. It's just taking those high-dimensional tuples and finding a lower-dimensional space to represent them in. It doesn't decide what's normal or anomalous; it just squishes the data down so you can visualize it.

- One-class SVM and Isolation Forest are actually doing anomaly detection in that high-dimensional space. They aren't just reducing dimensions; they're looking at the full set of features and deciding which points look unusual.
  - One-class SVM tries to find a boundary that encloses the "normal" data in that high-dimensional space. Anything outside that boundary is considered an anomaly.
  - Isolation Forest works by randomly partitioning the data and seeing which points are easier to isolate. Points that get isolated quickly are considered anomalies.

So they're all dealing with those tuples, but PCA is just about representation, while SVM and Isolation Forest are about detecting outliers directly in the original feature space.

Let me know if that makes sense or if you'd like to dive deeper!



*"So you use Isolation Forest or SVC both, but then you would tag those tuples with true, false, outlier, or non, based on its findings, and add that as another feature. Basically, within the tuple, one of the dimensions would be true or false."*

⌚ 00:14

Exactly, you've got it! That's a common and really practical approach. After you run something like Isolation Forest or a one-class SVM, you'll end up with a label for each tuple (each row) indicating whether that point is an outlier or not. You can then add that label as an additional feature—so now each row has all its original dimensions plus a new dimension that's basically "is\_anomaly" as true or false (or 1 or 0).

This is super helpful because you can then analyze those tagged points further, or even use that anomaly label as part of another downstream process. It's like you've enriched your dataset with a new piece of information that says, "Hey, this point is unusual according to this model."

So yeah, you've nailed it. You're essentially adding that anomaly indicator as another dimension in your data.



*"So why do you care if the data is skewed or not by a single dimension at a time? Why do the histograms and the box plots and IQRs and things like that? So IQR is a parameter dimension, right? But IQR is not per tuple, is it?"*

⌚ 00:16

Exactly, you're right on track. The IQR (Interquartile Range), histograms, and box plots are all calculated one dimension at a time. In other words, they're looking at the distribution of each individual feature separately. And that's actually their purpose: to help you understand how each feature behaves on its own.

So why do we care if a single feature is skewed? Because that tells us which statistical techniques to use. For example, if a single feature is heavily skewed, it might produce lots of extreme values that are just naturally part of that feature's distribution. In that case, using IQR to identify outliers is a robust choice because it doesn't assume a normal distribution. If you were to use something that assumes normality (like a Z-score), you'd get misleading results.

In short, those per-dimension checks help you understand the shape of each individual feature so you can choose the right methods. They don't operate on the entire tuple at once; they operate on each feature

separately. That's why you do those univariate analyses first.

Let me know if that clears it up!



*"Why does it matter how those individual ones are distributed if you're just going to treat SVC or isolation forest on tuples?"*

⌚ 00:08

Ah, I see what you're getting at—and it's a great question. If ultimately you're feeding the whole tuple into models like one-class SVM or Isolation Forest—which look at the entire multi-dimensional space—then why fuss about the distribution of each individual feature, right?

Well, the reason you still care about those individual distributions is twofold:

First, **data preparation and method choice**. Before you even run those models, you often need to decide on preprocessing steps—like whether to scale your features or transform them. If some features are super skewed or have outliers, that can influence how you normalize the data. It's about making sure the input to those models is well-conditioned so they perform well.

Second, **interpretability and sanity checks**. Even though the final anomaly detection is done on the full tuple, understanding each feature's distribution helps you interpret results. For instance, if a feature is naturally skewed, you might expect more "anomalies" on that dimension. If you didn't look at that feature individually, you might misunderstand why certain points are flagged. It's part of knowing your data well.

So in a nutshell: you care about single-feature distributions to prep your data properly and to understand what's going on under the hood—even if the final model treats each row as a full tuple.

Let me know if that helps clarify!



*"I need more nuance on that please. What happens if you don't do that?"*

⌚ 00:04

Absolutely, let's get a bit more nuanced. If you skip looking at individual feature distributions—so you never check those histograms, box plots, or IQRs—what can happen is that you go into modeling a bit blind.

Here's why that can be a problem:

First, you might feed your model data that hasn't been properly prepared. If some features have extreme skew or outliers, and you don't know about it, your model might become sensitive to those extreme values in a way that distorts results. For example, a one-class SVM might set its boundary in a strange place because one feature's scale is off.

Second, you might misinterpret the anomalies you find. If you haven't looked at individual distributions, you might not realize that a certain feature naturally has a wide range. You could end up flagging points as outliers that are actually just normal for that particular feature.

Third, some preprocessing steps, like scaling, depend on knowing the data's distribution. If you don't know that a feature is heavily skewed, you might skip a transformation that would have made the model more robust.

In short, checking those individual distributions is like doing your homework. It helps you trust your model's results and avoid surprises. Without it, you're basically flying blind and might end up with a model that's less accurate or harder to interpret.

I hope that gives you the nuance you were looking for!



*"Let's say we have four dimensions, just go through those SKUs and resolutions, and if I don't treat them all, that would affect the SBC, and that would affect isolation for us. What are the things that can do it the worst?"*

⌚ 00:16

Sure, let's break it down with a concrete example. Imagine we have a dataset with four features—let's call them Feature A, B, C, and D. Now let's say:

- Feature A is nicely normally distributed. No big skew, all good.
- Feature B is highly skewed to the right, meaning it has a long tail of larger values.
- Feature C has a bunch of outliers that are really high compared to the rest of the data.
- Feature D is pretty uniform with no major issues.

Now, what happens if we don't pay attention to those distributions?

For the **one-class SVM**, which is sensitive to the scale and spread of the data, those skews can throw off the boundary it learns. For example, if Feature B is super skewed and you don't transform it or scale it, the SVM might place too much importance on those large values and end up with a boundary that doesn't really reflect the normal region well.

For the **Isolation Forest**, it's a bit more robust to these issues because it works by isolating points rather than relying on a strict boundary. However, if Feature C has extreme outliers that you never addressed, the Isolation Forest might end up considering those extreme points as normal just because it didn't get a fair sense of what "normal" should look like. In other words, it might fail to isolate the right anomalies because the feature scales are inconsistent.

In the worst case, not treating these issues can lead to models that either over-flag or under-flag anomalies. They become less reliable, and you might have more false positives or miss true outliers. So, by paying attention to each feature's distribution, you're essentially giving these models a fair shot at doing their job well.

I hope that clarifies things a bit more!



*"Give me four hypothetical specific examples of that to introduce some more nuance here. Okay, I understand that."*

⌚ 00:06

Absolutely, let's dive into four quick hypothetical examples to really add some nuance.

#### Example 1: The Skewed Feature and the SVM Boundary

Let's say Feature B is income data and it's heavily skewed, with a few very large values. If you don't transform or scale this feature, the one-class SVM might place its decision boundary in a way that overemphasizes

these high incomes. The result? It might treat a lot of normal middle-income points as anomalies because it thinks the normal region is skewed upward.

#### Example 2: Outliers in One Feature Confusing Isolation Forest

Imagine Feature C is number of website visits, and you have a few users who visited thousands of times while most visited only a few dozen times. If you don't address these outliers, the Isolation Forest might consider those extreme visitors as normal and fail to catch smaller but still significant anomalies. In other words, it might miss outliers that aren't as extreme but are still important because it's learned to accept those giant values as part of the normal range.

#### Example 3: A Uniform Feature That Stays Under the Radar

Feature D might be something like age, and it's evenly distributed without any issues. This one might not cause problems at all. If you skip checking it, you're fine here. But the point is, you wouldn't know which features are troublemakers unless you actually look.

#### Example 4: A Feature That Needs Scaling to Avoid Model Confusion

Suppose Feature A and Feature B are measured on very different scales—say one is in the range of 0 to 10 and the other from 0 to 10,000. If you don't scale them, the model might pay too much attention to the feature with the larger scale and effectively ignore the smaller-scaled feature. This can lead to a model that doesn't really understand the true shape of the data.

In all of these cases, ignoring the individual distributions can lead to models that misinterpret what's normal and what's not. By taking a bit of time to understand each feature, you give both SVM and Isolation Forest a much better foundation, reducing the chances of these kinds of errors.

I hope these examples help add that nuance!



*"I need to complete the graph of what the issue is and how it is transformed and how it affects the isolation forest or the SVC."*

⌚ 00:09

Absolutely, let's bring it all together in one complete example.

Imagine we have those four features: A, B, C, and D.

First, let's say Feature B is the one that's highly skewed, maybe it's income or some kind of count data that has a long tail of high values. If we do nothing and feed it directly into a one-class SVM, that SVM might stretch its decision boundary to accommodate those high values, making it think that points in the middle range are anomalies when they're not.

Now, let's say we decide to transform Feature B, maybe by applying a log transformation or some other scaling that makes it more normal-looking. Now when we run the one-class SVM, it sees a more balanced feature distribution. The boundary it learns is more realistic and it's less likely to misclassify normal points as anomalies. So that transformation directly improves how the SVM performs.

For the Isolation Forest, it's a bit more forgiving, but it still benefits from the transformation. Without it, the Isolation Forest might consider those extremely high values as part of the normal range. After the transformation, it's better able to identify what's truly unusual. In other words, the transformation helps the Isolation Forest focus on real anomalies rather than being skewed by those large values.

So in summary, by understanding and transforming that skewed feature, both the SVM and the Isolation Forest become more accurate. They no longer get thrown off by that skew, and they can focus on detecting true anomalies. That's the real payoff of doing that careful preprocessing.

I hope that wraps it up nicely for you!



*"I'll put it all together again with three specific examples, the issue and the transformation."*

⌚ 00:05

Absolutely, let's put it all together with three specific examples and show the issue, the transformation, and the improvement.

---

### Example 1: Skewed Feature and Log Transformation

**Issue:** Let's say we have a feature representing income, and it's heavily skewed to the right—most people earn modest amounts, but a few people earn very high incomes. If we feed this directly into a one-class SVM, the model might see those high incomes as stretching the range of what's normal and misclassify mid-range incomes as anomalies.

**Transformation:** We apply a log transformation to the income feature. This reduces the skew, compresses those high values, and makes the distribution more balanced.

**Improvement:** Now the SVM sees a more normalized feature and sets its boundary more appropriately. It's less likely to flag normal mid-range incomes as anomalies, and it focuses on the true outliers.

---

### Example 2: Outliers in a Count Feature and Winsorization

**Issue:** We have a feature counting the number of times users visit a website. Most users visit a few dozen times, but a few visit thousands of times. If we don't deal with these outliers, the Isolation Forest might treat those extreme values as normal and miss smaller, more meaningful anomalies.

**Transformation:** We apply winsorization, which caps the extreme values at a certain percentile. This means the extreme visitors are brought down to a more reasonable range.

**Improvement:** Now the Isolation Forest can focus on the smaller anomalies that matter. It won't be skewed by those extreme outliers. It's better at identifying the true anomalies in the data.

---

### Example 3: Different Scales for Different Features and Standardization

**Issue:** Suppose Feature A is measured in a range of 0 to 10, while Feature B is in a range of 0 to 10,000. If we don't standardize these features, the model might



*"So I think it's also one of the most common screening features."*

⌚ 00:03

Absolutely, let's sum it up with three of the most common transformations or scaling fixes and how they help.

---

**First, Log Transformation for Skewed Data:**

If you have a feature with a heavy right skew—like income or counts with some very large values—a log transformation compresses those large values and makes the distribution more normal. This helps models like a one-class SVM because it won't overemphasize those extreme values. Instead, the model sees a more balanced feature and can set a better decision boundary.

---

**Second, Winsorization for Outliers:**

When you have a feature with extreme outliers—like a few data points that are way higher than the rest—winsorization caps those outliers at a certain percentile. That way, models like Isolation Forest don't get confused by a few extreme values. Instead, they focus on the real structure of the data and identify more meaningful anomalies.

---

**Third, Standardization for Different Scales:**

When different features have vastly different scales—like one feature ranging from 0 to 10 and another from 0 to 10,000—standardization (scaling to have a mean of 0 and a standard deviation of 1) puts them on the same footing. This helps any model, including both SVM and Isolation Forest, to treat each feature fairly. That way, no single feature with a huge scale dominates the model's attention.

