RAILS — Railbed Analysis & Image Learning System

"RAILS" ist ein fiktiver Projektname und steht in keiner Verbindung zu bestehenden Produkten, Marken oder Organisationen, etwaige Namensähnlichkeiten sind zufällig und nicht beabsichtigt.

Dieses Notebook behandelt die Analyse und das Clustering von Schienenuntergrund-Bilddaten im Rahmen des Master Moduls "Maschinelles Lernen". Grundlage sind rund 50.000 Graustufenbilder aus Messfahrten mehrerer europäischer Städte, die verschiedene Oberbautypen wie Schotter, Asphalt oder Rasen zeigen.

Ziel ist es, mit Hilfe von **Clustering- und Klassifikationsverfahren** Muster und Strukturen in den Daten zu erkennen und die Leistungsfähigkeit unterschiedlicher Ansätze zu vergleichen. Dazu werden die Bilder vorverarbeitet, mithilfe eines vortrainierten CNN in Embeddings überführt und anschließend mit Methoden wie KMeans und DBSCAN gruppiert.

Das Notebook ist so strukturiert, dass es den gesamten Workflow von der technischen Vorbereitung bis zur Auswertung abbildet:

- Zunächst erfolgt das Setup der Umgebung sowie die Konfiguration der Pfade und Parameter.
- Anschließend werden Datensatzstruktur und Metadaten untersucht, bevor die Feature-Extraktion mit einem CNN durchgeführt wird.
- Die resultierenden Features werden normalisiert und mittels PCA reduziert, um sie für Clustering-Algorithmen vorzubereiten.
- Im Kernteil werden **KMeans** und **DBSCAN** angewendet, systematisch evaluiert und visuell miteinander verglichen.
- Schließlich werden die Cluster-Ergebnisse gespeichert, Reports erzeugt und eine detaillierte Tenant-Analyse erstellt.

Im Fokus steht die praktische Anwendung moderner Machine-Learning-Techniken auf reale Daten sowie eine transparente Dokumentation der Ergebnisse mit Metriken und Visualisierungen

Inhaltsverzeichnis

- Einleitung
- 1. Setup: Importe & Umgebung
- 2. Konfiguration: Pfade, Modellparameter
- 3. Ergebnisse-Verzeichnis & Datensatz-Check
- 4. Dateiname-Parsing, Dataset-Metadaten & Tenant-Verteilung

- 5. Feature-Extraktion
- 5.1 Feature-Extraktion vorbereiten: Funktionen & Pipeline
- 5.2 Feature-Extraktion ausführen (CPU-Only, Timing & Valid-Filter)
- 6. Feature-Nachbearbeitung (Normalisierung & PCA → Vorbereitung fürs Clustering)
- 7. K-Means
- 7.1 K-Means: k-Sweep & Clusterbewertung (Inertia, Silhouette, Clustergrößen)
- 7.2 K-Means Evaluation visualisieren & k bestimmen
- 7.3 Finales K-Means mit optimalem k & Clusteranalyse
- 7.4 K-Means-Clusterbeispiele: Visualisierung von Beispielbildern
- 8. DBSCAN
- 8.1 DBSCAN: Parameter-Grid, Heatmaps & Best-Selection
- 9. Visualisierung: K-Means & DBSCAN (Side-by-Side) mit t-SNE
- 9.1 K-Nearest Neighbor Grafik
- 10. Cluster-Ergebnisse speichern
- 10.1 Speicher-Helfer definieren (Ordner/Bildkopie/Metadaten)
- 10.2 K-Means-Cluster speichern (Ausführung)
- 10.3 DBSCAN-Cluster speichern (Ausführung)
- 11. Tenant-Cluster-Analyse (Heatmap & Detailstatistik)
- 12. Clustering-Report (JSON) erstellen & Kernergebnisse ausgeben
- 13. Ergebnisse der Clustering Phase

1. Setup: Importe & Umgebung

Was:

• Import zentraler Bibliotheken (Datenhandling, Visualisierung, ML/DL).

Warum:

• Konsistente, reproduzierbare Läufe und Zentralisierung.

```
# Import Required Libraries
import os
import shutil
import numpy as np
import pandas as pd
import matplotlib
import matplotlib.pyplot as plt
import seaborn as sns
from pathlib import Path
import json
import time
import cv2
from collections import Counter, defaultdict
from PIL import Image
# Machine Learning Libraries
from sklearn.cluster import KMeans, MiniBatchKMeans, DBSCAN
```

```
from sklearn.decomposition import PCA
from sklearn.manifold import TSNE
from sklearn.metrics import silhouette score, silhouette samples
from sklearn.preprocessing import StandardScaler, normalize
# Deep Learning Libraries - Import AFTER setting environment variables
import tensorflow as tf
from tensorflow.keras.applications import ResNet50
from tensorflow.keras.applications.resnet50 import preprocess input
from tensorflow.keras.applications.vgg16 import preprocess input
from tensorflow.keras.preprocessing import image
# Image Processing
from img preprocessing import ImagePreprocessor
# Visualization
from matplotlib.patches import Rectangle
import warnings
warnings.filterwarnings('ignore')
# Set random seeds for reproducibility
np.random.seed(42)
tf.random.set_seed(42)
2025-09-07 15:06:41.342615: E
external/local xla/xla/stream executor/cuda/cuda fft.cc:485] Unable to
register cuFFT factory: Attempting to register factory for plugin
cuFFT when one has already been registered
2025-09-07 15:06:41.358084: E
external/local xla/xla/stream executor/cuda/cuda dnn.cc:8454] Unable
to register cuDNN factory: Attempting to register factory for plugin
cuDNN when one has already been registered
2025-09-07 15:06:41.362708: E
external/local xla/xla/stream executor/cuda/cuda blas.cc:1452] Unable
to register cuBLAS factory: Attempting to register factory for plugin
cuBLAS when one has already been registered
2025-09-07 15:06:41.373812: I
tensorflow/core/platform/cpu feature guard.cc:210] This TensorFlow
binary is optimized to use available CPU instructions in performance-
critical operations.
To enable the following instructions: AVX2 FMA, in other operations,
rebuild TensorFlow with the appropriate compiler flags.
2025-09-07 15:06:42.152338: W
tensorflow/compiler/tf2tensorrt/utils/py_utils.cc:38] TF-TRT Warning:
Could not find TensorRT
```

2. Konfiguration: Pfade, Modellparameter

Was:

- Lauf-zeitgestempelte Ergebnisordner anlegen (Analyse + Clusterbilder).
- Zentrale Hyperparameter für Feature-Extraktion und Clustering definieren.

Warum:

- TIMESTAMP: Versioniert jeden Run → kein Überschreiben, einfache Nachverfolgung & Vergleichbarkeit.
- **DATASET_PATH=...sample_100**: Kleine Stichprobe zum schnellen Iterieren/Debuggen. Skaliert später auf größere Samples.
- BASE_RESULTS_PATH/RESULTS_PATH/CLUSTERS_PATH: Klare Trennung von Analyseartefakten und exportierten Cluster-Bildern.
- BATCH SIZE=32: Bestimmt wie viele Bilder zeitgleich in den RAM geladen werden.
- **IMG_SIZE=(224,224)**: Erwartete Eingabegröße für ResNet50 (ImageNet-Pretraining) → kompatible Modeleingabe.
- **FEATURE_DIM=2048**: Output-Dimensionalität von ResNet50 → korrektes Erwartungs-Shape für Downstream-Schritte.
- **N_CLUSTERS_RANGE=range(3,16)**: Typischer, kompakter k-Bereich für K-Means-Sweep (Balance aus Rechenzeit und Abdeckung kleiner/mittlerer k).
- **PCA_COMPONENTS=50**: Anzahl der Principal Componentes. Angewandt zur Dimensionsreduktion.
- RANDOM STATE=42: Reproduzierbarkeit über PCA/t-SNE/K-Means hinweg.

Besonderheiten:

- TIMESTAMP prägt alle Output-Pfade (kein Überschreiben alter Ergebnisse).
- N CLUSTERS RANGE=3..15 für den k-Sweep (K-Means/MiniBatchKMeans).

- Konsolenhinweis mit Zielpfaden (RESULTS PATH, CLUSTERS PATH).
- Keine Dateien an dieser Stelle nur Konfiguration.

```
from datetime import datetime

TIMESTAMP = datetime.now().strftime('%Y%m%d_%H%M%S')
print(f"Analysis timestamp: {TIMESTAMP}")

DATASET_PATH = "./datasets/clustering_sample_10000"

BASE_RESULTS_PATH = f"./results_{TIMESTAMP}"

RESULTS_PATH = f"{BASE_RESULTS_PATH}/clustering_analysis"
CLUSTERS_PATH = f"{BASE_RESULTS_PATH}/clustered_images"
```

```
BATCH_SIZE = 32
IMG_SIZE = (224, 224)
FEATURE_DIM = 2048
N_CLUSTERS_RANGE = range(3, 16)
PCA_COMPONENTS = 50
RANDOM_STATE = 42

print(f"Results will be saved to:")
print(f" Analysis results: {RESULTS_PATH}")
print(f" Clustered images: {CLUSTERS_PATH}")

Analysis timestamp: 20250907_150642
Results will be saved to:
   Analysis results: ./results_20250907_150642/clustering_analysis
   Clustered images: ./results_20250907_150642/clustered_images
```

3. Ergebnisse-Verzeichnis & Datensatz-Check

Was:

- Anlage laufzeitgestempelter Ergebnisordner (Analyse, Clusterbilder), Ausgabe der Pfade.
- Sanity-Check des Datensatzpfads; Fallback: Auflistung vorhandener Datasets mit Bildanzahl.
- Zählen aller .png-Dateien im gewählten Dataset.
- Persistieren einer run metadata. ison (Pfad- und Konfig-Snapshot).

Warum:

- Ordnererstellung verhindert Fehler bei wiederholten Läufen.
- Pfad-/Existenz-Check reduziert Fehlersuche bei falschen Datasetangaben.
- **Bildzählung** schafft Transparenz (Basis für spätere Prozentangaben, Laufzeitabschätzungen).
- **run_metadata.json** dokumentiert Pfade & Konfiguration (Reproduzierbarkeit, Vergleichbarkeit zwischen Runs).

- Verzeichnisse: RESULTS PATH, CLUSTERS PATH
- Datei: RESULTS PATH/run metadata.json
- Konsolen-Logs mit Pfaden und Bildanzahl

```
# Create timestamped result roots (idempotent: no error if folders
already exist)
Path(RESULTS PATH).mkdir(parents=True, exist ok=True)
Path(CLUSTERS PATH).mkdir(parents=True, exist ok=True)
print(f"Created timestamped directories:")
print(f"Dataset path: {DATASET PATH}")
print(f"Analysis results path: {RESULTS PATH}")
print(f"Clustered images path: {CLUSTERS PATH}")
# Check dataset existence; if missing, enumerate available subfolders
under ./datasets
if not os.path.exists(DATASET PATH):
    print(f"Error: Dataset path {DATASET PATH} does not exist!")
    print("Available dataset directories:")
    datasets dir = Path("./datasets")
    if datasets dir.exists():
        for subdir in datasets dir.iterdir():
            if subdir.is dir():
                # Count only files ending with '.png' (case-sensitive)
                img count = len([f for f in subdir.iterdir() if
f.suffix == '.png'])
                print(f" {subdir.name}: {img count} images")
else:
    # Count .png files in the selected dataset (flat folder expected)
    img count = len([f for f in Path(DATASET PATH).iterdir() if
f.suffix == '.png'l)
    print(f"Found {img count} images in dataset")
# Build a metadata snapshot for this run (paths, counts, and core
configuration)
run metadata = {
    'timestamp': TIMESTAMP, # run identifier
    'dataset path': str(Path(DATASET PATH).resolve()),
    'total images found': img count if os.path.exists(DATASET PATH)
else 0,
    'analysis results path': <mark>str</mark>(Path(RESULTS PATH).resolve()),
    'clustered images path': str(Path(CLUSTERS PATH).resolve()),
    'configuration': {
        'batch size': BATCH SIZE,
        'img_size': IMG_SIZE,
        'feature dim': FEATURE DIM,
        'n_clusters_range': list(N_CLUSTERS RANGE),
        'pca components': PCA COMPONENTS,
        'random state': RANDOM STATE
    }
}
# Persist metadata to JSON for reproducibility/audit
with open(f"{RESULTS PATH}/run metadata.json", 'w') as f:
```

```
json.dump(run_metadata, f, indent=2)

print(f"\nRun metadata saved to: {RESULTS_PATH}/run_metadata.json")

Created timestamped directories:
Dataset path: ./datasets/clustering_sample_10000
Analysis results path: ./results_20250907_150642/clustering_analysis
Clustered images path: ./results_20250907_150642/clustered_images
Found 10000 images in dataset

Run metadata saved to:
./results_20250907_150642/clustering_analysis/run_metadata.json
```

4. Dateiname-Parsing, Dataset-Metadaten & Tenant-Verteilung

Was:

- Parsen der Dateinamen mit Suffix _C.png, um tenant, SID und original_filename zu extrahieren.
- Einlesen des Datasets zu einer Dateiliste und Aggregation der Tenant-Verteilung.
- Ausgabe von **Gesamtzahl**, **#Tenants** und **Prozentanteilen** je Tenant.

