Generative Neural Networks for the Sciences - Sample Solution **Exercise 1** For this sample solution, we chose the submission of Paul Saegert, Nikita Tatsch and Christian Kleiber. 1 Two-dimensional data In [29]: import numpy as np from sklearn.base import BaseEstimator, TransformerMixin from sklearn.cluster import kmeans plusplus # For GMM initialization In [30]: | # Implement a custom 2D histogram compatible with the sklearn API class Histogram(BaseEstimator, TransformerMixin): def \_\_init\_\_(self, bins: tuple[int] = None, range\_: tuple[int] = None): if bins is None: bins = (10, 10)else: assert len(bins) == 2, "bins must be a tuple of length 2" self.bins = bins self.range = range self.histogram = None def fit(self, X, y = None): # Calculate the range in x and y directions if self.range is None:  $self.range_ = ((X[:, 0].min(), X[:, 0].max()), (X[:, 1].min(), X[:, 1].max()))$ # Calculate the bin edges self.bin edges = [ np.linspace(self.range\_[0][0], self.range\_[0][1], self.bins[0] + 1), # xnp.linspace(self.range\_[1][0], self.range\_[1][1], self.bins[1] + 1) # y ] # Create an empty histogram self.histogram = np.zeros(self.bins) # Calculate the bin indices for each sample # Use numpy.digitize to bin the data (faster than for loops) bin indices = np.array([ np.digitize(X[:, 0], self.bin edges[0]) - 1, np.digitize(X[:, 1], self.bin edges[1]) - 1 # Count the number of samples in each bin for i in range(self.bins[0]): for j in range(self.bins[1]): self.histogram\_[i, j] = np.sum((bin\_indices[0] == i) & (bin indices[1] == j)) self.histogram /= np.sum(self.histogram ) return self def predict(self, X): # For a given sample, find the bin it belongs to and return the bin's value bin indices = np.array([ np.digitize(X[:, 0], self.bin edges[0]) - 1, np.digitize(X[:, 1], self.bin edges[1]) - 1 ]) values = np.zeros(X.shape[0]) # Where the sample is outside the range, return 0 # Where the sample is inside the range, return the bin's value for i in range(self.bins[0]): for j in range(self.bins[1]): values[(bin\_indices[0] == i) & (bin\_indices[1] == j)] = self.histogram\_[i, j] return values def sample(self, n=1, noise=True): # Sample from the histogram # Calculate the probability of each bin bin probabilities = self.histogram / np.sum(self.histogram ) # Sample from the bin probabilities bin\_indices = np.random.choice(self.bins[0] \* self.bins[1], size=n, p=bin\_probabilities.flatten ()) # Convert the bin indices to x and y coordinates x = self.bin edges[0][bin indices // self.bins[1]] y = self.bin edges[1][bin indices % self.bins[1]] # If noise is enabled, add uniform noise to the samples (to avoid degenerate solutions) if noise: x += np.random.uniform( -0.5 \* (self.bin\_edges[0][1] - self.bin\_edges[0][0]), 0.5 \* (self.bin\_edges[0][1] - self.bin\_edges[0][0]), size=n) y += np.random.uniform( -0.5 \* (self.bin edges[1][1] - self.bin edges[1][0]),0.5 \* (self.bin\_edges[1][1] - self.bin\_edges[1][0]), size=n) return np.vstack([x, y]).T In [31]: class Gaussian(BaseEstimator, TransformerMixin): def init (self): self.mean = None self.covariance = None self.determinant = None self.inverse = None def fit(self, X, y = None): # Calculate the mean self.mean = np.mean(X, axis = 0)# Calculate the covariance matrix self.covariance\_ = np.cov(X, rowvar = False) # Calculate the determinant and inverse of the covariance matrix self.determinant\_ = np.linalg.det(self.covariance\_) self.inverse\_ = np.linalg.inv(self.covariance\_) return self def predict(self, X): # Calculate the value of the Gaussian for each sample values = np.zeros(X.shape[0]) for i in range(X.shape[0]):  $values[i] = np.exp(-0.5 * (X[i] - self.mean_) @ self.inverse_ @ (X[i] - self.mean_)) / np.s$ qrt(self.determinant \* (2 \* np.pi) \*\* 2) return values def sample(self, n=1): # First, sample from a standard normal distribution x = np.random.normal(size=(n, self.mean .shape[0])) # Then, transform the samples to match the covariance matrix # Compute the eigendeomposition of the covariance matrix U and