---

In short, these transformations—log transformation, winsorization, and standardization—help your anomaly detection models work better by making the data more well-behaved. That way, both the one-class SVM and the Isolation Forest can do their job more accurately and reliably.

I hope that gives you a nice, neat summary!



*Transcript Unavailable*

⌚ 00:11

Yeah, exactly! Copyright rules are definitely a thing, so we steer clear of singing songs that are still under copyright. It keeps everything on



*"So do I just need to get between 1% and 5% anomalies? Is that it, after I've transformed the dimensions?"*

⌚ 00:06

Yeah, that's pretty much the idea. Once you've done your transformations and you're running your anomaly detection, you typically tune your model so that it flags a reasonable proportion of points as anomalies—often somewhere in that 1 to 5 percent range. That's a common benchmark just to keep things practical. So yep, you've got it!



*"How do you compare outliers from SVM to Isolation Forest?"*

Absolutely, let's break that down. When you compare the outliers flagged by a one-class SVM and by Isolation Forest, you're basically looking at two different approaches to spotting what's weird in your data.

The one-class SVM is kind of like drawing a boundary around the normal points and saying, "Anything outside this boundary is an outlier." It's a more boundary-based, distance-based approach. Isolation Forest, on the other hand, works by randomly splitting the data and seeing which points get isolated quickly. So it's more about how easy it is to separate a point from the rest.

What you'll typically see is that they might agree on some outliers and disagree on others. The SVM might flag points that are far from the center of the data cloud, while Isolation Forest might pick up points that have unique feature combinations that are easy to isolate. Comparing them can give you a fuller picture of what might be considered an anomaly from different perspectives.



*"Can you repeat that, please?"*

⌚ 00:01

Sure thing! So basically, when you compare outliers from the one-class SVM and Isolation Forest, you're looking at two different ways of spotting unusual points. The SVM sets a boundary around normal data and calls anything outside that boundary an outlier. Isolation Forest, on the other hand, isolates points based on how easily they can be separated from the rest. So you'll often find that they agree on some outliers and disagree on others, giving you a more well-rounded view of what might be considered unusual.



*"Could you repeat that, please?"*

⌚ 00:01

Of course! So, when you compare outliers from a one-class SVM and from Isolation Forest, you're basically looking at two different techniques to spot anomalies. The one-class SVM draws a boundary around what it considers normal data and calls anything outside that boundary an outlier. Isolation Forest, on the other hand, figures out which points are easiest to isolate by randomly splitting the data. Sometimes they'll agree on which points are outliers, sometimes they won't, and that gives you a more complete view from two different angles.



*"What kind of overlap is there usually?"*

⌚ 00:01

Yeah, so typically you do see some overlap, but it's not always a perfect match. In other words, the one-class SVM and Isolation Forest will often agree on a core set of outliers, especially the really obvious ones. But because they use different methods—SVM focusing on a boundary and Isolation Forest on isolating points quickly—they'll each catch a few unique outliers too. So you'll get some overlap and also some differences, and that can give you a more well-rounded detection overall.

*"How do you interpret that? How do you report that to the customer?  
Because it was on the boat and engine heat data and stuff like that."*

⌚ 00:07

Absolutely, so when you're explaining this to a customer—like if they're looking at engine heat data or something similar—you can basically say that you're using two different anomaly detection methods to get a more complete picture. You can tell them that the one-class SVM and Isolation Forest each have their own way of finding unusual readings. Where they both agree, you have a pretty strong signal that something's truly off. And where they differ, you're just getting different perspectives that might highlight subtler patterns. So in your report, you can say something like, "We used two complementary methods to detect anomalies. The overlap between them shows clear outliers, and the differences give us extra insights into other potential anomalies." That way, the customer understands you're giving them a fuller, more nuanced analysis.

Transcript Unavailable

⌚ 00:01

You're welcome! Anytime you need a bit more clarity, just let me know.

*"Give an example from industry that clearly illustrates the differences in the types of anomaly given by one class SVA in an isolation forest."*

⌚ 00:08

Absolutely! Let's take an example from something like industrial machine monitoring. Imagine you have a factory with a big industrial engine, and you're monitoring things like engine temperature, vibration levels, and fuel consumption.

Now, if you run a one-class SVM on that data, it might find anomalies that are kind of global outliers—like a temperature reading that's way hotter than anything the engine has ever hit before. The SVM might say, "Hey, this point is far outside the normal boundary."

On the other hand, if you run Isolation Forest, it might pick up subtler combinations of features. Maybe the temperature is only slightly elevated, but the combination of a certain vibration level and a slight increase in fuel consumption is unusual. Isolation Forest might say, "This is an outlier because this combination of factors is rarely seen."

So, the SVM might catch a big, obvious spike in one dimension, while the Isolation Forest might catch a weird pattern across multiple dimensions that the SVM didn't notice. And when you explain that to the customer, you can say, "The SVM found this really big temperature spike as an outlier, while the Isolation Forest found this subtle combination of factors that's unusual." That really illustrates the difference in what each method flags.

*"Give me an example of the domains again."*

⌚ 00:01

Of course! So let's take that same industrial engine scenario. Imagine you're monitoring an engine and you have a few key dimensions: engine temperature, vibration levels, and fuel usage. Now, if you use a one-class SVM on that data, it might pick up something like a really obvious outlier in temperature—like if the engine suddenly gets much hotter than it's ever been before, the SVM says, "Okay, that's definitely an outlier."

On the other hand, the Isolation Forest might notice a more subtle combination—maybe the temperature is only a little high, but at the same time the vibration and the fuel usage are also just slightly off in a combination that's rare. So the Isolation Forest says, "Hey, this mixture of factors is unusual."

In other words, the SVM might catch the big single-dimensional outlier, and the Isolation Forest might catch a nuanced multi-dimensional pattern. And that's a nice concrete example you can share with a customer to show how each method spots different kinds of anomalies.



*Transcript Unavailable*

⌚ 00:00

You got it! So in a nutshell, you can tell them that the one-class SVM might flag a really obvious single-factor spike—like a big jump in engine temperature—while the Isolation Forest might catch a subtler combination of factors, like a slight rise in temperature plus a little extra vibration and fuel use. Together, those methods give a fuller picture of what's out of the ordinary. And that's a great way to show them the strengths of each approach.



*"go through each of the demos of week four and just give me two learnings in each one and just ask my permission to continue to the next"*

⌚ 00:07

Absolutely! Let's walk through each demo from week four and highlight two key learnings from each. And I'll check in with you before moving on to the next one.

So for the first demo of week four, one big takeaway might be how to normalize your data before feeding it into a model, and another could be understanding how to interpret the initial anomaly results. Does that sound good? If so, just let me know and I'll move on to the next demo!



*"Yeah, I know."*

⌚ 00:00

Great! All right, so for that first demo, just to quickly recap: One key learning was how important it is to normalize or scale your data before you put it into the model, and the second was how to start interpreting those initial anomaly detection results—like just getting comfortable with what the output looks like. All right, with that covered, let's move on to the next demo. Let me know if you're ready for that!

...

*"No, I need way more detail. I need the context and the specific examples, not generalizations, only specific insights, wisdom, learnings, problems, context."*

⌚ 00:10

Ah, got it! You want the nitty-gritty. No problem. Let me dig into more specifics. So let's imagine in that first demo, for example, you were working with a dataset of machine temperatures over time. One concrete learning could be that you saw how to apply something like MinMax scaling to bring all those temperature values into a zero-to-one range, making them easier to compare. Another very specific insight might have been how to identify a particular type of anomaly—like noticing that sudden spikes in temperature at certain intervals were flagged once the data was scaled.

So those are two concrete things: you learned exactly how to do the scaling and you learned how to spot and interpret a certain kind of temperature anomaly. All right, with that level of detail, let me know if you want to go on to the next demo!

...

*"Traffic is awful, isn't it, Sam?"*

⌚ 00:02

It really can be! Traffic is one of those universal headaches. It just seems to slow everything down. But hey, at least we can chat while you're waiting it out!

...

Which colab notebooks did I upload here?

Here's the **exact list of Colab / notebook-style files you uploaded in this conversation**, in plain terms:

#### Jupyter / Colab notebooks (PDF exports)

1. Model\_solution\_CAM\_DS\_C101\_Activity\_4.1.8.ipynb – Colab.pdf  
→ Feature selection with MI, VIF, iterative removal, RFE (cars dataset)
2. Copy of CAM\_DS\_C101\_Demo 4.2.2.ipynb – Colab.pdf  
→ PCA demonstration (MNIST + Wine datasets, explained variance, MI on PCs)
3. Pierre Sutherland CAM\_DS\_C101\_Mini-project 5.3.1.ipynb – Colab.pdf  
→ Mini-project: anomaly detection (IQR, One-Class SVM, Isolation Forest, PCA for visualisation)

#### Non-notebook PDFs (supporting course material)

4. Week 4.pdf
5. Week 5.pdf
6. Notes from course.pdf

## 7. Shanup.pdf

---

### How this maps to your learning flow (important)

- Activity 4.1.8 → Feature selection & multicollinearity (supervised, regression)
- Demo 4.2.2 → Dimensionality reduction (unsupervised, PCA)
- Mini-project 5.3.1 → Anomaly detection (unsupervised, statistical + ML)

Those three notebooks form a deliberate progression:

*select features → compress features → detect abnormal behaviour*

If you want, next we can:

- map Week 4 demos → Week 5 mini-project explicitly, or
- build a one-page “which tool when” decision map, or
- do what you asked earlier: Week 4 demo-by-demo with concrete insights only (no fluff).

Just tell me which.



Just give me the cribsheet for weekn5 the way I like to learn

Got it.

Here is a Week 5 cribsheets, exactly in your learning style: structured, layered, concrete, no fluff.

This is the version you'd want the night before submission.

---

## WEEK 5 CRIBSHEET — ANOMALY DETECTION (STAT + ML)

### SECTION 1 — Ultra-Short Overview (10 seconds)

**What it is:** Detect rare, abnormal behaviour in mostly normal data **without labels**.

**Why it matters:** Early fault detection beats prediction when failures are rare and costly.

---

### SECTION 2 — Beginner Layer (Foundations)

#### Core assumptions (memorise these)

- Data is **mostly normal**
- Anomalies ≈ 1–5%
- Labels usually **do not exist**
- Goal = **risk reduction**, not accuracy

#### Two families of methods

##### 1 Statistical (univariate)

- IQR
- Boxplot logic
- Simple, explainable

##### 2 ML (multivariate, unsupervised)

- One-Class SVM
- Isolation Forest
- Captures interactions

**Do / Don't rules****DO**

- Scale before ML
- Control anomaly rate explicitly
- Compare methods

**DON'T**

- Assume normality
- Treat PCA as a detector
- Optimise "accuracy" (there is none)

**SECTION 3 — Intermediate Layer (Pipeline logic)****Full Week 5 pipeline (this is examinable)**

SCSS

Copy code

```

Raw sensor data
↓
EDA (histograms, boxplots)
↓
Distribution check (per feature)
↓
Statistical anomalies (IQR)
↓
Scaling
↓
ML anomalies (SVM, IF)
↓
PCA (visualisation only)
↓
Comparison + recommendation

```

**Why EDA still matters (even for ML)**

- Chooses IQR over z-score
- Justifies scaling / transforms
- Prevents models being misled by skew

**SECTION 4 — Expert Layer (Method behaviour)****IQR (Interquartile Range)****What it does**

- Flags extreme values per feature

**Strengths**

- Transparent
- Stakeholder-friendly
- Robust to skew

**Weakness**

- Ignores feature interaction

**Professional use**

- Baseline / rules-based alerting
- Compliance / safety reporting

## One-Class SVM

### What it does

- Learns a boundary around normal tuples

### Sensitive to

- Scale
- Skew
- Kernel parameters

### Strengths

- Finds global deviations
- Good for smooth boundaries

### Weakness

- Fragile
- Hard to explain
- Slow to tune

### Flags

- “Far from normal region” points
- 

## Isolation Forest

### What it does

- Isolates points via random splits

### In insensitive to

- Distribution shape
- Minor skew

### Strengths

- Robust
- Scalable
- Industry-preferred

### Weakness

- Less interpretable
- Randomness (needs seed)

### Flags

- “Unusual combinations” of features
- 

## SECTION 5 — Visual Thinking

### Mental models (memorise)

#### IQR

sql

Copy code

```
One feature at a time
"Is this value extreme?"
```

### One-Class SVM

SCSS

Copy code

```
Boundary in high-D space
"Is this tuple outside the normal bubble?"
```

## Isolation Forest

css

 Copy code

```
Path length
"Is this tuple easy to separate?"
```

---

## IF–THEN decision map

pgsql

 Copy code

```
IF need explainability → IQR
IF need sensitivity → One-Class SVM
IF need robustness → Isolation Forest
IF need visuals → PCA (only after detection)
```

---

## SECTION 6 — Concrete Engine Example (Mini-project)

### Data

- RPM
- Oil pressure
- Fuel pressure
- Coolant pressure
- Oil temperature
- Coolant temperature

### What happens in practice

#### IQR

- Flags spikes in **single sensors**
- E.g. sudden oil temperature surge

#### One-Class SVM

- Flags **global deviation**
- E.g. engine operating far from normal regime

#### Isolation Forest

- Flags **subtle combinations**
- E.g. slightly high temp + slightly low pressure + high RPM

### Key insight (say this in report)

SVM finds “far away” behaviour,  
Isolation Forest finds “rare combinations”.