Warum:

- Die Metadaten aus dem Dateinamen erlauben **Slicing** (z. B. Auswertung pro Tenant) und **Qualitätskontrollen** (Ungleichgewichte erkennen).
- Die Fokussierung auf _C.png stellt sicher, dass nur **konforme, bereinigte** Bildvarianten verarbeitet werden (einheitliche Pipeline).

- image files (Liste mit Pfad + extrahierten Metadaten)
- tenant distribution (Dict mit Z\u00e4hlungen)
- Konsolen-Logs (Totals, #Tenants, Verteilung in %)

```
def parse_filename(filename: str):
    """Parse filename to extract tenant, SID, and original
filename."""
    # Expect filenames ending with '_C.png' (case-sensitive)
    # Pattern convention: {tenant}_{sid}_{original}_{c.png}
    if not filename.endswith('_C.png'):
        return None, None
    name_without_ext = filename[:-6] # Remove '_C.png' (6 characters)
```

```
parts = name without ext.split(' ')
    # Require at least 3 parts: tenant, sid, and the remaining
original name
    if len(parts) >= 3:
        tenant = parts[0]
        sid = parts[1]
        original filename = ' '.join(parts[2:])
        return tenant, sid, original filename
    # Fallback if naming does not match the expected convention
    return None, None, None
def load dataset info(dataset path: str):
    """Load and analyze dataset information."""
    # Build file index and aggregate tenant counts based on parsed
filenames
    image files = []
    tenant_distribution = defaultdict(int)
    # Non-recursive, case-sensitive pattern: only matches '* C.png' in
the given folder
    for file path in Path(dataset path).glob('* C.png'):
        filename = file path.name
        tenant, sid, original_name = parse_filename(filename)
        # Keep only files that match the naming convention
        if tenant:
            image files.append({
                'filepath': str(file path),
                'filename': filename,
                'tenant': tenant,
                'sid': sid,
                'original name': original name
            })
            tenant distribution[tenant] += 1
    return image files, dict(tenant distribution)
# Load dataset information (flat folder expected)
print("Loading dataset information...")
image files, tenant distribution = load dataset info(DATASET PATH)
# Summary (assumes >=1 valid image; add guard if needed)
print(f"\nTotal images: {len(image files)}")
print(f"Number of tenants: {len(tenant distribution)}")
print("\nTenant distribution:")
for tenant, count in sorted(tenant distribution.items()):
    percentage = (count / len(image files)) * 100
    print(f" {tenant}: {count} images ({percentage:.1f}%)")
```

```
Loading dataset information...

Total images: 10000
Number of tenants: 8

Tenant distribution:
   ava: 1250 images (12.5%)
   bernmobil: 1250 images (12.5%)
   bvb: 1250 images (12.5%)
   cts: 1250 images (12.5%)
   gent: 1250 images (12.5%)
   gvb: 1250 images (12.5%)
   retm: 1250 images (12.5%)
   vbz: 1250 images (12.5%)
```

5. Feature-Extraktion

5.1 Feature-Extraktion vorbereiten: Funktionen & Pipeline

Was:

 Hilfsfunktionen zum Laden und ggf. Vorverarbeiten einzelner Bilder, Erzeugen des ResNet50-Encoders und batchweises Ableiten der Feature-Embeddings (2048-D).

Warum:

• Saubere Trennung von I/O, Modellkonstruktion und Batch-Verarbeitung erleichtert Debugging und spätere Modellaustausche (z. B. anderer Encoder).

Besonderheiten:

• 5 mögliche Vorverarbeitungsfunktionen (img_processing.py)

Outputs:

• Keinerlei Dateien. Rückgaben sind In-Memory: Feature-Matrizen (N×2048) und gültige Pfade.

```
def load_and_preprocess_image(image_path: str, target_size: tuple =
IMG_SIZE):
    """Load and preprocess image for ResNet50."""
    try:
        img = cv2.imread(image_path)
        img = cv2.resize(img, target_size)
        # insert preprocessing here
        # for exmaple:
        #img = ImagePreprocessor.method_3_gamma_correction(img)
        img_array = image.img_to_array(img)
        img_array = np.expand_dims(img_array, axis=0)
        img_array = preprocess_input(img_array)
        return img_array
```

```
except Exception as e:
        print(f"Error loading {image path}: {e}")
        return None
def create feature extractor():
    """Create ResNet50 feature extractor (without top classification
laver)."""
    print("Loading ResNet50 model...")
    base model = ResNet50(
        weights='imagenet',
        include top=False,
        input shape=(IMG_SIZE[0], IMG_SIZE[1], 3),
        pooling='avg' # Global average pooling
    )
    # The model output will be (batch size, 2048) features
    print(f"Feature extractor output shape:
{base model.output shape}")
    return base model
def extract features batch(model, image paths: list, batch size: int =
BATCH SIZE):
    """Extract features from images in batches."""
    features = []
    valid paths = []
    print(f"Extracting features from {len(image paths)} images...")
    for i in range(0, len(image paths), batch size):
        batch paths = image paths[i:i + batch size]
        batch images = []
        batch valid paths = []
        # Load batch images
        for img path in batch paths:
            img array = load and preprocess image(img path)
            if img array is not None:
                batch_images.append(img_array[0]) # Remove batch
dimension
                batch valid paths.append(img path)
        if batch images:
            # Convert to numpy array and predict
            batch images = np.array(batch images)
            batch_features = model.predict(batch_images, verbose=0)
            features.extend(batch features)
            valid paths.extend(batch valid paths)
```

```
# Progress update
if (i // batch_size + 1) % 10 == 0:
    print(f" Processed {min(i + batch_size,
len(image_paths))}/{len(image_paths)} images")
return np.array(features), valid_paths
```

5.2 Feature-Extraktion ausführen (CPU-Only, Timing & Valid-Filter)

Was:

- Initialisieren des ResNet50-Feature-Extractors, Sammeln der image_paths und batchweise Extraktion der Embeddings.
- Messen der Laufzeit und Ausgeben von Kernwerten (Shape, Anzahl gültiger Bilder).
- Filtern nicht ladbarer Bilder und Aktualisieren von image_files auf die valide Teilmenge.

Warum:

- Laufzeitmessung hilft bei der Abschätzung von Skalierung und Batchgrößen.
- Der Valid-Filter stellt sicher, dass nachfolgende Schritte (Clustering) nur konsistente Daten verarbeiten.

Besonderheiten:

- Erwartete Feature-Form: (N, 2048) (ResNet50 + GlobalAvgPooling).
- Die Reihenfolge der valid_paths bleibt mit image_files konsistent (wichtig für spätere Zuordnungen).

- In-Memory: features (N×2048), valid_paths, bereinigtes image_files.
- Konsole: Laufzeit, Shape, Zählstatistik.

```
# Extract features using ResNet50
print("=" * 80)
print("FEATURE EXTRACTION")
print("=" * 80)

# Create feature extractor
feature_extractor = create_feature_extractor() # builds ResNet50
backbone

# Extract image paths
image_paths = [item['filepath'] for item in image_files] # preserve
```

```
order for alignment with features
# Extract features
start time = time.time()
features, valid paths = extract features batch(feature extractor,
image_paths) # batched inference
extraction time = time.time() - start time
print(f"\nFeature extraction completed in {extraction time:.2f}
seconds")
print(f"Extracted features shape: {features.shape}") # expect
(N valid, 2048)
print(f"Valid images: {len(valid paths)}/{len(image paths)}")
# Update image files to only include valid images
valid image files = []
for img file in image files:
   if img file['filepath'] in valid_paths: # keep only successfully
processed paths
       valid image files.append(img file)
image files = valid image files # downstream steps use the filtered
metadata list
print(f"Updated image files: {len(image files)}")
FEATURE EXTRACTION
______
Loading ResNet50 model...
WARNING: All log messages before absl::InitializeLog() is called are
written to STDERR
I0000 00:00:1757250402.789817 129943 cuda executor.cc:1015]
successful NUMA node read from SysFS had negative value (-1), but
there must be at least one NUMA node, so returning NUMA node zero. See
more at
https://github.com/torvalds/linux/blob/v6.0/Documentation/ABI/testing/
sysfs-bus-pci#L344-L355
I0000 00:00:1757250402.823497 129943 cuda executor.cc:1015
successful NUMA node read from SysFS had negative value (-1), but
there must be at least one NUMA node, so returning NUMA node zero. See
https://github.com/torvalds/linux/blob/v6.0/Documentation/ABI/testing/
sysfs-bus-pci#L344-L355
I0000 00:00:1757250402.843440 129943 cuda executor.cc:1015]
successful NUMA node read from SysFS had negative value (-1), but
there must be at least one NUMA node, so returning NUMA node zero. See
more at
```

```
https://github.com/torvalds/linux/blob/v6.0/Documentation/ABI/testing/
sysfs-bus-pci#L344-L355
I0000 00:00:1757250402.850191 129943 cuda executor.cc:1015]
successful NUMA node read from SysFS had negative value (-1), but
there must be at least one NUMA node, so returning NUMA node zero. See
https://github.com/torvalds/linux/blob/v6.0/Documentation/ABI/testing/
sysfs-bus-pci#L344-L355
I0000 00:00:1757250402.854495 129943 cuda executor.cc:1015]
successful NUMA node read from SysFS had negative value (-1), but
there must be at least one NUMA node, so returning NUMA node zero. See
https://github.com/torvalds/linux/blob/v6.0/Documentation/ABI/testing/
sysfs-bus-pci#L344-L355
I0000 00:00:1757250402.859837 129943 cuda executor.cc:1015]
successful NUMA node read from SysFS had negative value (-1), but
there must be at least one NUMA node, so returning NUMA node zero. See
more at
https://github.com/torvalds/linux/blob/v6.0/Documentation/ABI/testing/
sysfs-bus-pci#L344-L355
I0000 00:00:1757250403.002160 129943 cuda executor.cc:1015]
successful NUMA node read from SysFS had negative value (-1), but
there must be at least one NUMA node, so returning NUMA node zero. See
more at
https://github.com/torvalds/linux/blob/v6.0/Documentation/ABI/testing/
sysfs-bus-pci#L344-L355
I0000 00:00:1757250403.004022 129943 cuda executor.cc:1015]
successful NUMA node read from SysFS had negative value (-1), but
there must be at least one NUMA node, so returning NUMA node zero. See
more at
https://github.com/torvalds/linux/blob/v6.0/Documentation/ABI/testing/
sysfs-bus-pci#L344-L355
I0000 00:00:1757250403.005700 129943 cuda executor.cc:1015
successful NUMA node read from SysFS had negative value (-1), but
there must be at least one NUMA node, so returning NUMA node zero. See
more at
https://github.com/torvalds/linux/blob/v6.0/Documentation/ABI/testing/
sysfs-bus-pci#L344-L355
2025-09-07 15:06:43.007203: I
tensorflow/core/common runtime/gpu/gpu device.cc:2021] Created
device /job:localhost/replica:0/task:0/device:GPU:0 with 1302 MB
memory: -> device: 0, name: NVIDIA GeForce RTX 3070 Laptop GPU, pci
bus id: 0000:01:00.0, compute capability: 8.6
Feature extractor output shape: (None, 2048)
Extracting features from 10000 images...
WARNING: All log messages before absl::InitializeLog() is called are
written to STDERR
I0000 00:00:1757250405.988169 130039 service.cc:146] XLA service
```

0x7171c01498b0 initialized for platform CUDA (this does not guarantee
that XLA will be used). Devices:
I0000 00:00:1757250405.988191 130039 service.cc:154] StreamExecutor
device (0): NVIDIA GeForce RTX 3070 Laptop GPU, Compute Capability 8.6
2025-09-07 15:06:46.057031: I
tensorflow/compiler/mlir/tensorflow/utils/dump_mlir_util.cc:268]
disabling MLIR crash reproducer, set env var
`MLIR_CRASH_REPRODUCER_DIRECTORY` to enable.
2025-09-07 15:06:46.488177: I
external/local_xla/xla/stream_executor/cuda/cuda_dnn.cc:531] Loaded
cuDNN version 8907
I0000 00:00:1757250409.045439 130039 device_compiler.h:188] Compiled
cluster using XLA! This line is logged at most once for the lifetime
of the process.

Processed 320/10000 images Processed 640/10000 images Processed 960/10000 images Processed 1280/10000 images Processed 1600/10000 images Processed 1920/10000 images Processed 2240/10000 images Processed 2560/10000 images Processed 2880/10000 images Processed 3200/10000 images Processed 3520/10000 images Processed 3840/10000 images Processed 4160/10000 images Processed 4480/10000 images Processed 4800/10000 images Processed 5120/10000 images Processed 5440/10000 images Processed 5760/10000 images Processed 6080/10000 images Processed 6400/10000 images Processed 6720/10000 images Processed 7040/10000 images Processed 7360/10000 images Processed 7680/10000 images Processed 8000/10000 images Processed 8320/10000 images Processed 8640/10000 images Processed 8960/10000 images Processed 9280/10000 images Processed 9600/10000 images Processed 9920/10000 images

Feature extraction completed in 57.72 seconds Extracted features shape: (10000, 2048)

```
Valid images: 10000/10000
Updated image files: 10000
```

6. Feature-Nachbearbeitung (Normalisierung & PCA → Vorbereitung fürs Clustering)

Was:

- L2-Normierung der Embeddings (zeilenweise) und optionale PCA-Reduktion auf PCA COMPONENTS.
- Ausgeben von Kennzahlen vor/nach Normalisierung sowie erklärter Gesamtvarianz der PCA.