Lambda eigenvalues, eigenvectors = np.linalg.eig(self.covariance ) # Compute the square root of Lambda Lambda\_sqrt = np.diag(np.sqrt(eigenvalues)) # Transform the samples via x = U Lambda\_sqrt z + mutransformed x = []for i in range(n): transformed x.append(eigenvectors @ Lambda sqrt @ x[i] + self.mean ) return np.array(transformed x) In [32]: class GMM(BaseEstimator, TransformerMixin): def init (self, L: int = 1): L: The number of Gaussian components self.L = Lself.weights\_ = np.empty(L) self.means = None # Will be initialized after X's shape is known self.covariances\_ = np.empty((L, 2, 2)) # Assuming 2 dimensions for simplicity  $self.inverse_ = np.empty((L, 2, 2))$ self.determinant = np.empty(L) def update\_determinant\_inverse(self): for i, covariance in enumerate(self.covariances): self.determinant [i] = np.linalg.det(covariance) self.inverse [i] = np.linalg.inv(covariance) def fit(self, X, y=None, max iter: int = 100): # Regularization term to prevent singular covariance matrix epsilon = 1e-6# Initialize mu l using kmeans++ mu, = kmeans plusplus(X, n clusters=self.L, random state=0) self.means = mu # Now we initialize it with the right shape # Initialize the weights to be uniform self.weights = np.ones(self.L) / self.L # Initialize the covariances to diagonals self.covariances = np.array([np.diag(np.var(X, axis=0))] \* self.L) self.update determinant inverse() # Begin expectation maximization for \_ in range(max iter): # E-step: Calculate the responsibilities gamma il responsibilities = np.zeros((X.shape[0], self.L)) for l in range(self.L): diff = X - mu[1]exponent = np.einsum('ij,ij->i', np.dot(diff, self.inverse [1]), diff) responsibilities[:, 1] = self.weights\_[1] \* np.exp(-0.5 \* exponent) / np.sqrt(self.dete rminant\_[1] \* (2 \* np.pi) \*\* X.shape[1]) responsibilities += epsilon responsibilities /= np.sum(responsibilities, axis=1, keepdims=True) # M-step: Update the means and variances for l in range(self.L): self.weights [1] = np.sum(responsibilities[:, 1]) / X.shape[0] # Update the means mu[l] = np.sum(responsibilities[:, l].reshape(-1, 1) \* X, axis=0) / np.sum(responsibili ties[:, 1]) # Update the covariances diff = X - mu[1]self.covariances [1] = np.dot(responsibilities[:, 1] \* diff.T, diff) / np.sum(responsib ilities[:, 1]) self.covariances\_[1] += np.eye(X.shape[1]) \* epsilon # Regularization term self.weights /= np.sum(self.weights ) self.update determinant inverse() self.means = mureturn self def predict(self, X): # Calculate the total probability density of each sample under the model probabilities = np.zeros(X.shape[0]) for l in range(self.L): diff = X - self.means [1]exponent = np.einsum('ij,ij->i', np.dot(diff, self.inverse\_[l]), diff) probabilities += self.weights\_[1] \* np.exp(-0.5 \* exponent) / np.sqrt(self.determinant\_[1] \* (2 \* np.pi) \*\* X.shape[1]) return probabilities def sample(self, n=1): # Sample from the GMM component = np.random.choice(self.L, size=n, p=self.weights ) samples = np.array([np.random.multivariate normal(self.means [1], self.covariances [1]) for 1 i n component]) return samples In [33]: class KDE(BaseEstimator, TransformerMixin): def init (self, bandwidth): self.bandwidth = bandwidth self.points = [] def fit(self, data): self.points = data return self def \_gaussian\_kernel(self, x, y, x0, y0): coeff = 1 / (2 \* np.pi \* self.bandwidth \*\* 2) exp val = -((x - x0) \*\* 2 + (y - y0) \*\* 2) / (2 \* self.bandwidth \*\* 2)return coeff \* np.exp(exp val) def predict(self, X): # Initialize the predicte value to 0 value = np.zeros(X.shape[0]) # For every point in X, calculate the value of the KDE for i, (xi, yi) in enumerate(X): # Add the value of the KDE for each point for x0, y0 in self.points: value[i] += self. gaussian kernel(xi, yi, x0, y0) # Normalize the value value[i] /= len(self.points) return value def sample(self, n=1): # Sample from the KDE # Sample a point from the points points ids = np.random.choice(len(self.points), size=n) points = self.points[points ids] # Sample from the