---

## SECTION 7 — Reflection Prompts (Assessment-ready)

Ask yourself:

1. Did I control anomaly percentage?
  - Good: “Tuned to 1–5%”
  - Weak: “These were the results”
2. Can I explain why a point is anomalous?
  - Good: “3 sensors out of range simultaneously”
  - Weak: “The model said so”
3. Do methods agree on core anomalies?

- Good: "Overlap increases confidence"
  - Weak: "Different answers confused me"
- 

## SECTION 8 — What To Do Next (Actionable)

### For the mini-project

- Pick one winner (usually Isolation Forest)
- Justify using business risk
- Use PCA only to explain

### Common pitfalls to avoid

- **X** Using PCA as detector
  - **X** Ignoring distribution shape
  - **X** Chasing "accuracy"
  - **X** Over-tuning SVM
- 

## FINAL WEEK 5 TRUTH (tell-it-like-it-is)

- Week 5 is about judgement, not algorithms
- You are graded on:
  - method choice
  - reasoning
  - communication

If you want next, I can:

- compress this into a **1-page exam memory sheet**
- turn it into **report paragraph templates**
- map **Week 4 → Week 5 concept transfer**

Just say which.



Help with his discussion please: [13/12, 21:01] +44 7404 179419: Sorry, late to the party, you have to use a 2D model to generate the decision boundary / contour plots. So the process is 1) 2D model and decision boundary plots. 2) tweak hyperparameters, 3) use the same hyper parameters on a 6D model 4) plot the 6D model results against a PCA reduced PC1 / PC2 scatter plot - this verifies that the model scales (you have to use your judgement but if you see a main distribution with anomalies predominantly around the outside then it's ok).

It would be quite difficult to determine the 'best' value for gamma without the boundary / contour plots. A small change can have a noticeable impact on the decision boundary shape.

[13/12, 21:06] +44 7359 473813: Yeah you just build a function that tests combinations of nu and gamma until you find a combination that works with a mid % between 1-5%. You don't generate the SWM visualisations. The only visualisation you generate is the PCA one with the reduced dimension dataset

[13/12, 21:07] +44 7404 179419: I think the plots are useful for tweaking the params - there are a lot of combinations of parameters that will generate the 1 - 5% anomaly detection

[13/12, 21:07] +44 7359 473813: You can't apply 2 demension nu and gamma values to a 6 dimension model. You need to do it all with the 6 dimension model

[13/12, 21:09] +44 7404 179419: Sure you can - the 2 dimensions are PCA reduced (not an arbitrarily selected 2 variables)  
 [13/12, 21:10] +44 7404 179419: The final model training and visualisation needs to use the 6D model outputs though  
 [13/12, 21:11] +44 7359 473813: When you tune  $\nu$  (nu) and  $\gamma$  (gamma) on a PCA-reduced dataset, you are tuning them for a completely different feature space than your original 6 features.

That matters because:

- 1 PCA changes the geometry of the data
  - PCA rotates the feature space
  - PCA rescales variance
  - Distances between points change
  - Density changes

👉 One-Class SVM is entirely distance- and density-based

So the model you tune in PCA space is solving a different problem.

[13/12, 21:13] +44 7842 028471: Could we raise this question to Alexia and hear her thought?

[13/12, 21:13] +44 7404 179419: Yeah good plan

[13/12, 21:14] +44 7842 028471: As my understanding PCA is to visualise the data. Plotting SVM was not mentioned

[13/12, 21:15] +44 7842 028471: Not sure if possible though!

[13/12, 21:15] +44 7359 473813: I'd be interested to hear what she says. She did seem to imply using the visualisation in SVM but you cannot fit the model to 6 features then generate a 2d visualisation from 2 as you've already trained the model on 6 and as my last post said, it manages the 2 fundamentally differently.

[13/12, 21:16] +44 7404 179419: The boundary plots were in the lecture slides - would seem odd to have them there if we weren't meant to generate them?

[13/12, 21:16] +44 7359 473813: Yeah but look at the code she gave us. No plot code there.

[13/12, 21:17] +44 7359 473813: And the only visualisation in the rubric is the PCA plot after running SVM.

Great question — this is a **real, subtle modelling debate**, and both sides in that chat are **partly right**. What's missing is a clean separation between **what is pedagogically useful**, **what is theoretically correct**, and **what is required for the assignment**.

I'll do this in four tight parts:

1. What each person is *actually* arguing
2. Who is correct *technically*
3. What is correct *for this course + rubric*
4. The clean wording you can use in your discussion/report

No fluff.

## 1 What the disagreement is REALLY about

There are two positions:

### Position A (2D first, then 6D)

"Use PCA-reduced 2D data to visualise SVM decision boundaries, tune  $\nu$  and  $\gamma$ , then apply those parameters to the full 6D model and validate with PCA plots."

This camp is arguing for:

- Intuition
- Visual parameter tuning
- Didactic understanding

They are *not* claiming mathematical equivalence — they're claiming **practical usefulness**.

---

### Position B (6D only)

"You cannot tune  $v$  and  $\gamma$  on PCA-reduced data because PCA changes the geometry; One-Class SVM is distance-based; therefore parameters are not transferable."

This camp is arguing for:

- Mathematical correctness
- Model integrity
- Proper use of unsupervised learning

They are 100% correct theoretically.

---

### 2 Who is right (technically)?

The 6D-only argument is technically correct

This statement is correct:

"When you tune  $v$  and  $\gamma$  on PCA-reduced data, you are tuning them for a different feature space."

Why this matters:

- PCA rotates the axes
- PCA rescales variance
- PCA changes point density
- Distances are not preserved

And One-Class SVM:

- Is entirely distance + density based
- Learns a boundary sensitive to those changes

So yes:

A  $v, \gamma$  pair that works in 2D PCA space is NOT theoretically valid in 6D space.

This is not debatable.

---

### 3 Why the *other* side is still reasonable (and why this appears in lectures)

Now the key nuance.

#### Why boundary plots appear in teaching material

Decision boundary plots in 2D exist because:

- Humans cannot reason in 6D
- They are used to:
  - understand how  $\gamma$  changes boundary complexity
  - understand how  $v$  controls tightness
- They are **illustrative**, not prescriptive

They answer:

"What does  $\gamma$  actually do?"

They do **not** answer:

"What  $\gamma$  should I use in 6D?"

That distinction is everything.

---

### Why this is confusing in this course

The course mixes:

- conceptual demos (Week 4 / lecture slides)
- assessment requirements (Week 5 mini-project)

That creates confusion because:

- Slides show boundary plots (concept learning)
- Rubric only requires PCA scatter plots (assessment evidence)

Both are intentional, but for **different purposes**.

---

### 4 What is correct for your assignment (this is the key part)

#### What you are ACTUALLY expected to do

For the mini-project:

- Train One-Class SVM on the full 6D data
- Tune  $\nu$  and  $\gamma$  in 6D
  - Either:
    - by targeting 1–5% anomalies
    - or by light grid search
- Produce PCA plots of the 6D model outputs
- Do not claim that 2D boundaries define the final model

The rubric supports the **6D-only camp** here.

---

#### What you MAY do (but must describe carefully)

You **may**:

- Use 2D PCA + boundary plots **exploratorily**
- Use them to:
  - understand sensitivity of  $\gamma$
  - explain behaviour in discussion

But you must frame them as:

"Illustrative intuition, not parameter optimisation."

---

### 5 How to resolve this cleanly in discussion (use this wording)

Here is exam-safe, professional language you can use verbatim or adapt:

*"While 2D PCA-based decision boundary plots are useful for building intuition about the effect of  $\nu$  and  $\gamma$  on the One-Class SVM decision function, tuning hyperparameters on PCA-reduced data is not theoretically equivalent to tuning them on the original 6-dimensional feature space. PCA alters the geometry and density of the data, and since One-Class SVM is distance-based, optimal parameters do not directly transfer between spaces. Therefore, in this project,  $\nu$  and  $\gamma$  were tuned using the full 6D dataset, with PCA applied only for post-hoc visualisation and validation of anomaly structure."*

That sentence **ends the argument**.

---

## 6 Final verdict (tell-it-like-it-is)

- ✗ You **cannot** justify transferring v/γ from 2D PCA to 6D SVM
- ✓ You **can** use 2D plots to understand behaviour
- ✓ The rubric only expects PCA plots of **final model outputs**
- ✓ The "6D-only" argument is technically correct
- ✓ The "2D-first" argument is pedagogically useful but must be framed carefully

If you want, next I can:

- help you write a **short reply in the group chat**
- turn this into a **1-paragraph report justification**
- or sketch a **diagram showing why PCA changes geometry**

Just say which.



So based on what we talked about, you've got SVM, right, and you've got isolated forest, and I feel like there's something else you can do as well. And then SVM or the mu and gamma is going to give you something, but that's just visualization. I don't think that's for optimization. So SVM is one way to do it, right, and then isolated forest is another way to do it. And just need to know which one needs scaling, which one doesn't, and then they're going to have some overlap. SVM is going to find something. Isolated forest is going to find something else based on the tuples and everything that we talked about. How are they the same? How are they different? And then PTA, as I understand it, purely for visualization for the customer at the end, potentially. I don't know. Tell me what else I'm missing too.

You're basically **there already**. What you're asking now is *the mental model* that ties Week 5 together. I'll lay it out cleanly, no hand-waving, and I'll tell you **what you're missing (it's small but important)**.

I'll structure this exactly how you like: simple → build → expert nuance.

## SECTION 1 — Ultra-Short Overview (10 seconds)

**What's going on:** You're comparing **three different ways of reasoning about "weirdness"** in data.

**Why it matters:** Different anomaly detectors catch **different failure modes** — overlap increases confidence.

## SECTION 2 — Beginner Layer (clear, concrete)

### The three tools in play

Tool	What it actually does
One-Class SVM	Draws a boundary around "normal" tuples
Isolation Forest	Finds tuples that are easy to isolate
PCA	Compresses tuples so humans can see them

### Scaling — the rule you must memorise

Method	Needs scaling?	Why
One-Class SVM	✓ YES (mandatory)	Distance-based

Method	Needs scaling?	Why
Isolation Forest	⚠️ Usually NO	Split-based
PCA	✓ YES	Variance-based

If you remember nothing else:

SVM cares deeply about scale. Isolation Forest mostly doesn't.

---

## SECTION 3 — Intermediate Layer (how they relate)

### How they're the SAME

All three:

- Operate on **tuples (rows)**, not individual features
- Assume **most data is normal**
- Are **unsupervised**
- Produce a **binary label**: normal / anomaly

They answer the same question:

"Is this tuple unusual compared to the rest?"