Warum:

- L2-Normierung macht Distanzen vergleichbar (≈ spherical K-Means) und stabilisiert Metriken.
- PCA reduziert Dimensionen, Rauschen und Rechenzeit. kann die Trennbarkeit für K-Means/DBSCAN verbessern.

Besonderheiten:

- PCA-Fit erfolgt auf normalisierten Features; random_state f
 ür Reproduzierbarkeit gesetzt.
- Default für das Clustering sind die **voll normalisierten** Features. PCA-Features optional testen/umschalten.

- features_normalized, features_pca
- Konsolen-Stats (vor/nach Normalisierung, PCA-Varianz, Shapes)

```
# Normalize features to unit length per sample (stabilizes distances
for K-Means/DBSCAN)
print("Normalizing features...")
features_normalized = normalize(features, norm='l2', axis=1)

# Basic sanity statistics before/after normalization
print(f"Original feature statistics:")
print(f" Mean: {features.mean():.4f}")
print(f" Std: {features.std():.4f}")
print(f" Min: {features.min():.4f}")
print(f" Max: {features.max():.4f}")

print(f"\nNormalized feature statistics:")
print(f" Mean: {features_normalized.mean():.4f}")
```

```
print(f" Std: {features normalized.std():.4f}")
print(f" L2 norm (first sample):
{np.linalg.norm(features normalized[0]):.4f}")
# Optional dimensionality reduction (denoising + speed-up for
clustering/TSNE)
print(f"\nApplying PCA to reduce dimensions from {FEATURE DIM} to
{PCA COMPONENTS}...")
pca = PCA(n_components=PCA_COMPONENTS, random_state=RANDOM_STATE)
features_pca = pca.fit_transform(features_normalized)
# Report explained variance (sum) and resulting shape
print(f"PCA explained variance ratio:
{pca.explained_variance_ratio_.sum():.4f}")
print(f"PCA features shape: {features pca.shape}")
Normalizing features...
Original feature statistics:
 Mean: 0.2479
 Std: 0.8876
 Min: 0.0000
 Max: 22.0882
Normalized feature statistics:
  Mean: 0.0059
 Std: 0.0213
  L2 norm (first sample): 1.0000
Applying PCA to reduce dimensions from 2048 to 50...
PCA explained variance ratio: 0.9154
PCA features shape: (10000, 50)
```

7. K-Means

7.1 K-Means: k-Sweep & Clusterbewertung (Inertia, Silhouette, Clustergrößen)

Was:

- k-Sweep: systematisches Durchtesten mehrerer Clusterzahlen k (z. B. 3–15), um anhand von Metriken (Silhouette/Inertia) das sinnvollste k zu wählen
- Systematischer k-Sweep über N_CLUSTERS_RANGE auf features_pca (standardmäßig MiniBatchKMeans).
- Für jedes k: Fit & Predict → Inertia, Silhouette-Score und Clustergrößen (min/max, Verteilung); Modell wird mitgespeichert.

Warum:

- Der k-Sweep liefert eine **datengetriebene Wahl** der Clusterzahl **Silhouette** bewertet Trennung/Kompaktheit (höher = besser), **Inertia** zeigt den "Elbow" (abnehmender Grenznutzen).
- **MiniBatchKMeans** skaliert besser auf größere N, ist für Embeddings meist ausreichend präzise.

Besonderheiten:

n init=10 reduziert die Chance auf schlechte lokale Minima.

- kmeans_results: Liste von Dicts {k, inertia, silhouette_score, min_cluster_size, max_cluster_size, cluster_sizes, model}
- Konsolen-Logs pro k (Inertia, Silhouette)

```
def evaluate kmeans clusters(features, k range, use minibatch=True):
    # Assumes features are L2-normalized for stable distance geometry
(spherical k-means behavior).
    # Computes inertia, silhouette, and size diagnostics per k. stores
the fitted model for later reuse.
    """Evaluate K-Means clustering for different k values."""
    results = []
    print(f"Evaluating K-Means for k in {list(k range)}...")
    for k in k_range:
        print(\overline{f}" Testing k=\{k\}...")
        # Use MiniBatchKMeans for efficiency with large datasets
        if use minibatch:
            kmeans = MiniBatchKMeans(
                n clusters=k,
                random state=RANDOM STATE,
                batch size=100,
                n init=10
        else:
            kmeans = KMeans(
                n clusters=k,
                random state=RANDOM STATE,
                n init=10
            )
        # Fit and predict
        cluster labels = kmeans.fit predict(features)
        # Calculate metrics
        inertia = kmeans.inertia
        silhouette avg = silhouette score(features, cluster labels)
```

```
# Cluster sizes
       cluster_sizes = Counter(cluster_labels)
       min cluster size = min(cluster sizes.values())
       max cluster size = max(cluster sizes.values())
       results.append({
           'k': k,
           'inertia': inertia,
           'silhouette score': silhouette avg,
           'min_cluster_size': min cluster size,
           'max_cluster_size': max_cluster_size,
           'cluster sizes': dict(cluster sizes),
           'model': kmeans
       })
       print(f" Inertia: {inertia:.2f}, Silhouette:
{silhouette_avg:.4f}")
   return results
# Evaluate K-Means clustering
print("=" * 80)
print("K-MEANS CLUSTERING EVALUATION")
print("=" * 80)
# Runs the k-sweep and collects metrics/models per k
kmeans results = evaluate kmeans clusters(features pca,
N_CLUSTERS_RANGE)
______
K-MEANS CLUSTERING EVALUATION
______
Evaluating K-Means for k in [3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14,
15]...
 Testing k=3...
   Inertia: 1568.23, Silhouette: 0.3852
 Testing k=4...
   Inertia: 1353.45, Silhouette: 0.3997
 Testing k=5...
   Inertia: 1276.90, Silhouette: 0.3439
 Testing k=6...
   Inertia: 1068.08, Silhouette: 0.4285
 Testing k=7...
   Inertia: 1046.21, Silhouette: 0.3492
 Testing k=8...
   Inertia: 953.05, Silhouette: 0.3791
 Testing k=9...
```

```
Inertia: 909.24, Silhouette: 0.3696
Testing k=10...
    Inertia: 855.68, Silhouette: 0.3423
Testing k=11...
    Inertia: 848.12, Silhouette: 0.3061
Testing k=12...
    Inertia: 807.52, Silhouette: 0.3383
Testing k=13...
    Inertia: 793.73, Silhouette: 0.3650
Testing k=14...
    Inertia: 785.57, Silhouette: 0.3083
Testing k=15...
    Inertia: 763.51, Silhouette: 0.3358
```

7.2 K-Means Evaluation visualisieren & k bestimmen

Was:

- 2×2-Dashboard: Elbow (Inertia), Silhouette, Clustergrößen (min/max), kombinierte Metriken.
- Bestimmung von optimal k über das Maximum des Silhouette-Scores.

Warum:

- Inertia zeigt den "Knick" (abnehmender Grenznutzen), Silhouette misst Trennung & Kompaktheit.
- **Kombination** (1–normierte Inertia & normierte Silhouette) hilft, widersprüchliche Signale zu balancieren.

Besonderheiten:

- 1 norm inertias sorgt für gleiche Zielfunktion ("höher ist besser").

Outputs:

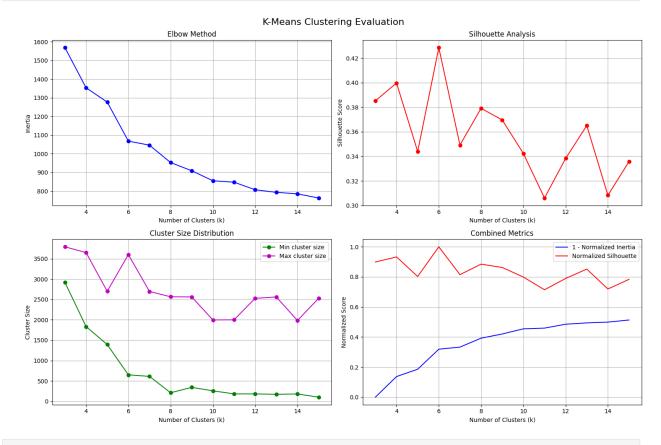
• Plot kmeans evaluation.png, optimal k, bester Silhouette-Wert.

```
# --- Visualization of k-sweep metrics & selection of k* ---
# Plot K-Means evaluation results
fig, axes = plt.subplots(2, 2, figsize=(15, 10))
fig.suptitle('K-Means Clustering Evaluation', fontsize=16)

# Extract data for plotting (one value per tested k)
k_values = [r['k'] for r in kmeans_results]
inertias = [r['inertia'] for r in kmeans_results]
silhouette_scores = [r['silhouette_score'] for r in kmeans_results]
```

```
min_cluster_sizes = [r['min_cluster_size'] for r in kmeans_results]
max cluster sizes = [r['max cluster size'] for r in kmeans results]
# --- Elbow plot (Inertia vs k): look for the knee / diminishing
returns ---
axes[0, 0].plot(k values, inertias, 'bo-')
axes[0, 0].set xlabel('Number of Clusters (k)')
axes[0, 0].set ylabel('Inertia')
axes[0, 0].set_title('Elbow Method')
axes[0, 0].grid(True)
# --- Silhouette score vs k: pick the maximum as primary criterion ---
axes[0, 1].plot(k values, silhouette scores, 'ro-')
axes[0, 1].set xlabel('Number of Clusters (k)')
axes[0, 1].set ylabel('Silhouette Score')
axes[0, 1].set_title('Silhouette Analysis')
axes[0, 1].grid(True)
# --- Cluster size diagnostics: min/max sizes vs k (imbalances, tiny
clusters) ---
axes[1, 0].plot(k values, min cluster sizes, 'go-', label='Min cluster
size')
axes[1, 0].plot(k_values, max_cluster_sizes, 'mo-', label='Max cluster
axes[1, 0].set xlabel('Number of Clusters (k)')
axes[1, 0].set ylabel('Cluster Size')
axes[1, 0].set title('Cluster Size Distribution')
axes[1, 0].legend()
axes[1, 0].grid(True)
# --- Combined metrics (normalized): align direction to "higher is
better" ---
                                                        # scale
norm inertias = np.array(inertias) / max(inertias)
to [0,1]
norm silhouettes = np.array(silhouette scores) /
max(silhouette scores) # scale to [0,1]
axes[1, 1].plot(k values, 1 - norm inertias, 'b-', label='1 -
Normalized Inertia')
axes[1, 1].plot(k values, norm silhouettes, 'r-', label='Normalized
Silhouette')
axes[1, 1].set xlabel('Number of Clusters (k)')
axes[1, 1].set ylabel('Normalized Score')
axes[1, 1].set title('Combined Metrics')
axes[1, 1].legend()
axes[1, 1].grid(True)
plt.tight layout()
plt.savefig(f"{RESULTS PATH}/kmeans evaluation.png", dpi=300,
bbox inches='tight')
plt.show()
```

```
# --- Select optimal k by maximum silhouette (primary criterion) ---
best_silhouette_idx = np.argmax(silhouette_scores)
optimal_k = k_values[best_silhouette_idx]
print(f"\nOptimal k based on silhouette score: {optimal_k}")
print(f"Best silhouette score:
{silhouette_scores[best_silhouette_idx]:.4f}")
```



Optimal k based on silhouette score: 6 Best silhouette score: 0.4285

7.3 Finales K-Means mit optimalem k & Clusteranalyse

Was:

- Finales Fitting von MiniBatchKMeans mit k=optimal_k.
- Anreicherung von image_files um das Feld cluster.
- Aggregation einer Clusterübersicht inkl. Tenant-Verteilung je Cluster.

Warum:

- Nach dem k-Sweep wird das beste k produktiv angewendet. Die resultierenden Labels bilden die Basis für Analyse, Export und Visualisierung.
- Tenant-Verteilungen helfen, **Bias/Imbalance** zu erkennen und Cluster zu interpretieren.

Besonderheiten:

- n init=20 senkt das Risiko schlechter lokaler Minima im finalen Fit.
- Die Reihenfolge von image_files muss den cluster_labels entsprechen (hier gegeben).
- Prozentanteile werden je Cluster relativ zu dessen Größe berechnet.