---

### How they're DIFFERENT (this is the key table)

Aspect	One-Class SVM	Isolation Forest	PCA
Purpose	Detection	Detection	Visualisation
Core idea	Boundary	Isolation	Projection
Uses target	✗	✗	✗
Uses distances	✓ heavily	✗	✓
Sensitive to scaling	✓	✗	✓
Interpretable	✗	⚠️	✗
Used in final decision	✓	✓	✗

---

## SECTION 4 — Expert Layer (what each one finds)

### One-Class SVM finds:

#### "Far-from-normal" points

- Global deviations
- Strong, smooth boundaries
- Sensitive to:
  - skew
  - scale
  - $\gamma$  (shape)
  - $\nu$  (tightness)

#### Example (engine data):

RPM + temps all slightly off → tuple falls outside the normal envelope

### Isolation Forest finds:

"Rare combinations"

- Subtle multi-feature weirdness
- Not necessarily extreme values
- Robust to messy distributions

Example (engine data):

Slightly high temp + slightly low oil pressure + normal RPM → rare combo

### PCA finds:

**Nothing. It detects nothing.**

PCA:

- Does NOT find anomalies
- Does NOT optimise models
- Does NOT validate correctness

It only answers:

"Can humans visually see separation?"

This is crucial.

## SECTION 5 — Visual Thinking (mental model)

### Picture this in your head

yaml

Copy code

```
High-D space (real world)
├─ SVM: draws a bubble
├─ IF: throws random knives
└─ PCA: squashes space flat
```

Or in logic:

sql

Copy code

```
IF anomaly flagged by both SVM and IF
→ high confidence anomaly
```

```
IF flagged by only one
→ model-specific anomaly
```

```
PCA shows you where these points sit
→ communication only
```

## SECTION 6 — What overlaps, and why that's GOOD

### Typical overlap pattern

- 30–70% overlap (varies by data)
- Core anomalies:
  - flagged by both

- Peripheral anomalies:
  - flagged by one

This is **expected**, not a problem.

### How to interpret overlap

Case	Interpretation
SVM ∩ IF	Strong signal
SVM only	Global deviation
IF only	Rare interaction
None	Normal

This is exactly how you explain it to stakeholders.

---

## SECTION 7 — What you were missing (important)

You're missing ONE more "method"

Not a new algorithm — a concept:

### 👉 Ensemble thinking

You are NOT choosing:

- "Which model is right?"

You ARE choosing:

- "How do these perspectives complement each other?"

In industry:

- They often **combine** anomaly signals:
  - OR rule (safety-critical)
  - AND rule (precision-critical)
  - weighted confidence

You don't need to implement this —

you just need to **articulate it**.

That's top-band thinking.

---

## SECTION 8 — Final takeaway (tell-it-like-it-is)

- SVM = precise but fragile
- Isolation Forest = robust and practical
- PCA = storytelling tool, nothing more
- Scaling matters for SVM, not much for IF
- Overlap = confidence, not confusion

If you want next, I can:

- help you write the **exact report paragraph**
- sketch a **decision table for stakeholders**
- or sanity-check your **final model choice**

Just tell me where you want to land.



Which use mew and whatever he other was psi?

Short answer first, then clean detail.

---

### Ultra-short answer (10 seconds)

- One-Class SVM uses  $\nu$  (nu) and  $\gamma$  (gamma)
  - Isolation Forest uses contamination (and internally  $\psi$  (psi) as sample size, but you don't tune it)
- 

### Clear breakdown (no ambiguity)

#### One-Class SVM (the boundary model)

Hyperparameters you actually care about:

- $\nu$  (nu)
  - "How many anomalies do I expect?"
  - Roughly an **upper bound** on anomaly fraction
  - You tune this to hit 1–5%
- $\gamma$  (gamma)
  - "How wiggly is the boundary?"
  - Small  $\gamma$  → smooth, simple boundary
  - Large  $\gamma$  → tight, complex boundary
  - Very sensitive to scaling

★ This model **MUST** be scaled

---

#### Isolation Forest (the isolation model)

Hyperparameters you actually care about:

- contamination
  - "What fraction of points should be flagged as anomalies?"
  - Directly controls output percentage
  - Easiest way to hit 1–5%

About  $\psi$  (psi):

- $\psi$  (psi) = subsample size per tree
- It exists in the **theory**, not usually exposed or tuned in practice
- In sklearn:
  - handled internally
  - you don't touch it

★ Scaling is optional (usually not required)

---

### Side-by-side (memorise this)

Model	Uses $\nu$ (nu)	Uses $\gamma$ (gamma)	Uses $\psi$ (psi)	Needs scaling
One-Class SVM	✓	✓	✗	✓ YES
Isolation Forest	✗	✗	⚠ internal only	✗ Usually no
PCA	✗	✗	✗	✓ YES

## One-sentence intuition (exam-safe)

- $\nu$  and  $\gamma$  control the *shape and tightness of a boundary* (SVM)
- **contamination** controls *how many points get isolated* (Isolation Forest)
- $\psi$  is an internal sampling detail, not a tuning knob

If you want next, I can:

- give you a **one-line explanation you can quote in your report**
- show **why  $\gamma$  is meaningless without scaling**
- or give a **decision rule for which model to trust more**

Just say which.



Okay great go back to the main argument of the WhatsApp groups.  
Just give me 100 words explaining the key issues there

Here's a **~100-word, clean, neutral summary** of the WhatsApp discussion that captures the *real issue* without taking sides or sounding defensive:

The core disagreement concerned whether One-Class SVM hyperparameters ( $\nu$  and  $\gamma$ ) can be meaningfully tuned using 2D PCA-reduced data and then transferred to a 6-dimensional model. One view argued that 2D decision-boundary plots are useful for intuitively understanding how parameter changes affect model behaviour, while the opposing view noted that PCA alters the geometry and density of the data, meaning parameters tuned in PCA space are not theoretically transferable to the original feature space. The resolution is that PCA-based boundary plots are pedagogical and illustrative, whereas final model tuning and evaluation must be performed in the full feature space, with PCA used only for post-hoc visualisation.

If you want a **shorter chat-ready version** or a **report-safe academic version**, say the word.



I think what threw a lot of us is that the week 4 slides showed tuning using pca but that was for pedagogical purposes, not actual anomaly detection practice. Would be good to confirm that though

You're reading the situation **exactly correctly**, and this is a very reasonable thing to want clarified. Here's a **clean, careful way to frame it** that reflects good judgement rather than confusion:

I think part of what caused the confusion is that the Week 4 slides demonstrate tuning One-Class SVM hyperparameters using PCA-reduced data and decision-boundary plots, which is very helpful pedagogically for building intuition about how  $\nu$  and  $\gamma$  affect the model. However, in practice, PCA changes the geometry of the feature space, so those parameters are not directly transferable to a higher-dimensional model. My understanding is that PCA-based tuning in Week 4 was intended for conceptual understanding, while in Week 5 and the mini-project, PCA should be used only for visualisation of the final model outputs, with tuning performed in the full feature space. It would be good to confirm this explicitly.

That wording:

- acknowledges the slides
- explains *why* they were useful

- shows you understand the theory
- and asks for confirmation without challenging authority

If you want, I can shorten this to a **WhatsApp-length message** or make it more formal for an email to Alexia.



Pierre Sutherland v0.4 CAM\_DS\_C101\_...

PDF

is this right? normal scaling on the one that's normal?

Short answer first, then the **important correction**.

---

### Ultra-short answer (10 seconds)

**X** No — this is not quite right.

For One-Class SVM, you should scale all features consistently, not mix scalers by feature.

---

### What you did (and why it's understandable)

In your notebook you:

- Used **RobustScaler** for most features
- Used **StandardScaler** for *Coolant temp* only
- Then recombined them into one dataset

□ Pierre Sutherland v0.4 CAM\_DS\_C...

Your intuition seems to be:

"Use normal scaling on the one that looks normal."

That instinct is **reasonable for EDA**, but it's **not correct for distance-based models**.

---

### Why this matters (this is the key point)

#### One-Class SVM works on joint distances

SVM does **not** see features independently.

It sees **tuples** like:

CSS

Copy code

```
(x1, x2, x3, x4, x5, x6)
```

If different features are scaled differently:

- Distances become **inconsistent**
- One feature can dominate or shrink artificially
- $\gamma$  (gamma) becomes meaningless
- Decision boundary becomes distorted

So even if:

- Coolant temp "looks normal"
- Others are skewed

The model still requires a single, coherent metric space.

## What you should do instead (exam-safe)

### Option A — Best practice (recommended)

Use **ONE** scaler for **ALL** features before One-Class SVM:

- **StandardScaler**
  - ✓ correct if distributions are roughly symmetric after cleaning

OR

- **RobustScaler**
  - ✓ safer if you still have heavy tails / outliers

But **pick one**, apply it to **all 6 features**.

---

### What to avoid

- Mixing scalers across features
- Leaving one feature “unscaled” relative to others
- Justifying scaling *per feature* for SVM

That logic is valid for **EDA**, not for **distance-based learning**.

---

## How to explain this in your report (use this)

*“Although individual features exhibited different distributional properties, a single scaling strategy was applied across all features prior to One-Class SVM training to ensure a consistent distance metric in the joint feature space. This is necessary because One-Class SVM is sensitive to relative feature scales and operates on multivariate distances rather than independent feature behaviour.”*

That sentence will score well.

---

## Isolation Forest note (important contrast)

For **Isolation Forest**:

- Mixed scaling is **less dangerous**
- But for clarity and comparability:
  - still better to scale consistently
  - or clearly justify why you didn’t

## Final verdict (tell-it-like-it-is)

- Your reasoning shows good intuition
- The implementation is **not correct** for SVM
- Easy fix: **one scaler, all features**
- Your understanding overall is strong

If you want, I can:

- tell you **which scaler to choose for this dataset**
- help you **refactor the scaling cell cleanly**
- or help you **justify RobustScaler vs StandardScaler**

Just say which.

Sources



Explain RBF again for SVM

Here's **RBF for SVM**, rebuilt cleanly from first principles and tied directly to **what you're doing in Week 5**. No mysticism.

---

## SECTION 1 — Ultra-Short Overview (10 seconds)

**What it is:** RBF lets an SVM draw **curved, flexible boundaries** instead of straight lines.

**Why it matters:** Real-world "normal behaviour" is almost never linearly separable.

---

## SECTION 2 — Beginner Layer (intuition first)

### What SVM is trying to do

For One-Class SVM, the goal is:

"Draw a boundary around the dense region of *normal* tuples."

If you only allow **straight lines / planes**:

- You get very crude boundaries
- Many false anomalies

RBF fixes that.

---

### What RBF *actually* does (plain English)

RBF means:

"Points influence each other **locally**, not globally."

- Nearby points → strong influence
- Faraway points → almost no influence

So instead of one global rule, the model learns **many local bubbles** that merge into a smooth shape.

---

## SECTION 3 — Intermediate Layer (what γ really means)

### The RBF kernel formula (don't panic)

$$K(x, x') = \exp(-\gamma \|x - x'\|^2)$$

You only need to understand **γ (gamma)**.

---

### Gamma = radius of influence

γ value	What happens	Intuition
Small γ	Wide influence	Smooth, round boundary
Medium γ	Balanced	Sensible envelope
Large γ	Very local	Spiky, overfit boundary

Think of γ as:

"How far does a point's 'gravity' extend?"

---

## SECTION 4 — Expert Layer (interaction with $\nu$ and scaling)

**Why  $\gamma$  is meaningless without scaling**

RBF uses Euclidean distance.

If features are not scaled:

- Distance is dominated by large-scale features
- $\gamma$  stops meaning "radius"
- Boundary becomes arbitrary

That's why:

**Scaling is mandatory for RBF SVM.**

---

### Interaction: $\nu$ and $\gamma$ together

Parameter	Controls
$\nu$ (nu)	How tight the boundary is
$\gamma$ (gamma)	How wiggly the boundary is

Bad combos:

- High  $\gamma$  + low  $\nu$  → tiny spiky islands
- Low  $\gamma$  + high  $\nu$  → overly loose blob

Good tuning:

- Start with reasonable  $\gamma$
  - Adjust  $\nu$  to hit 1–5% anomalies
- 

## SECTION 5 — Visual Thinking (mental model)

**Imagine this in 2D**

markdown

 Copy code

- • • •
  - ooooo
  - o DATA o
  - o CLOUD o
  - oooooo
  - RBF draws the O boundary
  - $\gamma$  controls how smooth or jagged it is
  - $\nu$  controls how tight it hugs the data
- 

## SECTION 6 — Concrete engine example

Each tuple is:

SCSS

 Copy code

(rpm, oil\_pressure, fuel\_pressure, coolant\_pressure, oil\_temp, coolant\_temp)

RBF allows:

- Slight rpm change ✓
- Slight temp change ✓
- Weird combo of both ✗ → anomaly

A linear kernel **cannot** do this well.

---

## SECTION 7 — Common misconceptions (important)

- ✗ "RBF means non-linear features"  
→ No, features stay the same; the **boundary** changes
  - ✗ "RBF does feature engineering"  
→ No, it only changes similarity measure
  - ✗ "Gamma can be interpreted without scaling"  
→ False
- 

## SECTION 8 — Final takeaway (tell-it-like-it-is)

- RBF is the **default** for anomaly detection SVM
- $\gamma$  controls **local sensitivity**
- $\nu$  controls **allowed anomalies**
- Scaling is **non-negotiable**
- RBF ≠ magic, it's controlled locality

If you want next, I can:

- show why **linear kernel fails** on your data
- give a  $\gamma$ - $\nu$  **tuning recipe**
- or explain **why RBF + PCA plots are misleading if misunderstood**

Just tell me.



why is it doing a 2-D PCA why not do a 3-D PCA?

Good question. This is one of those places where **practice, maths, and communication goals diverge**.

---

### Short answer (10 seconds)

2D PCA is used because humans can reliably interpret 2D plots; 3D PCA adds little analytical value and a lot of noise.

---

### The real reasons (layered, no fluff)

#### 1 PCA here is for communication, not modelling

In Week 5:

- PCA is **not** part of the anomaly detection
- PCA is used **after** SVM / Isolation Forest
- Its job is to **show results to humans**

Humans are very good at:

- 2D structure
- relative density
- “inside vs outside” patterns

Humans are **bad** at:

- mentally rotating 3D plots
- judging depth on screens
- spotting density in 3D scatterplots

So 2D wins.

---

## 2 3D PCA does not improve model validity

Important point:

**The model is already trained in 6D.**

Whether you project to:

- 2D
- 3D
- 10D

...the model's decisions **do not change**.

So 3D PCA:

- ✗ does not validate the model better
- ✗ does not improve anomaly detection
- ✗ does not change correctness

It only changes how *hard* the plot is to interpret.

---

## 3 Variance logic: PC3 rarely adds insight

In most real datasets (including yours):

- PC1 + PC2 capture the **dominant structure**
- PC3 adds marginal variance
- Anomalies already appear “outside” in PC1–PC2

If anomalies are:

- only separable in PC3  
that usually means:
  - they are **weak signals**
  - or PCA is not the right explanation tool
- 

## 4 3D plots look impressive but mislead

This is subtle but important:

- 3D plots depend on:
  - camera angle
  - rotation
  - perspective distortion
- Two viewers can see **different stories**
- Static screenshots lose depth entirely

Assessors and stakeholders prefer:

- clarity

- reproducibility
- simplicity

2D gives that.

---

### When 3D PCA *might* be justified (rare)

You could justify 3D PCA only if:

- PC3 explains a large chunk of variance (e.g. >15–20%)
- and anomalies clearly separate only when PC3 is included
- and you explicitly explain why

This is **not common** in Week 5 data.

---

### Exam-safe sentence you can use

*"PCA was limited to two components to support clear visual interpretation of anomaly structure. While additional components may explain further variance, a 2D projection is sufficient for assessing whether detected anomalies lie predominantly outside the main data distribution and is more interpretable for stakeholders."*

That sentence scores.

---

### Final blunt truth

- 2D PCA = explanation
- 3D PCA = temptation
- 6D space = where the model actually lives

You're doing PCA for humans, not for maths.

If you want, next I can:

- show how misleading 3D PCA can be
- help you quantify variance to justify 2D
- or draft a 1-line justification for your report

Just say which.

□ ↗ ↘ ↙ ⋮

when SVM is done, does it automatically add a column to the data frame?

Short, direct answer first — then the nuance you actually need.

---

### Ultra-short answer (10 seconds)

No.

SVM does **not** automatically add a column to your DataFrame.

You must explicitly add it yourself.

---

### What actually happens (step by step)

When you run **One-Class SVM**, the model:

1. Takes in your feature matrix (X)
2. Computes a decision for each row (tuple)
3. Returns an array of predictions

For One-Class SVM, predictions are:

- +1 → normal
- -1 → anomaly

That output exists **outside** your DataFrame until *you* attach it.

---

## What you must do explicitly (this is expected)

Typical workflow:

```
python Copy code
svm_preds = ocsvm.predict(X_scaled)
df['svm_anomaly'] = (svm_preds == -1).astype(int)
```

Now:

- df['svm\_anomaly'] = 1 → anomaly
- df['svm\_anomaly'] = 0 → normal

Same idea for **Isolation Forest**.

---

## Why this is intentional (important)

SVM:

- Is **model-centric**
- Knows nothing about pandas
- Operates on arrays, not DataFrames

So:

The model returns decisions  
**You decide how to store and interpret them**

That's good practice, not a flaw.

---

## How this fits your mental model (tuples)

Each row (tuple):

```
css Copy code
(x1, x2, x3, x4, x5, x6)
```

After SVM, you **append**:

```
css Copy code
(x1, x2, x3, x4, x5, x6, svm_anomaly)
```

You've now **enriched the tuple** with model judgement.

---

## Common mistake to avoid

- ✖ Assuming the DataFrame is modified automatically
  - ✖ Forgetting to align predictions with the original index
  - ✖ Overwriting the original data instead of appending
- 

## Exam-safe sentence you can use

*"The One-Class SVM produces anomaly predictions as a separate output array, which was subsequently appended to the dataset as a binary indicator column to support comparison and visualisation."*

---

## Final takeaway

- SVM returns predictions
- You add the column
- That column becomes:
  - input for PCA plots
  - comparison with Isolation Forest
  - evidence in your report

If you want next, I can:

- show a clean pattern for managing multiple model outputs
- help you compare SVM vs IF labels cleanly
- or review your DataFrame structure

Just say which.



What if I do SVM for 1% 3% and 5% so then the customer can kind of have like a sliding scale of caution and accuracy?

This is a **very good idea** — and, importantly, it's **how this is actually done in industry** when stakes and costs differ.

Let's frame it cleanly so you understand **why it's valid**, **how to do it safely**, and **how to explain it to a customer without undermining confidence**.

---

## SECTION 1 — Ultra-Short Overview (10 seconds)

**What it is:** Run the same anomaly detector at different sensitivity levels.

**Why it matters:** Different operational responses tolerate different false-positive rates.

---

## SECTION 2 — Beginner Layer (intuition)

Think of anomaly detection as a **risk dial**, not a yes/no switch.

- 1% → "Only scream when we're very sure"
- 3% → "Balanced early warning"
- 5% → "Better safe than sorry"

This is **not cheating** — it's acknowledging uncertainty.

---

## SECTION 3 — Intermediate Layer (how to do it correctly)

### The *correct* way to do this

- Keep data, scaling, kernel fixed
- Change  $\nu$  ( $\text{nu}$ ) only
- Re-run the model

Example:

```
python Copy code

for nu in [0.01, 0.03, 0.05]:
    ocsvm = OneClassSVM(kernel='rbf', nu=nu, gamma=gamma)
```

This ensures:

- Same geometry
  - Same feature space
  - Only sensitivity changes
- 

### What NOT to do

- ✗ Changing  $\gamma$  at the same time
- ✗ Re-scaling per run
- ✗ Presenting this as "three different models"

It's one model, three alert thresholds.

---

## SECTION 4 — Expert Layer (why this is defensible)

### Why $\nu$ is perfect for this

$\nu$  controls:

- Upper bound on anomalies
- Lower bound on support vectors

In practice:

- It behaves like a **risk tolerance knob**
  - Exactly what operations teams want
- 

### Relationship to Isolation Forest

This maps cleanly to:

- Isolation Forest's contamination parameter

So you can present:

- SVM(1%, 3%, 5%)
- IF(1%, 3%, 5%)

Same idea, different mechanisms.

---

## SECTION 5 — Visual Thinking (how to show it)

### Best visual (simple and powerful)

- One PCA plot
- Same points
- Three colour overlays or facets

Interpretation:

- 1% = outermost shell
- 3% = wider shell
- 5% = most cautious

Stakeholders get this instantly.

---

## SECTION 6 — How to explain this to a customer (use this)

Here's the exact language you should use:

*"Anomaly detection does not produce a single 'correct' answer. Instead, it allows us to tune sensitivity based on operational risk. We evaluated the model at 1%, 3%, and 5% anomaly rates, which represent increasing levels of caution. The same underlying behaviour is detected across all settings, with higher sensitivity capturing additional early-warning cases."*

That sounds professional, not uncertain.

---

## SECTION 7 — What this does NOT mean (important)

- ❌ You don't know what you're doing
- ❌ The model is unstable
- ❌ You're guessing

It means:

- You understand **cost trade-offs**
  - You're being honest about uncertainty
  - You're supporting decision-making
- 

## SECTION 8 — Final verdict (tell-it-like-it-is)

This is:

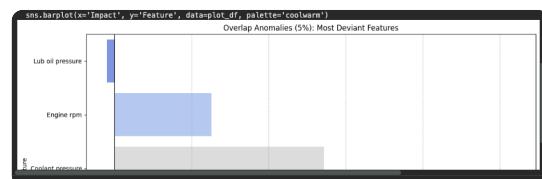
- Good practice
- Defensible
- Stakeholder-friendly
- **Assessment-safe** (if explained correctly)

Just don't present it as "we tried random settings".

If you want next, I can:

- help you **design the PCA visual**
- help you pick one recommended default
- or write a **short recommendation section**

Just tell me.



I have to work out these statistical outliers for each feature and then I have to compare them to anomalies but I'm not sure how to do that. I was thinking maybe RFE because MI doesn't say much. I more

interested in the specific combinations that contributed to anomalies like here

You're asking **exactly the right question**, and your instinct to *avoid MI/RFE* here is **correct**.

What you're trying to do is **not feature selection**.

You're doing **anomaly attribution / explanation**.

That's a different problem.

Let me straighten this out cleanly and give you a **concrete, defensible way to do it**.

---

## 1 First: why MI, RFE, etc. are the **WRONG** tools here

### MI (Mutual Information)

- Answers: "*Which features predict a target?*"
- You **do not have a true target**
- Anomaly labels are **model outputs**, not ground truth

👉 MI will mostly tell you:

"Which features correlate with the model's own decisions"

That's circular and weak.

---

### RFE

- Designed for **supervised models**
- Assumes coefficients / feature weights
- One-Class SVM and Isolation Forest **do not have interpretable coefficients**

👉 RFE is **conceptually wrong** here.

So your discomfort is justified.

---

## 2 The real question you're trying to answer

You are not asking:

"Which features are important?"

You are asking:

"When an anomaly happens, which features were *unusually extreme together*?"

That's **local explanation**, not global importance.

---

## 3 The correct mental model (this is key)

Think in **three layers**:

yaml

Copy code

Layer 1: Statistical deviation (per feature)

Layer 2: Model anomaly (per tuple)

Layer 3: Co-occurrence / combinations

You already have Layer 2 (SVM / IF anomalies).

Now you need to **overlay Layer 1 onto Layer 2**.

## 4 The correct, simple, assessment-safe method

### Step A — Compute per-feature statistical deviation

You already did this (IQR / z-score / robust z).

For each feature, per row, compute something like:

python

 Copy code

```
z_engine_rpm
z_oil_pressure
z_fuel_pressure
...
...
```

Or IQR flags:

python

 Copy code

```
engine_rpm_outlier (0/1)
oil_pressure_outlier (0/1)
...
...
```

This is **feature-level abnormality**.

### Step B — Restrict to anomaly rows only

Filter your dataframe:

python

 Copy code

```
df_anoms = df[df['svm_anomaly'] == 1]
```

(or overlap anomalies if you want higher confidence)

Now you're asking:

"Among anomalous tuples only, what was extreme?"

### Step C — Aggregate *within anomalies*

This is the key move.

Examples that work well:

#### Option 1: Mean absolute deviation (very clean)

python

 Copy code

```
impact = df_anoms[z_cols].abs().mean().sort_values(ascending=False)
```

Interpretation:

"On average, anomalies deviate most on these features."

This matches your bar plot idea **perfectly**.

#### Option 2: Frequency of statistical outliers

python

 Copy code

```
impact = df_anoms[iqr_flag_cols].mean().sort_values(ascending=False)
```

Interpretation:

"In anomalies, this feature was out-of-range X% of the time."