- In-Memory: cluster labels, angereichertes image files (mit cluster).
- Konsole: Größe je Cluster und Tenant-Rangfolge pro Cluster.

```
# Runs MiniBatchKMeans once more with stronger n init and assigns
labels to all samples
print(f"\nPerforming final K-Means clustering with k={optimal k}...")
final kmeans = MiniBatchKMeans(
    n clusters=optimal k,
    random state=RANDOM STATE,
    batch size=100,
    n_init=20 # More initializations for final model
cluster labels = final kmeans.fit predict(features pca)
# Enrich metadata: attach the integer cluster label to each image file
entry
for i, img file in enumerate(image files):
    img file['cluster'] = int(cluster labels[i])
# Cluster composition analysis (counts per cluster and tenant
distribution)
print(f"\nCluster Analysis:")
cluster stats = defaultdict(lambda: defaultdict(int))
for img file in image files:
    cluster = img file['cluster']
    tenant = img file['tenant']
    cluster_stats[cluster]['total'] += 1
    cluster stats[cluster][tenant] += 1
# Human-readable report per cluster (size + tenant ranking)
for cluster id in sorted(cluster stats.keys()):
```

```
stats = cluster_stats[cluster_id]
    total = stats['total']
    print(f"\nCluster {cluster_id}: {total} images")
    # Show tenant distribution in this cluster
    tenant counts = {k: v for k, v in stats.items() if k != 'total'}
    for tenant, count in sorted(tenant counts.items(), key=lambda x:
x[1], reverse=True):
        percentage = (count / total) * 100
        print(f" {tenant}: {count} ({percentage:.1f}%)")
Performing final K-Means clustering with k=6...
Cluster Analysis:
Cluster 0: 944 images
  cts: 528 (55.9%)
  gent: 250 (26.5%)
  bernmobil: 78 (8.3%)
  gvb: 56 (5.9%)
  vbz: 22 (2.3%)
  retm: 10 (1.1%)
Cluster 1: 3571 images
  bernmobil: 1105 (30.9%)
  gvb: 857 (24.0%)
  gent: 724 (20.3%)
  vbz: 561 (15.7%)
  cts: 241 (6.7%)
  retm: 43 (1.2%)
  bvb: 20 (0.6%)
 ava: 20 (0.6%)
Cluster 2: 2562 images
  bvb: 1226 (47.9%)
  vbz: 627 (24.5%)
  ava: 578 (22.6%)
  gvb: 122 (4.8%)
  retm: 9 (0.4%)
Cluster 3: 1345 images
  ava: 650 (48.3%)
  retm: 606 (45.1%)
  gvb: 28 (2.1%)
  bernmobil: 27 (2.0%)
  gent: 21 (1.6%)
  cts: 8 (0.6%)
  vbz: 5 (0.4%)
```

```
Cluster 4: 650 images
  retm: 548 (84.3%)
  gvb: 65 (10.0%)
  vbz: 23 (3.5%)
  cts: 9 (1.4%)
  bvb: 3 (0.5%)
  gent: 1 (0.2%)
  ava: 1 (0.2%)
Cluster 5: 928 images
  cts: 464 (50.0%)
  gent: 254 (27.4%)
  qvb: 122 (13.1%)
  bernmobil: 40 (4.3%)
  retm: 34 (3.7%)
  vbz: 12 (1.3%)
  bvb: 1 (0.1%)
  ava: 1 (0.1%)
```

7.4 K-Means-Clusterbeispiele: Visualisierung von Beispielbildern

Was:

- Zeigt pro Cluster eine Stichprobe zufälliger Bilder in einem Bildgrid (3 Spalten, mehrere Zeilen).
- Nutzt die finalen K-Means-Labels (image_files[i]['cluster']) als Grundlage.

Warum:

• Schnelle, visuelle Qualitätsprüfung der Clusterinhalte (Plausibilität, Ausreißer, Muster).

Besonderheiten:

- Zufallsstichprobe ≠ "repräsentativste" Beispiele.
- Fehlerhafte oder fehlende Dateien werden textuell im Grid gekennzeichnet.
- Ergebnisse werden als cluster <id> examples.png gespeichert.

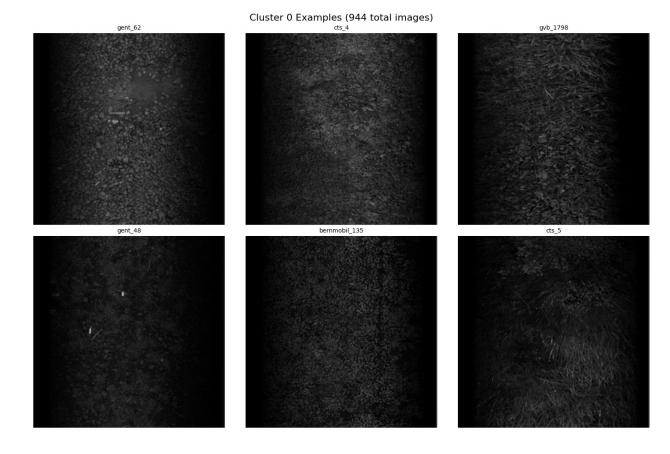
Outputs:

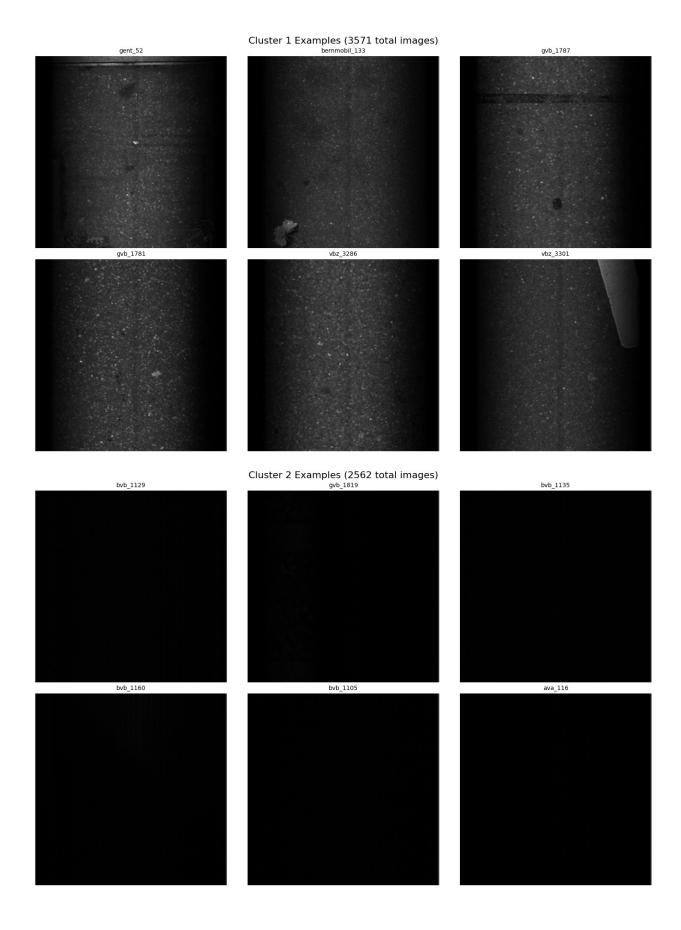
PNG-Bildtafeln je Cluster unter RESULTS_PATH, Konsolenlogs.

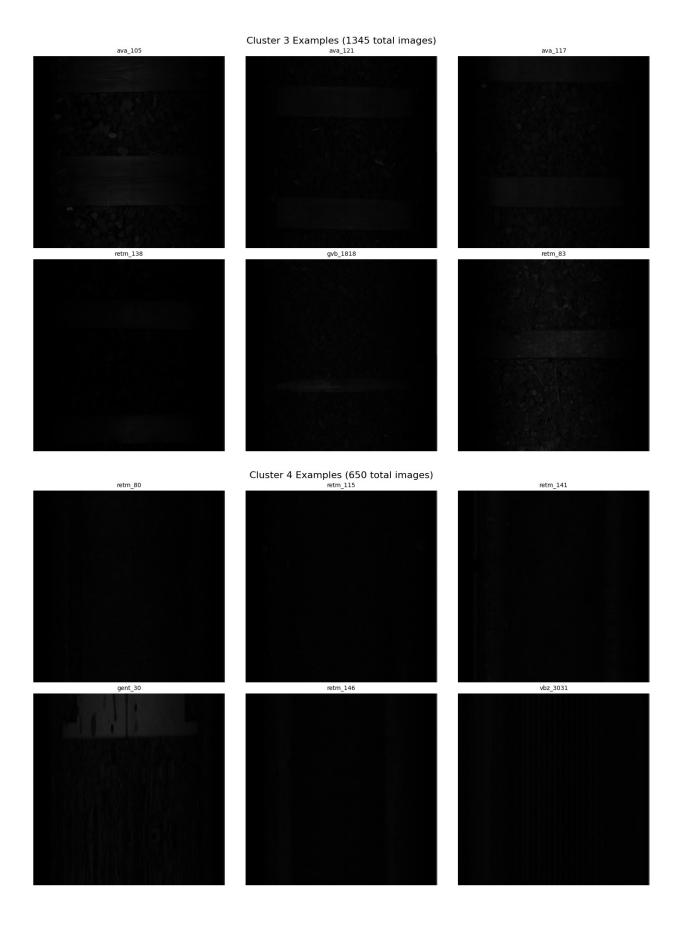
```
def display_cluster_examples(image_files, cluster_id, n_examples=6):
    """Display example images from a specific cluster."""
    # Collect all images that belong to the requested cluster
    cluster_images = [img for img in image_files if img['cluster'] ==
cluster_id]

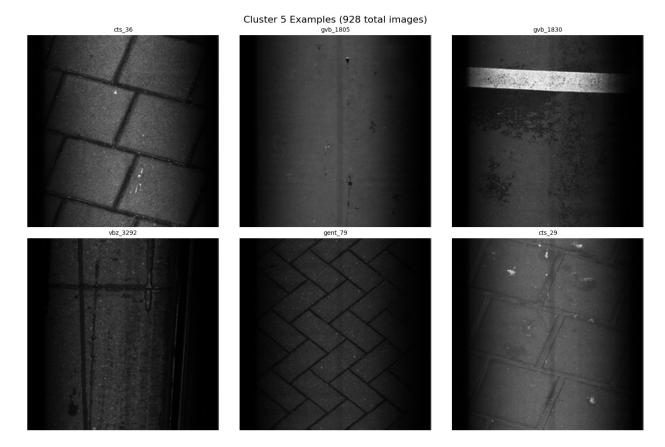
if not cluster_images:
    print(f"No images found for cluster {cluster_id}")
```

```
return
    # Randomly sample examples (set np.random.seed(...) earlier for
reproducibility)
    examples = np.random.choice(cluster images, min(n examples,
len(cluster images)), replace=False)
    # Create subplot grid (3 columns; rows computed from sample size)
    cols = 3
    rows = (len(examples) + cols - 1) // cols
    fig, axes = plt.subplots(rows, cols, figsize=(15, 5 * rows))
    if rows == 1:
        axes = axes.reshape(1, -1)
    fig.suptitle(f'Cluster {cluster id} Examples
({len(cluster images)} total images)', fontsize=16)
    for i, img_info in enumerate(examples):
        row = i // cols
        col = i % cols
        # Load and display image; on failure, render a textual
placeholder
        try:
            img = Image.open(img info['filepath'])
            axes[row, coll.imshow(img)
            axes[row,
col].set title(f"{img info['tenant']} {img info['sid']}", fontsize=10)
            axes[row, col].axis('off')
        except Exception as e:
            axes[row, col].text(0.5, 0.5, f"Error loading\
n{img_info['filename']}",
                               ha='center', va='center',
transform=axes[row, col].transAxes)
            axes[row, col].axis('off')
    # Hide any empty subplot cells (if sample size not divisible by
#cols)
    for i in range(len(examples), rows * cols):
        row = i // cols
        col = i % cols
        axes[row, col].axis('off')
    plt.tight layout()
    # Save a PNG panel per cluster to RESULTS PATH
    plt.savefig(f"{RESULTS PATH}/cluster_{cluster_id}_examples.png",
dpi=300, bbox inches='tight')
    plt.show()
```









8. DBSCAN

8.1 DBSCAN: Parameter-Grid, Heatmaps & Best-Selection

Was:

- Dichte-basiertes Clustering auf PCA-Features mit einem Grid aus eps × min_samples.
- Pro Kombination: Fit/Predict, Metriken (Cluster ohne Noise, Noise-Quote, Silhouette ohne Noise) und anschließende **3 Heatmaps**.
- Auswahl des "besten" Settings per Silhouette und Balanced Score silhouette * (1 noise ratio) (robuster).

Warum:

- DBSCAN ist empfindlich gegenüber eps/min_samples. ein Grid liefert eine datengetriebene Auswahl.
- Balanced Score verhindert triviale Lösungen mit hoher Silhouette aber extremer Noise-Quote.

Besonderheiten:

- Silhouette wird nur berechnet, wenn >1 Cluster vorhanden; **Noise (-1)** wird bei Silhouette ausgeschlossen.
- Für Heatmaps werden negative Silhouetten als **0** visualisiert (bessere Lesbarkeit).
- Bei sehr hoher Noise-Quote: Parameterbereich erweitern oder **PCA-Komponenten** anpassen; optional **k-Distance-Plot** bzw. **HDBSCAN** prüfen.