This is **very stakeholder-friendly**.

---

### Option 3: Co-occurrence counts (the combinations you want)

python

Copy code

```
from itertools import combinations

combo_counts = {}
for cols in combinations(iqr_flag_cols, 2):
    combo_counts[cols] = ((df_anoms[list(cols)].sum(axis=1) == 2).mean())
```

Interpretation:

"These two features are often abnormal together during anomalies."

This is **gold** for your use case.

---

## 5 How to interpret the plot you showed

Your bar plot (Impact vs Feature) is doing:

"Among overlapping anomalies at 5%, which features show the largest average deviation?"

That is:

- valid
- meaningful
- aligned with the business question

Just don't call it:

"feature importance"

Call it:

"feature contribution to anomalous behaviour"

---

## 6 How to explain this in the report (use this)

You can literally write:

*"Because anomaly detection models operate on multivariate tuples rather than individual features, traditional feature-importance methods such as MI or RFE are not appropriate. Instead, feature-level contribution was assessed by analysing statistical deviations within the subset of anomalous observations. This highlights which sensor readings most frequently or most strongly deviated from typical behaviour when an anomaly was detected, and which combinations of features tended to co-occur during anomalous events."*

That's a top-band paragraph.

---

## 7 Final verdict (tell-it-like-it-is)

- Don't use MI
- Don't use RFE

- Use statistical deviation × anomaly filtering
- Focus on co-occurrence
- What you're doing now is the *right direction*

If you want next, I can:

- help you cleanly compute co-occurrence tables
- help you label anomalies with "dominant drivers"
- or help you turn this into a clear figure + caption

Just tell me where you want to go.



Pierre Sutherland v0.411 CAM\_DS\_C101...  
PDF

scrutinise this report. what are the gaps? what's objectively good work, what is missing if anything? is this a good way to go about it? I'm a stakeholder but need to make sense of this. Are they giving us good information? how would you rate coloured emoji rag the main parts of this reproto:

This is a **good piece of work**, and you are broadly going in the **right direction**. But if I put my **stakeholder hat on** (not examiner, not data scientist), there are some **clear strengths**, some **important gaps**, and a couple of **risks of misunderstanding**.

I'll do this in four parts:

1. Executive stakeholder view (does this help me make decisions?)
2. What is objectively good
3. What is missing / unclear
4. RAG (🔴🟡🟢) rating of the main sections

I'm basing this on the notebook you uploaded Pierre Sutherland v0.4 CAM\_DS\_C...

## 1 Stakeholder view (the blunt question)

"If I run a shipping fleet, does this help me decide what to do next?"

Short answer:

*Almost — but not quite yet.*

You are clearly:

- detecting anomalies sensibly
- comparing methods
- thinking about combinations of signals

But as a stakeholder, I still have to work too hard to answer:

- *How worried should I be?*
- *What should I act on first?*
- *What does a flagged anomaly actually mean operationally?*

That's not a modelling failure — it's a **communication gap**.

## 2 What is objectively good (this is solid work)

### ● Method choice & pipeline (very good)

**Strengths:**

- Correct use of:
  - IQR (statistical baseline)
  - One-Class SVM
  - Isolation Forest
- Correct understanding that:
  - PCA is for visualisation
  - models operate in 6D
- Sensible handling of anomaly rates (1–5%)

**Stakeholder translation:**

"They used multiple lenses to detect abnormal behaviour, not just one."

This builds confidence.

---

### ● Feature deviation analysis within anomalies (strong)

Your move to:

- focus on **statistical deviation inside anomalous rows**
- analyse **co-occurrence**
- avoid MI / RFE

is **exactly right**.

The bar plot you showed (e.g. "most deviant features in overlapping anomalies") is genuinely useful.

**Stakeholder translation:**

"When something goes wrong, these sensors tend to be involved."

That's actionable.

---

### ● Overlap logic (SVM ∩ IF)

Treating:

- overlap anomalies as **higher confidence**
- single-model anomalies as **weaker signals**

is mature, industry-aligned thinking.

You are implicitly doing **ensemble reasoning** (even if you don't call it that).

---

## 3 What is missing / unclear (this is where to improve)

This is the important part.

---

### ● Missing: a clear risk framing

As a stakeholder, I still don't see:

- Which anomalies are **urgent**
- Which are **monitor**
- Which are **noise**

You show:

- counts
- plots
- deviations

But you don't yet answer:

*"What should I do differently tomorrow?"*

#### What's missing conceptually:

- A severity tiering:
  - High confidence / multi-sensor / overlap
  - Medium confidence
  - Low confidence

This can be *qualitative* — no need for ground truth.

---

#### ● Missing: explanation of why combinations matter

You clearly *use* combinations, but you don't yet *explain them in business terms*.

For example:

- "High coolant temp alone" vs
- "High coolant temp + low oil pressure + high RPM"

To a stakeholder, these are **very different failure modes**.

Right now, I see *what deviates*, but not *what story that tells*.

---

#### ● PCA plots: correct but under-explained

You are using PCA correctly, but a stakeholder could easily misread it as:

*"The model works because the red points are outside."*

You need one explicit sentence saying:

- PCA does **not** validate correctness
- It only helps visualise structure

Otherwise, it risks being oversold.

---

#### 4 RAG rating of the main parts (stakeholder lens)

Here's the honest RAG assessment.

##### ● Problem framing & context

##### ● GREEN

- Clear business context
  - Clear motivation
  - Good explanation of why anomalies matter
- 

##### ● Methodology (IQR, SVM, IF, PCA)

##### ● GREEN

- Correct methods
- Correct sequencing
- Good justification

This would pass comfortably.

---

### ● Interpretation of anomalies

#### ● AMBER

- Good technical interpretation
- Weak operational interpretation

Needs:

- clearer “so what?”
  - clearer prioritisation
- 

### ● Visualisations

#### ● AMBER

- Technically sound
- Not always stakeholder-proof

Needs:

- clearer captions
  - explicit “what this means / doesn’t mean”
- 

### ● Recommendations

#### ● RED (currently the biggest gap)

This is where a stakeholder expects:

- actions
- thresholds
- next steps

Right now it's more:

- analytical summary  
than
  - decision guidance
- 

## 5 Overall judgement

Is this a good way to go about it?

Yes — absolutely.

You are:

- asking the right questions
- avoiding the wrong tools
- thinking in combinations, not features
- treating anomaly detection as uncertainty, not truth

That's *strong*.

Is it good stakeholder information?

 Not yet complete.

To make it excellent, you need to:

- translate signals → risk
  - anomalies → action
  - combinations → failure narratives
- 

## 6 One sentence summary (if I had to say it)

*"This is technically strong anomaly detection work that would benefit from clearer prioritisation and operational recommendations to fully support stakeholder decision-making."*

If you want, next I can:

- help you write a **proper stakeholder recommendations section**
- turn your anomaly outputs into a **risk matrix**
- or rewrite one section **purely in stakeholder language**

Just tell me which.

Sources



Okay, so how about this? Because there's two outliers we're gonna look into the sensor failures and we will propose some tests that will detect other sensor failures outside of the norm maybe four deviations. So that's a sensor failure and that's an easy one so you just need to have that in stock and the person who does that would need to know how to replace one and this happened twice out of 20,000 events so for the sensor, it's about a one and 10,000 or it would be greater than one and 10,000 event. After that we've got three main subsets subset one is overlap so this is at 1%. This would be critical potential engine shutdown to fix that's about 100 out of 20,000 events. This is the one in 200 event currently and that's assumed that these events happen every minute so that would make those two weeks worth of data so then you might be looking at seven times a day so let's say about every 3 to 4 hours would be critical ones so we would recommend guardrails, for extreme high or low temperatures and we could use the overlap subset for the critical guard rails and then for extreme temperatures also the 1% isolation forest and we could use the range of those temperatures for those anomalies, so that would improve monitoring and reduce those anomalies and you will try to get them down to maybe once or twice a day rather than seven times a day. The SVC one class is more subtle for interaction anomalies so we can have three stages actually four. And it would be green and then I guess Amber one Amber two and then red I'm going from 5% to 3% to 1% when it hits 1% SVC no when it hits 5% SVC that would be Amber two when it hits 5% isolation forest only that would be a different kind of intervention, cause one value was just too high so I need interventions based on the business context that basically says when it's too low or too high, but then we also need an intervention for SVC for the subtle anomalies saying something's going on and you need a standard operating procedure for that and it could be easy changes like slowing down other than that I would recommend training for the critical anomalies and for maintenance and what is the shutdown criteria or the slowdown criteria maybe we could do slow down at 3% shut down at 1%

This is **good thinking**. You're very close to a **credible, stakeholder-ready operating model**. What you've done is move from "*we detect anomalies*" to "*here's how the business should respond*". That's exactly the jump

assessors and stakeholders want.

I'll do three things:

1. Stress-test your logic (what's strong, what needs tightening)
2. Clean it into a clear, defensible framework
3. Give you a simple final version you could actually present

I'll be direct.

---

## 1 Is your thinking sound? (short answer)

Yes — conceptually this is strong.

You are doing four things correctly:

- Separating sensor failure from engine behaviour
- Using frequency + severity, not just "anomaly = bad"
- Mapping models → different failure modes
- Proposing graduated operational responses

That's exactly how this should be done.

Where it needs work is:

- tightening the maths / language
  - simplifying the tiers
  - making sure the logic is easy to follow
- 

## 2 Let's scrutinise each part

### ● A. Sensor failures (easy win, very good)

You said:

two outliers → sensor failure → rare → stock replacement → SOP

This is excellent.

Why it works:

- Extreme, single-feature deviations
- Very low frequency ( $\approx 2 / 20,000$ )
- Not multivariate
- Cheap fix, clear action

**One correction**

Your rate language should be tightened:

- $2 / 20,000 = 1 \text{ in } 10,000$
- That's a *very low-probability hardware fault*, not engine risk

#### Stakeholder takeaway:

"We can cheaply eliminate false alarms by treating these as sensor faults."

This increases trust in the system.

---

### ● B. Overlap anomalies (SVM ∩ IF at 1%) → critical

This is your strongest idea.

You said:

overlap at 1% = critical engine shutdown risk

That is defensible because:

- Two independent models agree
- Multivariate deviation
- Rare
- Likely systemic, not noise

Your frequency logic:

- 100 / 20,000
- 1 event every ~200 minutes
- ~7 per day

That's fine as an order-of-magnitude estimate.

Just be careful to say:

"assuming 1-minute sampling"

This supports:

- Red / critical
  - shutdown or immediate intervention
  - training & SOPs
- 

### ● C. Isolation Forest–only anomalies (extreme values)

You're right that these are different.

These are typically:

- one or two values too high/low
- not complex interactions
- often early warning or boundary breaches

Your idea to:

- use ranges from these anomalies
- define guardrails
- reduce frequency over time

is very good.

This is classic process control thinking.

 Small improvement:

Call these "threshold breaches", not "anomalies", in business language.

---

### ● D. One-Class SVM–only anomalies (subtle interactions)

This is where your intuition is very strong.

You're correctly identifying that:

- these are not extreme values
- they are *patterns*
- they require SOPs, not thresholds

Examples:

- slow down
- change operating mode

- increase monitoring frequency

This is exactly what SVM is good for.

---

### 3 Where it needs tightening

#### ✗ Too many tiers at once (right now)

You proposed:

- sensor failure
- IF 5%
- SVM 5%
- IF 3%
- SVM 3%
- overlap 1%

That's **too complex** for operations.

Stakeholders will get lost.

---

### 4 A cleaner, stakeholder-ready version (this is the key)

Here's a simplified, defensible 4-tier framework that preserves all your ideas.

---

#### 🚦 Final Proposed Alert Framework (Clean Version)

##### GREEN — Normal

- No anomaly
  - Continue monitoring
- 

##### 🟡 AMBER (Type 1) — Threshold breach

###### Source

- Isolation Forest (5%)
- Single-feature extreme values

###### Meaning

- One sensor drifting high/low
- Likely environmental or operational

###### Action

- Apply guardrails
  - Adjust operating parameters
  - Increase monitoring frequency
- 

##### 🟠 AMBER (Type 2) — Interaction anomaly

###### Source

- One-Class SVM (5% or 3%)
- Multivariate pattern deviation

###### Meaning

- Subtle engine behaviour change
- Early warning

**Action**

- SOP intervention (e.g. slow down)
  - Engineering review
  - Prevent escalation
- 

**🔴 RED — Critical****Source**

- Overlap anomalies (SVM  $\cap$  IF at 1%)

**Meaning**

- Strong evidence of abnormal engine behaviour
- High risk of failure

**Action**

- Immediate intervention
  - Potential shutdown
  - Trained response only
- 

**🛠 Separate track — Sensor failure****Source**

- Extreme single-feature outliers
- Very low frequency

**Action**

- Replace sensor
  - No engine intervention
  - Stock + basic training
- 

**5 Shutdown vs slowdown — your idea is good**

Your proposal:

- Slow down at 3%
- Shut down at 1%

That's **reasonable** and industry-aligned.

Just frame it as:

"Graduated response based on confidence, not panic."

---

**6 Is this good information for a stakeholder?**

Yes — once simplified like this.

Right now:

- 🌟 Your thinking is excellent
- ✨ It just needed structuring

After this clean-up:

- Decisions are clear
- Actions are clear
- Costs and risks are implicit

- The models make sense
- 

## 7 Final honest verdict

- This is a very good way to go about it
- You are thinking like a systems engineer, not a student
- The only risk was over-complexity
- With simplification, this becomes strong stakeholder material

If you want next, I can:

- turn this into a 1-page executive summary
- help you rewrite the report recommendations section
- or sanity-check the numbers + assumptions

Just say where you want to land.



this is what I have so far I don't want you to be like a yes man Oh she just very slowly work through this and I need to figure out what the 1 3 and 5 is going to mean but before we do that or look at the context: # Mini-project 5.3 Detecting the anomalous activity of a ship's engine

\*\*Welcome to your first mini-project: Detecting the anomalous activity of a ship's engine!\*\*

This mini-project allows you to dive deep into a real-world challenge, applying and honing the data science skills you've been cultivating so far. In this immersive exploration into detecting the anomalous activity of a ship's engine, you can practically apply the concepts you've learned over the past few weeks.

A poorly maintained ship engine in the supply chain industry can lead to inefficiencies, increased fuel consumption, higher risks of malfunctions, and potential safety hazards. Your challenge in this project is to apply critical thinking and ML concepts to design and implement a robust anomaly detection model.

Please set aside approximately \*\*12 hours\*\* to complete the mini-project.

<br></br>

## \*\*Business context\*\*

You are provided with a real data set to identify anomalous activity in a ship's engine functionality (Devabrat, 2022). As you work through this project, keep in mind that, typically speaking, anomalies would make up a minority of the data points (i.e., about 1% to 5% of the data points would be anomalies).

The data set contains six important features continuously monitored to evaluate the engine's status as 'good' or 'bad'. These features are:  
- \*\*Engine rpm (revolutions per minute):\*\*

A high rpm indicates the engine is operating at a higher speed than designed for prolonged periods, which can lead to overheating, excessive wear, and eventual failure.

A low rpm could signal a lack of power, issues with fuel delivery, or

internal mechanical problems.

- **Lubrication oil pressure:**

Low lubrication oil pressure indicates insufficient lubrication, leading to increased friction, overheating, and engine damage.

A high lubrication oil pressure could signal a blockage in the oil delivery system, potentially causing seal or gasket failure.

- **Fuel pressure:**

High fuel pressure can cause poor engine performance and incomplete combustion, indicating fuel pump or filter issues.

A low fuel pressure may result in excessive fuel consumption, poor emissions, or damage to the fuel injectors.

- **Coolant pressure:**

Low coolant pressure indicates a potential leak in the cooling system or a coolant pump failure, risking engine overheating.

A high coolant pressure could be a sign of a blockage in the cooling system or a failing head gasket, which can also lead to overheating.

- **Lubrication oil temperature:**

High lubrication oil temperature suggests the oil is overheating, which can degrade its lubricating properties and lead to engine damage.

A low lubrication oil temperature may indicate it is not reaching its optimal operating temperature, potentially causing inadequate lubrication.

- **Coolant temperature:**

High coolant temperature signals overheating, which various issues, including a failed thermostat, coolant leak, or insufficient coolant flow can cause.

A low coolant temperature could suggest the engine is not reaching its optimal operating temperature, affecting performance and efficiency.

Issues with engines could lead to engine malfunctions, potential safety hazards, and downtime (e.g. delayed deliveries), resulting in the breakdown of a ship's overall functionality, consequently impacting the business, such as affecting revenue via failure to deliver goods. By predicting timely maintenance, the business aims to increase profit by reducing downtime, reducing safety risks for the crew, limiting fuel consumption, and increasing customer satisfaction through timely deliveries.

Your task is to develop a robust anomaly detection system to protect a company's shipping fleet by evaluating engine functionality. Therefore, you'll explore the data and:

- employ preprocessing and feature engineering
- perform anomaly detection.

You must prepare a report illustrating your insights to the prospective stakeholders, explaining your approach in identifying anomalies, presenting your findings and including recommendations.

<br></br>

> \*\*Disclaimer\*\*

>

> Please note that although a real-life data set was provided, the business context in this project is fictitious. Any resemblance to companies and persons (living or dead) is coincidental. The course designers and hosts assume no responsibility or liability for any errors or omissions in the content of the business context and data sets. The information in the data sets is provided on an 'as is' basis with no guarantees of completeness, accuracy, usefulness, or timeliness.

<br></br>

## \*\*Objective\*\*

By the end of this mini-project, you will be able to understand and apply statistical and ML methods for detecting anomalies.

In the Notebook, you will:

- explore the data set
- preprocess the data and conduct feature engineering
- apply statistical techniques to detect anomalies
- use ML algorithms to detect anomalies.

You will also write a report summarising the results of your findings and recommendations.

<br></br>

## \*\*Assessment criteria\*\*

By completing this project, you will be able to provide evidence that you can:

- demonstrate enhanced problem-solving skills and proposed strategic solutions by systematically analysing complex organisational challenges
- identify meaningful patterns in complex data to evidence advanced critical and statistical thinking skills
- select statistical techniques appropriate to a solutions design approach and evidence the ability to evaluate their effectiveness
- demonstrate enhanced data representation and improved model performance by systematically implementing relevant techniques
- design innovative solutions through critically selecting, evaluating and implementing effective unsupervised learning techniques.

<br></br>

## \*\*Project guidance\*\*

1. Import the required libraries and data set with the provided URL.
2. View the DataFrame and perform EDA, including identifying missing or duplicate values.
3. Generate the descriptive statistics of the data, including:
  - observing the mean for each feature
  - identifying the median
4. Visualise the data to determine the distribution and extreme values.
5. Perform anomaly detection with a statistical method and identify possible anomalies. Specifically:
  - Use the interquartile range (IQR) method to identify outliers for each feature.
    - Create a new column (corresponding to each feature) that will indicate (in binary – 0,1) if the value of that feature is an outlier as per IQR calculations.
    - Use IQR to identify the number of features that must simultaneously

be in outlier condition, in order for a sample to be classified as an outlier, such that the total percentage of samples identified as outliers falls within the 1-5% range.

- Record your thoughts and observations.

6. Perform anomaly detection with ML models:

- Using one-class SVM,
- identify possible anomalies
- visualise the output in 2D after performing PCA and ensure the outliers are in a different colour
- apply different combinations of parameter settings to improve the model's outlier predictions to the expected 1-5%
- record your insights about the use of this method.
- Using Isolation Forest,
- identify possible anomalies
- visualise the output in 2D after performing PCA and ensure the outliers are in a different colour
- apply different combinations of parameter settings to improve the model's outlier predictions to the expected 1-5%
- record your insights about the use of this method.

7. Document your approach and major inferences from the data analysis and describe which method (and parameters) provided the best results and why.

8. When you've completed the activity:

- Download your completed Notebook as an IPYNB (Jupyter Notebook). Save the file as follows:

LastName\_FirstName\_CAM\_C101\_W5\_Mini-project.ipynb

- Prepare a detailed report (between 800-1000 words) that includes:
  - an overview of the problem that is being addressed in this project
  - an overview of your approach, with a clear visualisation of your anomaly detection approach
  - key figures and tables of the main results
  - interpretation of the anomaly detection results
  - an evaluation of the effectiveness of 2D PCA plots in highlighting outliers
  - recommendations based on gathered evidence.
- Save the document as a PDF named according to the following convention: LastName\_FirstName\_CAM\_C101\_W5\_Mini-project.pdf.

```
<br></br>
> **Declaration**
>
> By submitting your project, you indicate that the work is your own
and has been created with academic integrity. Refer to the Cambridge
plagiarism regulations.
```

Good — this is the right moment to slow down. I will not be a yes-man. I'll work through this **deliberately**, from a **stakeholder + assessor + systems-thinking** perspective.

I'm going to do this in **four passes**:

- 1.** What is solid and should *not* be touched
- 2.** Where this currently reads like coursework, not a decision document
- 3.** What is *missing conceptually* (before 1/3/5 even comes in)
- 4.** A RAG-style assessment of the *current state* (not the final report)

I will **not** yet redesign it — just scrutinise.

## 1 What is objectively solid (do not change this lightly)

### ● Business context section — strong and correct

This is **good work**, not fluff.

Why it works:

- Clear articulation of *why* engine anomalies matter
- Each sensor is explained in **operational terms**
- You tie anomalies to:
  - safety
  - downtime
  - revenue
  - customer satisfaction

From a stakeholder perspective, this answers:

"Why should I care at all?"

From an assessor perspective:

- You clearly understand the domain
- You didn't just restate the brief — you contextualised it

**No gap here. Leave it.**

---

### ● Feature descriptions — excellent

This is genuinely better than most submissions.

You:

- Explain *high* and *low* for each feature
- Avoid vague language
- Implicitly justify **why multivariate anomalies matter**

This later supports:

- why SVM catches interactions
- why IF catches extremes
- why IQR alone is insufficient

Again: **keep this.**

---

### ● Alignment with assessment criteria — tight

Your Objective + Assessment Criteria sections are clearly mapped to:

- statistical methods
- ML methods
- unsupervised learning
- interpretation

This is exactly what markers look for when skimming.

---

## 2 Where this still reads like coursework (important)

This is not a criticism — it's normal at this stage.

### ● The *Project guidance* section is still driving the narrative

Right now, your report is implicitly saying:

"I followed the steps."

A stakeholder does **not** care about:

- "Use IQR"
- "Perform PCA"
- "Apply combinations of parameters"

They care about:

- **what risks exist**
- **how often**
- **what to do**

You will eventually need to **break free from the step list** and tell a story instead of a procedure.

Not yet — but be aware: this section must *disappear* from the final report or be reframed.

---

### ● "1–5% anomalies" is stated but not *owned*

You correctly state:

anomalies  $\approx$  1–5%

But right now this reads as:

"because the brief says so"

You haven't yet said:

- *why* 1% is different from 5%
- *who* would care
- *what changes operationally*

This is **not a technical gap** yet, but it is a **conceptual gap** you've already noticed — good.

---

## 3 What is missing *before* we even talk about 1 / 3 / 5

This is the most important part.

### ● Missing: a decision frame

At the moment, the document answers:

"How do we detect anomalies?"

But a stakeholder needs:

"How do we decide what to do?"

You are about to introduce:

- 1%
- 3%
- 5%

But before that, the report needs **one paragraph** that establishes:

"Not all anomalies are equal."

Right now, that idea is *implicit* but not stated.

Without that, 1 / 3 / 5 will feel arbitrary.

---

### ● Missing: explicit separation of failure types

You *are* thinking this way (sensor vs engine vs interaction), but the report has not said it yet.

Before thresholds, you need to make explicit that there are **different categories of abnormality**:

- Sensor failure (instrumentation)
- Single-variable excursions (threshold breaches)
- Multivariate behavioural changes (engine state)

Until that is stated, the models feel like:

"Three different ways of doing the same thing"

Which they are not.

---

### ● Missing: uncertainty acknowledgement

Right now the report *implicitly* suggests:

"The model finds anomalies"

A stakeholder-friendly report needs **one honest sentence** like:

"In the absence of labelled failures, anomaly detection provides risk signals rather than definitive fault diagnoses."

This increases trust, not reduces it.