Outputs:

• dbscan_parameter_optimization.png (Heatmaps), Konsolen-Log der besten Parameter, Objekt best_dbscan.

```
# DBSCAN Clustering
print("=" * 80)
print("DBSCAN CLUSTERING")
print("=" * 80)
# Use PCA features for DBSCAN (better performance in lower dimensions)
print("Applying DBSCAN on PCA-reduced features...")
# Create a grid of parameters to test
eps_values = [0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.2, 1.5]
min samples values = [3, 5, 7, 10, 15, 20]
print("\nTesting parameter combinations:")
print(f"eps values: {eps values}")
print(f"min samples values: {min samples values}")
print(f"Total combinations to test: {len(eps_values) *
len(min samples values)}")
dbscan results = []
# Test all combinations
for eps in eps values:
    for min samples in min samples values:
        print(f"\nTesting DBSCAN with eps={eps},
min samples={min samples}...")
        dbscan = DBSCAN(eps=eps, min samples=min samples) # density
params: neighborhood radius & min points
        dbscan labels = dbscan.fit predict(features pca) # run on
PCA-reduced features
        # Count clusters and noise points
        n clusters = len(set(dbscan labels)) - (1 if -1 in
dbscan labels else 0) # exclude noise from cluster count
        n noise = list(dbscan labels).count(-1)
        # Calculate silhouette score (only if we have more than 1
cluster)
```

```
if n clusters > 1:
            # Filter out noise points for silhouette calculation
            mask = dbscan labels != -1
            if mask.sum() > 1: # Need at least 2 points
                silhouette avg = silhouette score(features pca[mask],
dbscan labels[mask])
                silhouette avg = -1
        else:
            silhouette avg = -1
        result = {
            'eps': eps,
            'min samples': min samples,
            'n_clusters': n_clusters,
            'n noise': n noise,
            'noise ratio': n noise / len(dbscan labels),
            'silhouette_score': silhouette_avg,
            'labels': dbscan labels
        dbscan results.append(result)
        print(f" Clusters: {n clusters}")
        print(f" Noise points: {n noise}
({result['noise ratio']*100:.1f}%)")
        print(f" Silhouette: {silhouette avg:.4f}")
# Create results visualization
plt.figure(figsize=(15, 10))
# Create a matrix of results
eps_grid, min_samples_grid = np.meshgrid(eps values,
min samples values)
n_clusters_grid = np.zeros_like(eps_grid, dtype=float)
silhouette grid = np.zeros like(eps grid, dtype=float)
noise ratio grid = np.zeros like(eps grid, dtype=float)
# Fill heatmap matrices with metrics per (eps, min samples)
for result in dbscan results:
    i = min samples values.index(result['min samples'])
    j = eps values.index(result['eps'])
    n_clusters_grid[i, j] = result['n_clusters']
    silhouette grid[i, j] = max(result['silhouette score'], 0) #
Replace negative scores with 0 (visual clarity)
    noise ratio grid[i, j] = result['noise ratio']
# Plot number of clusters
plt.subplot(221)
plt.imshow(n clusters grid, aspect='auto', interpolation='nearest')
plt.colorbar(label='Number of Clusters')
```

```
plt.vlabel('min samples')
plt.xlabel('eps')
plt.title('Number of Clusters')
plt.xticks(range(len(eps values)), [f'{x:.1f}' for x in eps values],
rotation=45)
plt.yticks(range(len(min samples values)), min samples values)
# Plot silhouette scores
plt.subplot(222)
plt.imshow(silhouette grid, aspect='auto', interpolation='nearest')
plt.colorbar(label='Silhouette Score')
plt.ylabel('min samples')
plt.xlabel('eps')
plt.title('Silhouette Score')
plt.xticks(range(len(eps values)), [f'{x:.1f}' for x in eps values],
rotation=45)
plt.yticks(range(len(min samples values)), min samples values)
# Plot noise ratio
plt.subplot(223)
plt.imshow(noise ratio grid, aspect='auto', interpolation='nearest')
plt.colorbar(label='Noise Ratio')
plt.ylabel('min samples')
plt.xlabel('eps')
plt.title('Noise Ratio')
plt.xticks(range(len(eps values)), [f'{x:.1f}' for x in eps values],
plt.yticks(range(len(min samples values)), min samples values)
# Find best results
valid results = [r for r in dbscan results if r['silhouette score'] >
if valid results:
    # Sort by different metrics
    best silhouette = max(valid results, key=lambda x:
x['silhouette score']) # highest quality by silhouette
    balanced score = \max(valid results, key=lambda x:
x['silhouette score'] * (1 - x['noise ratio'])) # quality vs. noise
trade-off
    print("\nBest results:")
    print("\nBest by silhouette score:")
    print(f"eps={best silhouette['eps']},
min samples={best silhouette['min samples']}")
    print(f"Clusters: {best silhouette['n clusters']}")
    print(f"Noise points: {best silhouette['n noise']}
({best silhouette['noise ratio']*100:.1f}%)")
    print(f"Silhouette: {best silhouette['silhouette score']:.4f}")
    print("\nBest balanced (silhouette * (1 - noise ratio)):")
```

```
print(f"eps={balanced score['eps']},
min samples={balanced score['min samples']}")
    print(f"Clusters: {balanced_score['n_clusters']}")
    print(f"Noise points: {balanced score['n noise']}
({balanced score['noise ratio']*100:.1f}%)")
    print(f"Silhouette: {balanced score['silhouette score']:.4f}")
    # Use balanced score as best result (more robust in practice)
    best dbscan = balanced score
else:
    print("\nNo valid DBSCAN results found. Consider adjusting
parameters.")
    best dbscan = dbscan results[0] # Use first result as fallback
plt.tight layout()
plt.savefig(f"{RESULTS_PATH}/dbscan_parameter_optimization.png",
dpi=300, bbox inches='tight')
plt.show()
DBSCAN CLUSTERING
Applying DBSCAN on PCA-reduced features...
Testing parameter combinations:
eps values: [0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.2, 1.5]
min samples values: [3, 5, 7, 10, 15, 20]
Total combinations to test: 66
Testing DBSCAN with eps=0.2, min samples=3...
  Clusters: 60
  Noise points: 1827 (18.3%)
  Silhouette: 0.0045
Testing DBSCAN with eps=0.2, min samples=5...
  Clusters: 32
  Noise points: 2083 (20.8%)
  Silhouette: 0.1553
Testing DBSCAN with eps=0.2, min samples=7...
  Clusters: 28
  Noise points: 2333 (23.3%)
 Silhouette: 0.1114
Testing DBSCAN with eps=0.2, min samples=10...
  Clusters: 14
 Noise points: 2697 (27.0%)
  Silhouette: 0.2687
```

```
Testing DBSCAN with eps=0.2, min samples=15...
  Clusters: 12
 Noise points: 3096 (31.0%)
  Silhouette: 0.4528
Testing DBSCAN with eps=0.2, min samples=20...
  Clusters: 11
 Noise points: 3363 (33.6%)
 Silhouette: 0.4503
Testing DBSCAN with eps=0.3, min samples=3...
  Clusters: 23
 Noise points: 408 (4.1%)
  Silhouette: -0.1241
Testing DBSCAN with eps=0.3, min_samples=5...
  Clusters: 14
  Noise points: 521 (5.2%)
  Silhouette: -0.0639
Testing DBSCAN with eps=0.3, min samples=7...
  Clusters: 11
  Noise points: 602 (6.0%)
  Silhouette: -0.0738
Testing DBSCAN with eps=0.3, min samples=10...
  Clusters: 7
  Noise points: 699 (7.0%)
 Silhouette: 0.0164
Testing DBSCAN with eps=0.3, min_samples=15...
  Clusters: 4
 Noise points: 799 (8.0%)
 Silhouette: 0.1927
Testing DBSCAN with eps=0.3, min_samples=20...
  Clusters: 4
  Noise points: 878 (8.8%)
  Silhouette: 0.1968
Testing DBSCAN with eps=0.4, min_samples=3...
  Clusters: 3
  Noise points: 43 (0.4%)
  Silhouette: 0.1285
Testing DBSCAN with eps=0.4, min samples=5...
  Clusters: 3
 Noise points: 57 (0.6%)
  Silhouette: 0.1115
```

```
Testing DBSCAN with eps=0.4, min samples=7...
  Clusters: 3
 Noise points: 69 (0.7%)
 Silhouette: 0.1205
Testing DBSCAN with eps=0.4, min samples=10...
  Clusters: 2
 Noise points: 121 (1.2%)
 Silhouette: 0.1670
Testing DBSCAN with eps=0.4, min samples=15...
  Clusters: 2
 Noise points: 162 (1.6%)
 Silhouette: 0.2828
Testing DBSCAN with eps=0.4, min samples=20...
  Clusters: 2
  Noise points: 180 (1.8%)
  Silhouette: 0.2834
Testing DBSCAN with eps=0.5, min samples=3...
  Clusters: 2
  Noise points: 3 (0.0%)
  Silhouette: 0.1845
Testing DBSCAN with eps=0.5, min samples=5...
  Clusters: 1
  Noise points: 7 (0.1%)
 Silhouette: -1.0000
Testing DBSCAN with eps=0.5, min samples=7...
  Clusters: 1
 Noise points: 7 (0.1%)
 Silhouette: -1.0000
Testing DBSCAN with eps=0.5, min samples=10...
  Clusters: 1
 Noise points: 7 (0.1\%)
  Silhouette: -1.0000
Testing DBSCAN with eps=0.5, min_samples=15...
  Clusters: 1
  Noise points: 7 (0.1\%)
  Silhouette: -1.0000
Testing DBSCAN with eps=0.5, min samples=20...
  Clusters: 1
 Noise points: 14 (0.1%)
  Silhouette: -1.0000
```

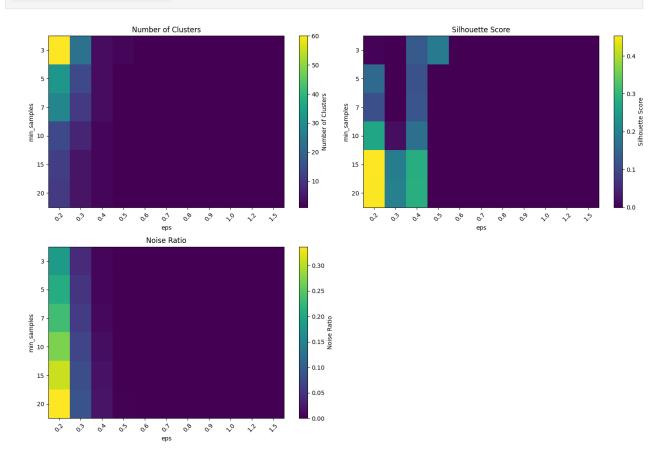
```
Testing DBSCAN with eps=0.6, min samples=3...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=0.6, min samples=5...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=0.6, min samples=7...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=0.6, min samples=10...
  Clusters: 1
  Noise points: 1 (0.0%)
  Silhouette: -1.0000
Testing DBSCAN with eps=0.6, min samples=15...
  Clusters: 1
  Noise points: 1 (0.0%)
  Silhouette: -1.0000
Testing DBSCAN with eps=0.6, min samples=20...
  Clusters: 1
 Noise points: 1 (0.0\%)
 Silhouette: -1.0000
Testing DBSCAN with eps=0.7, min samples=3...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=0.7, min samples=5...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=0.7, min_samples=7...
  Clusters: 1
  Noise points: 0 (0.0\%)
  Silhouette: -1.0000
Testing DBSCAN with eps=0.7, min samples=10...
  Clusters: 1
 Noise points: 0 (0.0%)
  Silhouette: -1.0000
```

```
Testing DBSCAN with eps=0.7, min samples=15...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=0.7, min samples=20...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=0.8, min samples=3...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=0.8, min samples=5...
  Clusters: 1
  Noise points: 0 (0.0\%)
  Silhouette: -1.0000
Testing DBSCAN with eps=0.8, min samples=7...
  Clusters: 1
  Noise points: 0 (0.0\%)
  Silhouette: -1.0000
Testing DBSCAN with eps=0.8, min samples=10...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=0.8, min samples=15...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=0.8, min samples=20...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=0.9, min_samples=3...
  Clusters: 1
  Noise points: 0 (0.0\%)
  Silhouette: -1.0000
Testing DBSCAN with eps=0.9, min samples=5...
  Clusters: 1
 Noise points: 0 (0.0%)
  Silhouette: -1.0000
```

```
Testing DBSCAN with eps=0.9, min samples=7...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=0.9, min samples=10...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=0.9, min samples=15...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=0.9, min samples=20...
  Clusters: 1
  Noise points: 0 (0.0\%)
  Silhouette: -1.0000
Testing DBSCAN with eps=1.0, min samples=3...
  Clusters: 1
  Noise points: 0 (0.0\%)
 Silhouette: -1.0000
Testing DBSCAN with eps=1.0, min samples=5...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=1.0, min samples=7...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=1.0, min samples=10...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=1.0, min_samples=15...
  Clusters: 1
  Noise points: 0 (0.0\%)
  Silhouette: -1.0000
Testing DBSCAN with eps=1.0, min samples=20...
  Clusters: 1
 Noise points: 0 (0.0%)
  Silhouette: -1.0000
```

```
Testing DBSCAN with eps=1.2, min samples=3...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=1.2, min samples=5...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=1.2, min samples=7...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=1.2, min samples=10...
  Clusters: 1
  Noise points: 0 (0.0\%)
  Silhouette: -1.0000
Testing DBSCAN with eps=1.2, min samples=15...
  Clusters: 1
  Noise points: 0 (0.0\%)
 Silhouette: -1.0000
Testing DBSCAN with eps=1.2, min samples=20...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=1.5, min samples=3...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=1.5, min samples=5...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Testing DBSCAN with eps=1.5, min_samples=7...
  Clusters: 1
  Noise points: 0 (0.0\%)
  Silhouette: -1.0000
Testing DBSCAN with eps=1.5, min samples=10...
  Clusters: 1
 Noise points: 0 (0.0%)
  Silhouette: -1.0000
```

```
Testing DBSCAN with eps=1.5, min samples=15...
  Clusters: 1
 Noise points: 0 (0.0%)
  Silhouette: -1.0000
Testing DBSCAN with eps=1.5, min_samples=20...
  Clusters: 1
 Noise points: 0 (0.0%)
 Silhouette: -1.0000
Best results:
Best by silhouette score:
eps=0.2, min_samples=15
Clusters: 12
Noise points: 3096 (31.0%)
Silhouette: 0.4528
Best balanced (silhouette * (1 - noise_ratio)):
eps=0.2, min_samples=15
Clusters: 12
Noise points: 3096 (31.0%)
Silhouette: 0.4528
```