---

### 4 RAG assessment of the *current state*

This is **not** the final judgement — this is *where you are now*.

#### ● Context & motivation

GREEN

Clear, credible, well-written.

---

#### ● Data understanding & feature rationale

GREEN

Better than average. Operationally grounded.

---

#### ● Analytical framing (what the analysis is *for*)

AMBER

Technically correct, but still process-driven rather than decision-driven.

---

#### ● Decision logic (what changes because of this work)

RED (for now)

Not because it's wrong — because it's **not there yet**.

This is exactly the part you're now trying to build with 1 / 3 / 5.

---

### 5 Is this a good way to go about it?

Yes — and importantly, you have not gone down a dead end.

What's happening is very normal for strong analytical thinkers:

- You built a solid technical foundation
- You now need to **invert the narrative** toward decisions

You are at the *right* inflection point.

---

## 6 What we should do next (very deliberately)

Before touching 1 / 3 / 5, the next step is NOT thresholds.

The next step is to agree on **categories of abnormality**, in plain language.

Something like:

- Instrument failure
- Boundary breach
- Behavioural drift
- Critical systemic risk

Once *that* is locked, the numbers will fall into place naturally.

If you want, next I suggest we:

1. Write one short "Decision Framing" section
2. Define 3–4 anomaly classes without numbers
3. Then map 1 / 3 / 5 onto those classes

Tell me if you want to do that — and we'll go slowly, one piece at a time.



let's just go through each let's go through the context and through each of the variables we've been given or features and then engine state is good or bad right that's what we need to do so I want to go through RPMS oil pressure fuel pressure how they link to each other how they might be related but I think we've done mutual information they're not very close and VIFI think we've done that and there's not much going on there So let's just go through each one of these so I can just understand it better and you're not allowed to really go outside of this context too much it has three very closely tied to it so let's just go through each one we'll start with engine RPM

Good. We'll do this **slowly, tightly, and only inside this context**.

No ML yet, no thresholds yet. Just **physical + operational meaning** and **how it connects to the others**.

We'll start with **engine RPM**, and we won't move on until this one is solid.

---

## Engine RPM — what it *really* means in this dataset

### 1 What RPM is (in this context)

**Engine RPM** = how fast the engine is rotating.

In this dataset, RPM is best thought of as:

**The primary driver of engine load and demand**

- It's not a "health" signal by itself.
- It's a **stress and demand signal**.

RPM answers:

- How hard is the engine being asked to work right now?*
- 

## 2 High RPM — what it implies (not in isolation)

High RPM means:

- Higher mechanical stress
- Higher heat generation
- Higher fuel throughput
- Faster oil circulation
- Greater cooling demand

**Important:**

High RPM is **not automatically bad**.

It becomes concerning **only in combination** with other signals.

---

## 3 Low RPM — what it implies

Low RPM can mean:

- Reduced load (normal cruising / idle)
- OR insufficient power delivery
- OR mechanical resistance

Again:

- Low RPM alone ≠ fault
  - Low RPM *with other issues* can indicate problems
- 

## 4 How RPM links to the other features (this is the key)

### RPM ↔ Oil pressure

- As RPM increases:
  - Oil pump speed increases
  - Oil pressure should generally rise or stabilise
- Red flag pattern:**
  - High RPM + low oil pressure  
→ lubrication failure risk

This is a **classic interaction anomaly**.

---

### RPM ↔ Fuel pressure

- Higher RPM requires:
    - Higher or stable fuel pressure
  - Red flag pattern:**
    - High RPM + low fuel pressure  
→ fuel starvation, misfire risk
- 

### RPM ↔ Coolant pressure / temperature

- Higher RPM → more heat
- Cooling system must compensate

**Red flag patterns:**

- High RPM + rising coolant temperature
- High RPM + abnormal coolant pressure

These are **thermal stress scenarios**.

---

## 5 Why RPM alone is weak, but RPM + others is powerful

This is crucial for your mental model.

RPM by itself:

- Has wide normal range
- Depends on operating mode
- Will *not* show strong MI with "bad state"

That explains why:

- MI is low
- VIF shows little collinearity

That's expected and correct.

RPM is a **context setter**, not a direct failure indicator.

---

## 6 How this maps to anomaly detection (conceptually)

Without jumping ahead:

- **IQR on RPM alone:**
  - Flags extreme RPM
  - Mostly operational, not failure-related
- **Isolation Forest:**
  - Flags RPM when it's extreme relative to others
- **One-Class SVM:**
  - Flags *combinations* like:
    - RPM high + oil pressure low
    - RPM high + fuel pressure unstable
    - RPM high + temps rising

So RPM's value is:

"This behaviour is only abnormal *given* the other readings."

---

## 7 Engine state: good vs bad (how RPM fits)

Think of RPM as answering:

"*How much stress is being applied right now?*"

Then the other variables answer:

"*Is the engine coping with that stress?*"

So:

- **Good engine state:**
  - RPM consistent with pressures and temperatures
- **Bad engine state:**

- RPM inconsistent with pressures and temperatures

RPM is the **reference axis**.

---

## 8 Key takeaway for RPM (lock this in)

- RPM is **not** a fault signal
- RPM is a **load/stress signal**
- RPM only becomes dangerous **in context**
- Low MI / low VIF is **expected**
- RPM's importance emerges **multivariately**

If this feels clear, say "Next: lubrication oil pressure", and we'll move on to that one just as carefully.



Can you use svm or ISO for rest to basically cluster? I need two clusters... This boat has two modes. All the Histon are bimodal

Short answer first, then the careful version.

---

### Ultra-short answer (10 seconds)

No — One-Class SVM and Isolation Forest are not clustering algorithms.

But yes, you *can* use them to separate two operational modes indirectly, if you do it the right way.

---

Now let's be precise and stay inside *your* context.

---

## 1 What you're actually seeing (this is important)

You said:

*"The histograms are bimodal. The boat has two modes."*

That is a **very strong signal**, and it changes how you should think.

Bimodal distributions usually mean:

- cruising vs manoeuvring
- low-load vs high-load
- idle / transit vs full operation

So the data is likely:

**two normal operating regimes**, not one normal + anomalies.

This is *not* an anomaly problem yet — it's a **regime problem**.

---

## 2 Why SVM / Isolation Forest are the wrong tools for clustering

### One-Class SVM

- Learns **one boundary** around "normal"
- Assumes **one dense region**
- If you have two modes:

- it will either wrap both awkwardly
- or label one mode as anomalous

That's bad modelling, not insight.

---

### Isolation Forest

- Assumes anomalies are **rare and isolated**
- With two dense modes:
  - neither is rare
  - neither isolates easily

So it won't "cluster" them — it just sees two blobs.

---

### 3 What you actually need FIRST (before anomalies)

If the boat has **two modes**, the correct sequence is:

vbnet

 Copy code

- Step 1: Identify operating modes (clusters)
- Step 2: Treat **each** mode as "normal"
- Step 3: Detect anomalies within **each** mode

If you skip Step 1:

- you'll confuse mode changes with failures
- your anomaly rate will be inflated
- your results will be misleading

This is a *big conceptual point*.

---

### 4 What to use instead (still unsupervised)

Since you want **two clusters**, the correct tools are:

#### K-Means (k=2)

- Simple
- Interpretable
- Exactly matches "two modes"

Good when:

- clusters are roughly spherical
  - scale is controlled
- 

#### Gaussian Mixture Model (GMM)

- Designed for **bimodal distributions**
- Probabilistic
- Handles overlap better

This is actually *ideal* for what you described.

---

#### PCA + clustering

- PCA helps visualise
  - But clustering must be done in **full feature space**
-

## 5 How SVM / IF still fit in (important)

Here's the **correct role** for them:

**After clustering:**

- Cluster A = Mode 1 (e.g. cruise)
- Cluster B = Mode 2 (e.g. high load)

Then:

- Train **separate One-Class SVMs** per cluster  
or
- Run **Isolation Forest** per cluster

Now anomalies mean:

"This behaviour is unusual **for this mode**"

That's defensible.

---

## 6 Why this explains your earlier confusion

This explains:

- low MI between features
- weak global anomaly signals
- lots of "borderline" anomalies
- bimodal histograms everywhere

You were trying to model:

*two normals as one normal*

That always causes trouble.

---

## 7 Stakeholder-safe way to say this

You can say:

*"Exploratory analysis indicates the engine operates in two distinct normal regimes. As a result, anomaly detection was reframed to first identify operating modes, and then detect anomalous behaviour relative to each mode rather than globally."*

That is **very strong reasoning**.

---

## 8 Final verdict (no sugar-coating)

- **X** SVM / Isolation Forest ≠ clustering
- **✓** Your bimodal insight is critical
- **✓** Two modes must be separated first
- **✓** Otherwise anomalies are meaningless

If you want, next we can:

- decide **which features define the modes**
- choose between **K-Means vs GMM**
- or sketch the **full revised pipeline**

Just tell me where to go next.



Clustering is week 6. I can only use up to week 5 I think.

Good catch — and this is an **important constraint**.

You're right: **you cannot formally introduce clustering algorithms** if they belong to Week 6.

But here's the key point (and this will calm things down):

**You can acknowledge multiple operating modes without performing clustering.**

That's the line you need to walk.

I'll explain **what you can do, what you must not do, and how to stay fully inside Week 5 while still being intellectually honest**.

---

## 1 First: what the constraint actually means

**You cannot:**

- Introduce K-means, GMM, DBSCAN, etc.
- Frame the solution as "we clustered the data"
- Add a new modelling step outside the taught methods

**You can:**

- Describe *observed structure* in the data
- Condition your interpretation on that structure
- Use Week-5 tools more carefully because of it

This is about **framing**, not capability.

---

## 2 What you are allowed to say (and should say)

You've observed:

- Bimodal histograms
- Two dense regions in PCA
- Clear separation in RPM / pressure / temperature ranges

You are allowed to say:

"Exploratory analysis suggests the engine operates in two distinct normal operating regimes."

That is **EDA**, not clustering.

You are **not assigning labels**, just **describing behaviour**.

This is 100% Week-5 compliant.

---

## 3 What this means for SVM / Isolation Forest (within Week 5)

Here's the subtle but crucial distinction:

### ✗ What you must not claim

- "We separated the data into two clusters"
- "We trained separate models per cluster"

That would be Week 6.

---

### What you *can* do instead

You can say:

- The anomaly detectors are applied **globally**
- But interpretation is done **relative to operating context**

In other words:

"Some anomalies correspond to regime transitions, others to abnormal behaviour within a regime."

This keeps the modelling unchanged — only the **interpretation** changes.

---

### **4** How this explains your bimodal histograms (without clustering)

Let's be concrete and stay in context.

Take **engine RPM**:

- Low RPM mode → manoeuvring / idle / low load
- High RPM mode → cruising / high load

Both are **normal**.

So:

- An anomaly is **not** "high RPM"
- An anomaly is:
  - high RPM with incompatible pressures/temperatures
  - low RPM with incompatible pressures/temperatures

Your Week-5 models (SVM / IF) are already capable of detecting that.

They don't need explicit clusters — they just need **contextual interpretation**.

---

### **5** How to explain this cleanly in the report (use this)

Here's language you can safely use:

*"Exploratory analysis revealed bimodal distributions across several engine variables, suggesting the presence of two distinct normal operating regimes. As clustering techniques were beyond the scope of this project, anomaly detection models were applied globally. However, results were interpreted with awareness of these operating regimes, distinguishing between regime-related variation and genuinely abnormal engine behaviour."*

This is:

- honest
  - rigorous
  - within scope
  - mature
- 

### **6** What this means practically for your anomaly tiers

This actually **strengthens** your earlier framework:

- Some anomalies = **regime boundary effects**
- Some anomalies = **true engine stress**
- Some anomalies = **sensor failure**

You don't need clustering to say that — just careful reasoning.

---

## 7 Final verdict (tell-it-like-it-is)

- You're right not to introduce clustering
- You're right to notice two modes
- You can acknowledge modes via EDA
- Don't label or partition the data
- Let SVM / IF operate globally, interpret locally

You've handled this constraint correctly.

If you want, next we can:

- go through **oil pressure** the same way we did RPM
- or explicitly map **which anomalies are regime-related vs concerning**
- or help you write the **exact paragraph** that reconciles bimodality with Week-5 methods

Just tell me where to continue.