9. Reporting und Visualisierung

9.1 Visualisierung: K-Means & DBSCAN (Side-by-Side) mit t-SNE

Was:

- berechnet ein 2D-t-SNE auf den PCA-Features (features_pca) mit stabilen Parametern (init='pca', learning rate='auto', dynamische Perplexity)
- Erstellt Side-by-Side-Visualisierung der K-Means- und DBSCAN-Zuordnungen in separaten Panels
- Verwendet diskrete Farbkarten mit **BoundaryNorm** für saubere Cluster-Trennung und eindeutige Legendenbeschriftung

Warum:

- t-SNE wird genutzt, um die 50D-PCA-Features auf 2D zu reduzieren f
 ür eine intuitive Visualisierung der Cluster-Struktur
- Side-by-Side Vergleich ermöglicht direkten Vergleich der beiden Methoden
- stabile Parameter ermöglichen reproduzierbare Layouts für Vergleichbarkeit

Besonderheiten:

• Noise-Behandlung bei DBSCAN: Noise-Punkte (-1) werden explizit in grau dargestellt, reguläre Cluster erhalten tab10-Farben

- Side-by-Side Plot mit t-SNE-Projektion beider Cluster
- Erstellung der Datei clustering_tsne_visualization_fixed.png, die den Plot enthält

```
# Visualize clustering results with t-SNE (Fixed Colors & Legends)
print("=" * 80)
print("CLUSTER VISUALIZATION WITH t-SNE (IMPROVED)")
print("=" * 80)
print("Computing t-SNE embedding with stable parameters...")
N = len(features pca)
# Use stable t-SNE parameters for reproducible and better results
tsne = TSNE(
    n components=2,
    init='pca', # PCA initialization for better stability
    learning rate='auto', # Adaptive learning rate
    perplexity=min(50, max(5, int(N * 0.01))), # Dynamic perplexity
based on sample size
    max iter=1500, # More iterations for convergence
    random state=RANDOM STATE,
    metric='euclidean',
    early exaggeration=12.0
)
```

```
tsne features = tsne.fit transform(features pca)
print(f"t-SNE completed with perplexity={tsne.perplexity}")
# Create visualization with fixed discrete colors
fig, axes = plt.subplots(1, 2, figsize=(20, 8))
# === K-MEANS PLOT WITH DISCRETE COLORS ===
# Remap K-Means labels to 0..C-1 for consistent coloring
unique kmeans = sorted(set(cluster labels))
kmeans label map = {old: new for new, old in enumerate(unique kmeans)}
kmeans colors = np.array([kmeans label map[label] for label in
cluster labels])
# Create discrete colormap for K-Means
n kmeans clusters = len(unique kmeans)
kmeans cmap =
matplotlib.colors.ListedColormap(plt.cm.tab10(np.linspace(0, 1,
n kmeans clusters)))
kmeans norm = matplotlib.colors.BoundaryNorm(
    boundaries=np.arange(-0.5, n kmeans clusters, 1),
    ncolors=n kmeans clusters
)
scatter1 = axes[0].scatter(
    tsne features[:, 0],
    tsne features[:, 1],
    c=kmeans colors,
    cmap=kmeans cmap,
    norm=kmeans norm,
    alpha=0.7,
    s = 50
axes[0].set title(f'K-Means Clustering (k={optimal k})\nt-SNE
Visualization')
axes[0].set xlabel('t-SNE Component 1')
axes[0].set_ylabel('t-SNE Component 2')
# Discrete colorbar for K-Means
cbar1 = plt.colorbar(scatter1, ax=axes[0],
ticks=range(n kmeans clusters))
cbar1.set ticklabels([f'Cluster {unique kmeans[i]}' for i in
range(n kmeans clusters)])
cbar1.set label('K-Means Clusters')
# === DBSCAN PLOT WITH NOISE IN GREY ===
dbscan colors = best dbscan['labels'].copy()
unique dbscan = sorted(set(dbscan colors))
n dbscan clusters = len(unique dbscan) - (1 if -1 in unique dbscan)
else 0)
```

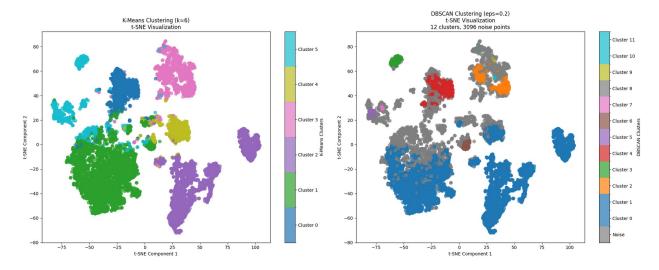
```
# Create color mapping: noise (-1) -> 0 (grey), clusters -> 1,2,3...
if -1 in unique dbscan:
    # Noise gets grey, clusters get tab10 colors
    colors = ['#808080'] # Grev for noise
    colors.extend(plt.cm.tab10(np.linspace(0, 1, n dbscan clusters)))
    # Map -1 to 0, others to 1,2,3...
    dbscan label map = \{-1: 0\}
    cluster idx = 1
    for label in unique dbscan:
        if label != -1:
            dbscan label map[label] = cluster idx
            cluster idx += 1
    total colors = \overline{len}(unique dbscan)
else:
    # No noise, just use tab10 for all clusters
    colors = plt.cm.tab10(np.linspace(0, 1, n dbscan clusters))
    dbscan_label_map = {label: idx for idx, label in
enumerate(unique dbscan)}
    total colors = n dbscan clusters
dbscan colors mapped = np.array([dbscan label map[label] for label in
dbscan colors])
# Create discrete colormap for DBSCAN
dbscan cmap = matplotlib.colors.ListedColormap(colors)
dbscan_norm = matplotlib.colors.BoundaryNorm(
    boundaries=np.arange(-0.5, total colors, 1),
    ncolors=total colors
)
scatter2 = axes[1].scatter(
    tsne features[:, 0],
    tsne features[:, 1],
    c=dbscan colors mapped,
    cmap=dbscan cmap,
    norm=dbscan norm,
    alpha=0.7,
    s = 50
)
axes[1].set title(f'DBSCAN Clustering (eps={best dbscan["eps"]})\nt-
SNE Visualization\n{n dbscan clusters} clusters,
{best dbscan["n noise"]} noise points')
axes[1].set xlabel('t-SNE Component 1')
axes[1].set ylabel('t-SNE Component 2')
# Discrete colorbar for DBSCAN
cbar2 = plt.colorbar(scatter2, ax=axes[1], ticks=range(total colors))
if -1 in unique dbscan:
    tick labels = ['Noise'] + [f'Cluster {i}' for i in
```

```
range(n_dbscan_clusters)]
else:
    tick_labels = [f'Cluster {unique_dbscan[i]}' for i in
range(n_dbscan_clusters)]
cbar2.set_ticklabels(tick_labels)
cbar2.set_label('DBSCAN Clusters')

plt.tight_layout()
plt.savefig(f"{RESULTS_PATH}/clustering_tsne_visualization_fixed.png",
dpi=300, bbox_inches='tight')
plt.show()

CLUSTER VISUALIZATION WITH t-SNE (IMPROVED)

Computing t-SNE embedding with stable parameters...
t-SNE completed with perplexity=50
```



9.2 K-Nearest Neighbor Grafik bei DBSCAN

Was:

- Berechnet für jeden Datenpunkt die Distanz zum k-ten nächsten Nachbarn (k = best_dbscan['min_samples']) auf den PCA-Features
- Sortiert diese k-Distanzen absteigend und visualisiert sie als Kurve (K-Distance Plot)
- Überlagert horizontale Referenzlinien für das gewählte best_eps (rot) und andere getestete Epsilon-Werte (grau)

Warum:

 Visuelle Epsilon-Validierung: Der Plot zeigt, ob das automatisch gewählte eps am "Elbow" (Knick) der Kurve liegt

- Datengetriebene Parameter-Wahl: Ergänzt die Grid-Search um eine theoretisch fundierte Visualisierung der Dichteverteilung
- Core-Point-Analyse: Punkte oberhalb der eps-Linie werden zu Core-Points → Einschätzung der Cluster-Dichte

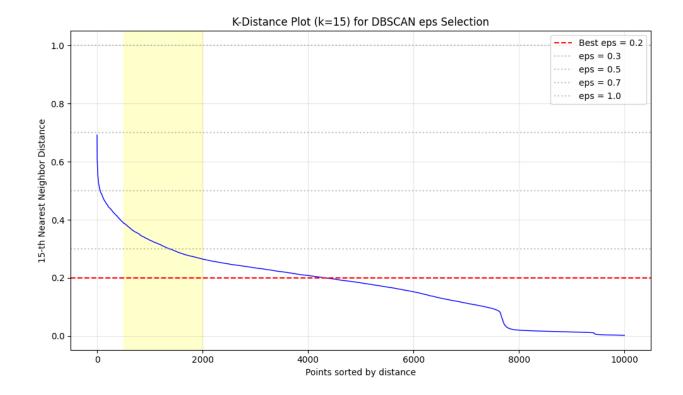
Besonderheiten:

- Gelber Bereich (5%-20% der sortierten Punkte) zeigt die typische Knick-Zone
- Zählt Punkte oberhalb des gewählten eps als potentielle Core-Points zur quantitativen Analyse
- Zeigt mehrere eps-Kandidaten zur Orientierung (0.3, 0.5, 0.7, 1.0)

- Plot: dbscan k distance.png mit sortierter k-Distanz-Kurve und eps-Referenzlinien
- Konsolen-Analyse: Interpretation des gewählten eps und Anzahl potentieller Core-Points

```
# K-Distance Plot for DBSCAN Parameter Guidance
print("=" * 80)
print("K-DISTANCE PLOT FOR DBSCAN EPS SELECTION")
print("=" * 80)
from sklearn.neighbors import NearestNeighbors
# Use the min samples from best DBSCAN result
k = best dbscan['min samples']
print(f"Computing {k}-distance plot for eps guidance...")
# Fit NearestNeighbors on PCA features
neighbors = NearestNeighbors(n neighbors=k, metric='euclidean')
neighbors.fit(features pca)
# Get distances to k-th nearest neighbor for each point
distances, indices = neighbors.kneighbors(features pca)
k distances = distances[:, k-1] # k-th distance (0-indexed)
# Sort distances in descending order
k distances sorted = np.sort(k distances)[::-1]
# Create the plot
plt.figure(figsize=(10, 6))
plt.plot(range(len(k distances_sorted)), k_distances_sorted, 'b-',
linewidth=1)
plt.axhline(y=best dbscan['eps'], color='red', linestyle='--',
           label=f'Best eps = {best dbscan["eps"]}')
# Add some reference lines for other tested eps values
for eps in [0.3, 0.5, 0.7, 1.0]:
    if eps != best dbscan['eps']:
        plt.axhline(y=eps, color='grey', linestyle=':', alpha=0.5,
```

```
label=f'eps = {eps}')
plt.xlabel('Points sorted by distance')
plt.ylabel(f'{k}-th Nearest Neighbor Distance')
plt.title(f'K-Distance Plot (k={k}) for DBSCAN eps Selection')
plt.legend()
plt.grid(True, alpha=0.3)
# Highlight the "elbow" region
elbow start = int(len(k distances sorted) * 0.05)
elbow end = int(len(k distances sorted) * 0.20)
plt.axvspan(elbow start, elbow end, alpha=0.2, color='yellow',
           label='Typical elbow region')
plt.tight layout()
plt.savefig(f"{RESULTS PATH}/dbscan k distance.png", dpi=300,
bbox inches='tight')
plt.show()
print(f"\nK-Distance Plot Analysis:")
print(f"- Red line shows selected eps = {best dbscan['eps']}")
print(f"- Look for 'elbow' in the curve to find optimal eps")
print(f"- Steep increase indicates good density separation")
print(f"- Current eps captures {np.sum(k distances sorted >=
best dbscan['eps'])} points as potential core points")
K-DISTANCE PLOT FOR DBSCAN EPS SELECTION
Computing 15-distance plot for eps guidance...
```



K-Distance Plot Analysis:

- Red line shows selected eps = 0.2
- Look for 'elbow' in the curve to find optimal eps
- Steep increase indicates good density separation
- Current eps captures 4325 points as potential core points

10. Cluster-Ergebnisse speichern

10.1 Speicher-Helfer definieren (Ordner/Bildkopie/Metadaten)

Was:

- es werden drei Hilfsfunktionen für die Speicherung der Cluster-Ergebnisse definiert
- create_cluster_directories(): Legt strukturierte Ordnerhierarchie an (method_name/cluster_<id>/ bzw. noise/ für DBSCAN)
- copy_images_to_clusters(): Kopiert Originalbilder in ihre jeweiligen Cluster-Ordner mit Duplikatsvermeidung
- save_cluster_metadata(): Erstellt detaillierte JSON-Metadaten pro Cluster mit Tenant-Statistiken und Bildlisten

Warum:

- Clustering-Ergebnisse werden dauerhaft und strukturiert gespeichert für spätere Analyse
- Bilder werden nach Clustern sortiert → vereinfacht manuelle Inspektion und Qualitätskontrolle der Clustering Verfahren

- JSON-File dokumentiert Cluster-Zusammensetzung, Tenant-Verteilung und verwendete Methodik
- Separierte Cluster ermöglichen gezielte Weiterverarbeitung einzelner Gruppen, hierdurch ist ein Labeln der Cluster einfach möglich, um eine spätere Klassifizierung von neuen Daten vornehmen zu können

Besonderheiten:

- Ordner-Erstellung und Dateikopien überschreiben nicht bei identischen Dateien (Größenvergleich)
- Noise-Punkte (-1) werden speziell im noise/-Ordner gesammelt, reguläre Cluster in cluster_<id>/
- Unterstützt sowohl K-Means (cluster_labels) als auch DBSCAN (dbscan_labels)
 Parameter

- Ordner mit kopierten Originalbildern im festgelegten Dateipfad: {base path}/{method name}/cluster <id>/
- Metadaten Dateien je Cluster mit Angabe der cluster_id, total_images, tenant distribution und den Details der Bilder
- Erstellung von Statistiken zur Anzahl der erfolgreichen Kopien, Anzahl der Fehler (wenn vorhanden) und die Größe der Cluster

```
def create cluster directories(base path, method name, cluster labels,
dbscan labels=None):
    """Create directory structure for clustered images."""
    method path = Path(base path) / method name
    method path.mkdir(parents=True, exist ok=True)
    if method name == 'kmeans':
        unique clusters = sorted(set(cluster labels))
    else: # dbscan
        unique clusters = sorted(set(dbscan labels))
        # Handle noise points (-1) separately
        if -1 in unique clusters:
            unique clusters = [c for c in unique clusters if c != -1]
+ [-1]
    cluster dirs = {}
    for cluster id in unique clusters:
        if cluster id == -1:
            cluster dir = method path / 'noise'
        else:
            cluster_dir = method_path / f'cluster_{cluster_id}'
        cluster dir.mkdir(exist ok=True)
        cluster dirs[cluster id] = cluster dir
    return cluster dirs
```

```
def copy images to clusters(image files, cluster_dirs, cluster_labels,
method name='kmeans', dbscan labels=None):
    """Copy images to their respective cluster directories."""
    print(f"\nCopying images to {method name.upper()} cluster
directories...")
    if method name == 'kmeans':
        labels to use = cluster labels
    else: # dbscan
        labels to use = dbscan labels
    copied count = 0
    error count = 0
    for i, img file in enumerate(image files):
        try:
            cluster id = labels to use[i]
            source_path = Path(img_file['filepath'])
            target dir = cluster dirs[cluster id]
            target path = target dir / source path.name
            # Copy file if it doesn't exist or is different
            if not target path.exists() or target path.stat().st size
!= source path.stat().st size:
                shutil.copy2(source path, target path)
                copied count += 1
        except Exception as e:
            print(f"Error copying {img file['filename']}: {e}")
            error_count += 1
    print(f"Successfully copied {copied count} images")
    if error count > 0:
        print(f"Errors: {error count}")
    return copied count, error count
def save cluster metadata(cluster dirs, image files, cluster labels,
method name='kmeans', dbscan labels=None):
    """Save metadata for each cluster."""
    print(f"\nSaving {method name.upper()} cluster metadata...")
    if method name == 'kmeans':
        labels to use = cluster labels
    else: # dbscan
        labels to use = dbscan labels
    for cluster_id, cluster_dir in cluster dirs.items():
        # Get images for this cluster
```

```
cluster images = []
        for i, img file in enumerate(image files):
            if int(labels to use[i]) == cluster id: # Convert numpy
int32 to Pvthon int
                cluster images.append({
                     'filename': img_file['filename'],
                     'tenant': img file['tenant'],
                     'sid': img file['sid'],
                     'original name': img file['original name']
                })
        # Calculate statistics
        tenant counts = Counter([img['tenant'] for img in
cluster images])
        metadata = {
             'cluster id': int(cluster id) if isinstance(cluster id,
(np.integer, np.int32, np.int64)) else cluster id, # Ensure
cluster id is JSON serializable
            'method': method name,
            'total images': <a href="length">len</a>(cluster images),
            'tenant distribution': dict(tenant counts),
            'images': cluster images
        }
        # Save metadata
        metadata_file = cluster_dir / 'cluster_metadata.json'
        with open(metadata_file, 'w') as f:
            json.dump(metadata, f, indent=2)
    print(f"Metadata saved for {len(cluster dirs)} clusters")
```

10.2 K-Means-Cluster speichern (Ausführung)

Was:

- Führt die K-Means-Cluster-Speicherung mit den in Abschnitt 10.1 definierten Hilfsfunktionen aus
- erstellt je gefundenem Cluster einen Ordner in der definierten Ordnerstruktur
- generiert die zuvor definierten Statistiken als JSON-Datei

Warum:

- vereinfachte visuelle Kontrolle
- persistente Archivierung zur späteren Analyse
- gezielte Weiterverarbeitung
- direkte Vergleiche mit vorherigen Läufen durch Anlage der Ordnerstruktur inklusive Timestamp

Besonderheiten:

- Zeitstempel-basierte Pfade für eindeutige Versionierung
- Ausgabe von detaillierten Statistiken und Fehler-Tracking

- kopierte Originalbilder in der gewählten Ordnerstruktur {CLUSTERS_PATH}/kmeans/cluster <0..k-1>/
- Metadaten Datei cluster metadata. json für jedes Cluster
- Anzeige der Anzahl erstellter Ordner, Cluster-Größen und Kopierstatistiken (Erfolg/Fehler)
- Nennung des Speicherorts als Bestätigung
 ./results {TIMESTAMP}/clustered images/kmeans/

```
# Save K-Means clustering results to timestamped directories
print("=" * 80)
print("SAVING K-MEANS CLUSTERS TO TIMESTAMPED DIRECTORIES")
print("=" * 80)
print(f"Using timestamped cluster directory: {CLUSTERS PATH}")
# Create K-Means cluster directories
kmeans dirs = create cluster directories(CLUSTERS PATH, 'kmeans',
cluster labels)
print(f"Created K-Means cluster directories:")
for cluster id, cluster dir in sorted(kmeans dirs.items()):
   cluster size = sum(1 for label in cluster labels if label ==
cluster id)
   print(f" {cluster dir.name}: {cluster size} images")
# Copy images to K-Means clusters
kmeans copied, kmeans errors = copy images to clusters(
   image files, kmeans dirs, cluster labels, 'kmeans'
)
# Save K-Means cluster metadata
save cluster metadata(kmeans dirs, image files, cluster labels,
'kmeans')
print(f"\nK-Means clustering results saved to: {Path(CLUSTERS PATH) /
'kmeans'}")
_____
SAVING K-MEANS CLUSTERS TO TIMESTAMPED DIRECTORIES
______
Using timestamped cluster directory:
./results 20250907 150642/clustered images
Created K-Means cluster directories:
 cluster 0: 944 images
```

```
cluster_1: 3571 images
  cluster_2: 2562 images
  cluster_3: 1345 images
  cluster_4: 650 images
  cluster_5: 928 images

Copying images to KMEANS cluster directories...
Successfully copied 10000 images

Saving KMEANS cluster metadata...
Metadata saved for 6 clusters

K-Means clustering results saved to:
  results_20250907_150642/clustered_images/kmeans
```

10.3 DBSCAN-Cluster speichern (Ausführung)

Was:

- Führt die DBSCAN-Cluster-Speicherung mit den in Abschnitt 10.1 definierten Hilfsfunktionen aus
- erstellt je gefundenem Cluster einen Ordner in der definierten Ordnerstruktur, zusätzlich wird ein Ordner für die noise Punkte eingeführt
- generiert die zuvor definierten Statistiken als JSON-Datei

Warum:

- Ermöglichung der Analyse anomaler Bilder zur Identifizierung von Ausreißern
- manuelle Überprüfung der dichtebasierten Gruppierung
- direkter Vergleich beider Clustering Ansätze möglich

Besonderheiten:

 Nutzt die "balanced score" Parameterwahl (silhouette * (1 - noise_ratio)) statt reiner Silhouette-Optimierung

- kopierte Originalbilder in der gewählten Ordnerstruktur {CLUSTERS PATH}/dbscan/cluster <0..n>/ + noise/
- Metadaten Datei cluster metadata. j son für jedes Cluster
- Anzeige der Anzahl erstellter Ordner, Cluster-Größen und Kopierstatistiken (Erfolg/Fehler)
- Nennung des Speicherorts als Bestätigung
 ./results {TIMESTAMP}/clustered images/dbscan/

```
# Save DBSCAN clustering results to timestamped directories
print("=" * 80)
print("SAVING DBSCAN CLUSTERS TO TIMESTAMPED DIRECTORIES")
print("=" * 80)
```

```
print(f"Using timestamped cluster directory: {CLUSTERS PATH}")
# Add DBSCAN cluster labels to image files for consistency
dbscan labels = best dbscan['labels']
for i, img file in enumerate(image files):
    img file['dbscan cluster'] = int(dbscan labels[i])
# Create DBSCAN cluster directories
dbscan dirs = create cluster directories(CLUSTERS PATH, 'dbscan',
None, dbscan labels)
print(f"Created DBSCAN cluster directories:")
for cluster id, cluster dir in sorted(dbscan dirs.items()):
    cluster size = sum(1 for label in dbscan labels if label ==
cluster id)
    if cluster id == -1:
        print(f" {cluster_dir.name} (noise): {cluster_size} images")
        print(f" {cluster_dir.name}: {cluster_size} images")
# Copy images to DBSCAN clusters
dbscan_copied, dbscan_errors = copy_images_to_clusters(
    image_files, dbscan_dirs, None, 'dbscan', dbscan_labels
)
# Save DBSCAN cluster metadata
save cluster metadata(dbscan dirs, image files, None, 'dbscan',
dbscan labels)
print(f"\nDBSCAN clustering results saved to: {Path(CLUSTERS PATH) /
'dbscan'}")
SAVING DBSCAN CLUSTERS TO TIMESTAMPED DIRECTORIES
Using timestamped cluster directory:
./results 20250907 150642/clustered images
Created DBSCAN cluster directories:
  noise (noise): 3096 images
  cluster 0: 2494 images
  cluster 1: 2890 images
  cluster 2: 477 images
  cluster 3: 166 images
  cluster 4: 537 images
  cluster 5: 98 images
  cluster 6: 123 images
  cluster 7: 41 images
```

```
cluster_8: 33 images
  cluster_9: 14 images
  cluster_10: 14 images
  cluster_11: 17 images

Copying images to DBSCAN cluster directories...
Successfully copied 10000 images

Saving DBSCAN cluster metadata...
Metadata saved for 13 clusters

DBSCAN clustering results saved to:
  results_20250907_150642/clustered_images/dbscan
```

11. Tenant-Cluster-Analyse (Heatmap & Detailstatistik)

Was:

- Baut eine Tenant×Cluster-Matrix auf mit zeilenweiser Normalisierung und berechnet Prozentanteile je Tenant pro Cluster
- Erstellt eine Seaborn-Heatmap (sns.heatmap) mit Zellbeschriftung und YlorRd-Farbskala zur Visualisierung der Verteilungen

Warum:

- Identifiziert tenant-spezifische Clustering-Muster. Zeigt an, ob bestimmte Verkehrsunternehmen charakteristische Untergrund-/Situationstypen aufweisen
- Starke Ungleichverteilungen können auf systematische Bias oder domänenspezifische Besonderheiten hinweisen
- Visualisiert, ob das Clustering echte visueller Muster oder nur tenant-basierte Artefakte erfasst hat

- Heatmap-Grafik: tenant_cluster_heatmap.png in RESULTS_PATH mit prozentualer Tenant-Verteilung über alle Cluster
- Konsolen-Report: Detaillierte Aufschlüsselung je Tenant mit Gesamtzahl und clusterspezifischen Prozent-/Absolutwerten

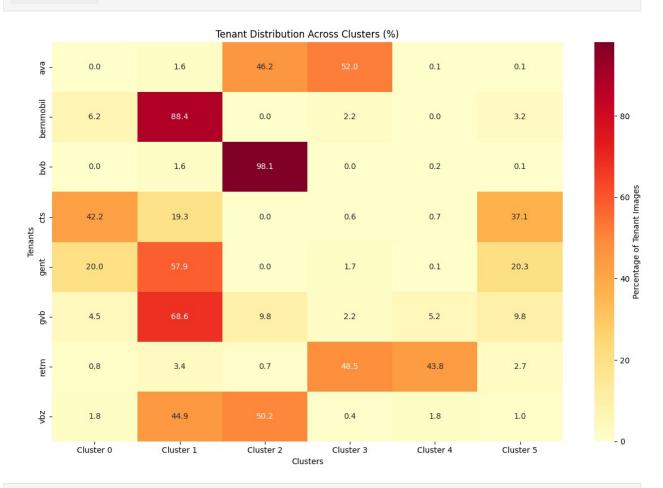
```
# Analyze tenant distribution across clusters
print("=" * 80)
print("TENANT DISTRIBUTION ANALYSIS")
print("=" * 80)

# Create tenant-cluster matrix
tenant_cluster_matrix = defaultdict(lambda: defaultdict(int))
total_by_tenant = defaultdict(int)

for img_file in image_files:
    tenant = img_file['tenant']
```

```
cluster = img file['cluster']
    tenant_cluster_matrix[tenant][cluster] += 1
    total by tenant[tenant] += 1
# Convert to DataFrame for easier visualization
tenants = sorted(total by tenant.keys())
clusters = sorted(set(cluster labels))
matrix data = []
for tenant in tenants:
    row = []
    for cluster in clusters:
        count = tenant cluster matrix[tenant][cluster]
        percentage = (count / total by tenant[tenant]) * 100
        row.append(percentage)
    matrix data.append(row)
# Create heatmap
plt.figure(figsize=(12, 8))
heatmap data = np.array(matrix data)
sns.heatmap(
    heatmap data,
    xticklabels=[f'Cluster {c}' for c in clusters],
    yticklabels=tenants,
    annot=True,
    fmt='.1f',
    cmap='Yl0rRd',
    cbar kws={'label': 'Percentage of Tenant Images'}
plt.title('Tenant Distribution Across Clusters (%)')
plt.xlabel('Clusters')
plt.ylabel('Tenants')
plt.tight layout()
plt.savefig(f"{RESULTS PATH}/tenant cluster heatmap.png", dpi=300,
bbox inches='tight')
plt.show()
# Print detailed statistics
print("\nDetailed Tenant-Cluster Distribution:")
for tenant in tenants:
    print(f"\n{tenant} ({total by tenant[tenant]} images):")
    for cluster in clusters:
        count = tenant cluster matrix[tenant][cluster]
        percentage = (count / total by tenant[tenant]) * 100
        if count > 0:
            print(f" Cluster {cluster}: {count} images
({percentage:.1f}%)")
_____
```

TENANT DISTRIBUTION ANALYSIS



Detailed Tenant-Cluster Distribution:

```
ava (1250 images):
    Cluster 1: 20 images (1.6%)
    Cluster 2: 578 images (46.2%)
    Cluster 3: 650 images (52.0%)
    Cluster 4: 1 images (0.1%)
    Cluster 5: 1 images (0.1%)

bernmobil (1250 images):
    Cluster 0: 78 images (6.2%)
    Cluster 1: 1105 images (88.4%)
    Cluster 3: 27 images (2.2%)
    Cluster 5: 40 images (3.2%)

bvb (1250 images):
```

Cluster 1: 20 images (1.6%)

```
Cluster 2: 1226 images (98.1%)
  Cluster 4: 3 images (0.2%)
  Cluster 5: 1 images (0.1%)
cts (1250 images):
  Cluster 0: 528 images (42.2%)
  Cluster 1: 241 images (19.3%)
  Cluster 3: 8 images (0.6%)
  Cluster 4: 9 images (0.7%)
  Cluster 5: 464 images (37.1%)
gent (1250 images):
  Cluster 0: 250 images (20.0%)
  Cluster 1: 724 images (57.9%)
  Cluster 3: 21 images (1.7%)
  Cluster 4: 1 images (0.1%)
 Cluster 5: 254 images (20.3%)
qvb (1250 images):
  Cluster 0: 56 images (4.5%)
  Cluster 1: 857 images (68.6%)
  Cluster 2: 122 images (9.8%)
  Cluster 3: 28 images (2.2%)
  Cluster 4: 65 images (5.2%)
  Cluster 5: 122 images (9.8%)
retm (1250 images):
  Cluster 0: 10 images (0.8%)
  Cluster 1: 43 images (3.4%)
  Cluster 2: 9 images (0.7%)
  Cluster 3: 606 images (48.5%)
  Cluster 4: 548 images (43.8%)
  Cluster 5: 34 images (2.7%)
vbz (1250 images):
  Cluster 0: 22 images (1.8%)
  Cluster 1: 561 images (44.9%)
  Cluster 2: 627 images (50.2%)
  Cluster 3: 5 images (0.4%)
  Cluster 4: 23 images (1.8%)
  Cluster 5: 12 images (1.0%)
```

12. Clustering-Report (JSON) erstellen & Kernergebnisse ausgeben

Was:

- erstellt clustering_report.json mit Zeitstempel-Informationen, Run-Metadaten und vollständigen Clustering-Ergebnissen
- Sammelt Dataset-Info (Bildanzahl, Feature-Dimension, PCA-Varianz), K-Means-Resultate (optimal_k, Silhouette-Scores, Evaluation-Historie) und DBSCAN-Parameter

• Integriert Tenant-Cluster-Analyse mit detaillierter Verteilungsmatrix pro Tenant über alle Cluster

Warum:

- Alle Parameter, Metriken und Ergebnisse werden zentral für Nachvollziehbarkeit und Vergleichbarkeit archiviert
- Run-spezifische Metadaten ermöglichen systematische Analyse von Clustering-Stabilität über mehrere Läufe
- Parallele Dokumentation von K-Means und DBSCAN erleichtert objektive Bewertung beider Ansätze
- Geschäftsspezifische Analyse zeigt, ob Clustering domänenrelevante Muster (Verkehrsunternehmen) erfasst

- JSON-Report clustering_report.json in RESULTS_PATH mit vollständiger Run-Dokumentation und Parametern
- Kompakte Übersicht mit Timestamp, optimalen Parametern, Cluster-/Noise-Anzahlen und PCA-Varianz in der Ausgabe
- Absolute Pfade zu Analysis- und Cluster-Verzeichnissen für einfache Navigation

```
# Generate comprehensive clustering report with timestamp info
print("=" * 80)
print("TIMESTAMPED CLUSTERING ANALYSIS SUMMARY")
print("=" * 80)
# Compile results with timestamp information
clustering report = {
    'run info': {
        'timestamp': TIMESTAMP,
        'run date': time.strftime('%Y-%m-%d %H:%M:%S'),
        'analysis_results_path': str(Path(RESULTS_PATH).resolve()),
        'clustered images path': str(Path(CLUSTERS PATH).resolve())
    },
    'dataset info': {
        'total images': int(len(image files)),
        'feature dimension': int(FEATURE DIM),
        'pca components': int(PCA COMPONENTS),
        'pca explained variance':
float(pca.explained variance ratio .sum()),
        'tenant distribution': {k: int(v) for k, v in
tenant_distribution.items()}
    },
    'kmeans results': {
        'optimal_k': int(optimal_k),
        'silhouette score':
float(silhouette scores[best silhouette idx]),
        'cluster_sizes': { int(k): int(v) for k, v in
Counter(cluster labels).items()},
```

```
'evaluation results': [
           {
                'k': int(r['k']),
                'inertia': float(r['inertia']),
                'silhouette score': float(r['silhouette score'])
           } for r in kmeans results
       ]
   },
    'dbscan results': {
        'best eps': float(best dbscan['eps']),
        'min samples': int(best dbscan['min samples']),
        'n clusters': int(best dbscan['n clusters']),
        'n_noise': int(best_dbscan['n_noise']),
        'silhouette score': float(best dbscan['silhouette score'])
    'tenant cluster analysis': {
       tenant: {
            'cluster distribution': {int(k): int(v) for k, v in
tenant cluster matrix[tenant].items()}
       } for tenant in tenants
   }
}
# Save results to timestamped directory
with open(f"{RESULTS PATH}/clustering report.json", 'w') as f:
   json.dump(clustering report, f, indent=2)
# Print summary
print(f"Analysis completed successfully!")
print(f"\nRun Information:")
print(f"- Timestamp: {TIMESTAMP}")
print(f"- Analysis results saved to: {RESULTS PATH}")
print(f"- Clustered images saved to: {CLUSTERS PATH}")
print(f"\nKey Findings:")
print(f"- Optimal number of clusters (K-Means): {optimal k}")
print(f"- Best silhouette score:
{silhouette scores[best silhouette idx]:.4f}")
print(f"- DBSCAN found {best dbscan['n clusters']} clusters with
{best dbscan['n noise']} noise points")
print(f"- PCA captured {pca.explained variance ratio .sum():.1%} of
the variance")
print(f"\nCluster sizes (K-Means):")
cluster sizes = Counter(cluster labels)
for cluster id, size in sorted(cluster sizes.items()):
    percentage = (size / len(cluster_labels)) * 100
   print(f" Cluster {cluster id}: {size} images ({percentage:.1f})
```

```
TIMESTAMPED CLUSTERING ANALYSIS SUMMARY
______
Analysis completed successfully!
Run Information:
- Timestamp: 20250907 150642
- Analysis results saved to:
./results_20250907_150642/clustering_analysis
- Clustered images saved to:
./results 20250907 150642/clustered images
Key Findings:
- Optimal number of clusters (K-Means): 6
- Best silhouette score: 0.4285
- DBSCAN found 12 clusters with 3096 noise points
- PCA captured 91.5% of the variance
Cluster sizes (K-Means):
 Cluster 0: 944 images (9.4%)
 Cluster 1: 3571 images (35.7%)
 Cluster 2: 2562 images (25.6%)
 Cluster 3: 1345 images (13.5%)
 Cluster 4: 650 images (6.5%)
 Cluster 5: 928 images (9.3%)
```

13. Ergebnisse der Clustering Phase

- Das dichtebasierte Cluster mit DBSCAN konnte keinen zuverlässigen Erfolg liefern, trotz vielfacher Anpassung der Parameter.
- Die Ergebnisse über die K-Means-Methode waren zufriedenstellend.
- Die Ergebnisse der Cluster wurden mit drei unterschiedlichen Metriken bewertet. Neben den gezeigten Metriken wurden in einer separaten Analyse weitere Cluster-Gütemaße evaluiert, diese Ergebnisse sind in diesem Notebook noch nicht enthalten. Konkret kamen der Silhouette Score, der Davies-Bouldin Index und der Calinski-Harabasz Index zum Einsatz. Für Hintergrund und einen vergleichenden Überblick siehe: Arbelaitz et al. (2013).
- Es wurde versucht mit Hilfe von einer Bildvorverarbeitung die Bilder vorzuverarbeiten, um z.B. dunkle Bilder aufzuhellen. Dies wurde im Schritt 5.1 optional in diesem Notebook eingebaut. Es konnte allerdings kein nennenswerter Effekt bzw. Verschlechterungen festgestellt werden, weshalb wir uns im folgenden dazu entschieden haben keine Bildvorverarbeitung vorzunehmen.
- Zusätzlich wurden folgende Konfigurationen getestet. Die Experimente wurden mit Hilfe des Python-Files kmeans_experiments.py
 - Feature-Extraction-Model: ResNet50,VGG16

```
{'layer': 'conv4_block6_out'/'block4_conv3'}
'low': {'layer': 'conv3 block4 out'/'block2 conv2'} }
```

- Als beste Konfiguration hat sich das ResNet50 mit conv4_block6_out als Layer und keiner Bildvorverarbeitung herausgestellt.
 - Die Ergebnisse aller Experimente sind in der mitgeschickten results.json.
- Es wurden zwei Clustering Läufe mit jeweils 10.000 Bildern initialisiert (also insgesamt 20.000 unterschiedlichen Bildern). Ein Test mit 50.000 Bildern führte zu nicht plausiblen Clustern mit K-Means und wurde deshalb verworfen. Eine Analyse, weshalb der Lauf mit 50.000 Bildern nicht funktionierte wurde nicht angestrebt, da ein Clustering mit 20.000 Bildern für unsere Zwecke vollkommen ausreichend ist.
- Die entstandenen 5 Cluster wurden anschließend manuell gesichtet und bereinigt. Es wurden folgende fünf Klassen identifiziert:
 - Beton/Asphalt
 - Gras/natürliche Untergründe (z.B. auch Laub)
 - Schotter
 - Stein (verschiedene Pflaster-Arten)
 - Messfehler (zu dunkle Bilder, verrauschte Bilder)
- Während der Bereinigung wurden fehlerhaft zugeordnete Bilder manuell entfernt, bevor ein Training des Klassifizierungsmodell stattfindet. Die entfernten Bilder wurden gesammelt und können somit später als Spezialfälle gesondert analysiert werden.
- Das Ziel durch das Clustering die Daten zu sortieren und für das Labeling vorzubereiten konnte dadurch erreicht werden.