KDE samples = []for i in range(n): samples.append(np.random.normal(loc=points[i], scale=self.bandwidth)) return np.array(samples) Results In [34]: from sklearn.datasets import make moons, make blobs import matplotlib.pyplot as plt In [35]: n samples list = [20, 50, 100, 500, 1000]X list = [make moons(n samples=n samples list, noise=0.1)[0] for n samples list in n samples list] # X list = [make blobs(n samples=n samples list)[0] for n samples list in n samples list] In [36]: # Fit the models hist list = [Histogram(bins=(20, 20)).fit(X) for X in X list] print("Histogram done") gaussian list = [Gaussian().fit(X) for X in X list] print("Gaussian done") gmm list = [GMM(L=20).fit(X, max iter = 100) for X in X list]print("GMM done") kde list = [KDE(bandwidth=0.1).fit(X) for X in X list] print("KDE done") Histogram done Gaussian done GMM done KDE done In [37]: grid range = (-2.5, 2.5)In [38]: x = np.linspace(\*grid range, 100)y = np.linspace(\*grid\_range, 100) xx, yy = np.meshgrid(x, y)X grid = np.vstack([xx.ravel(), yy.ravel()]).T In [39]: y pred hist list = [hist.predict(X grid).reshape(xx.shape) for hist in hist list] print("Histogram done") y pred gaussian list = [gaussian.predict(X grid).reshape(xx.shape) for gaussian in gaussian list] print("Gaussian done") y pred gmm list = [gmm.predict(X grid).reshape(xx.shape) for gmm in gmm list] print("GMM done") y pred kde list = [kde.predict(X grid).reshape(xx.shape) for kde in kde list] print("KDE done") Histogram done Gaussian done GMM done KDE done In [40]: | fig, ax = plt.subplots(4, len(n samples list), figsize=(20, 16)) for i, y pred model list in enumerate([y pred hist list, y pred gaussian list, y pred gmm list, y pred kde list]): for j in range(len(n samples list)): ax[i, j].contourf(xx, yy, y pred model list[j], alpha=0.5) ax[i, j].scatter(X\_list[j][:, 0], X\_list[j][:, 1], s=1, c="black") **if** i == 0: ax[i, j].set\_title(f"n\_samples = {n\_samples\_list[j]}") ax[i, j].set xlim(grid range) ax[i, j].set\_ylim(grid\_range)  $n_samples = 20$  $n_samples = 500$ n samples = 50n samples = 100n samples = 1000-1 **Observations:** Histogram: Fits well to the data but tends to overfit (extreme case: small dataset, where one bin size only captures one point) Gaussian: Does not fit the multimodal distribution of the data well, but approximates a continuous blob. **GMM:** Each Gaussian component captures a portion of the data. With n\_samples  $\geq$  100, the model begins to fit to the two moons fairly well. It is not constrained to a rectengular grid like the histogram and thus seems more natural. KDE: Same problem as the histogram for small sample sizes. However, it tries its best (depending on the bandwidth, of course) to interpolate the distribution between individual samples. For large sample sizes, the learned distribution comes very close to the ground truth. Sample In [41]: n samples = 1 000# Sample from the models X sample hist list = [hist.sample(n samples, noise=True) for hist in hist list] X sample gaussian list = [gaussian.sample(n samples) for gaussian in gaussian list] X sample gmm list = [gmm.sample(n samples) for gmm in gmm list] X sample kde list = [kde.sample(n samples) for kde in kde list] In [42]: fig, ax = plt.subplots(4, len(n\_samples\_list), figsize=(20, 16)) for i, X\_sample\_model\_list in enumerate([X\_sample\_hist\_list, X\_sample\_gaussian\_list, X\_sample\_gmm\_list, X sample kde list]): for j in range(len(n samples list)): ax[i, j].scatter(X\_sample\_model\_list[j][:, 0], X\_sample\_model\_list[j][:, 1], s=1, c="black") **if** i == 0: ax[i, j].set title(f"n samples = {n samples list[j]}") ax[i, j].set xlim(grid range) ax[i, j].set\_ylim(grid\_range) n\_samples = 50 n\_samples = 1000  $n_samples = 20$ n samples = 100 $n_samples = 500$ Observations: Histogram: The sampled data looks very blocky for small training sets because the distribution is sampled from only a few bins. We added uniform noise on the scale of a bin to partially account for this. Gaussian: The generated samples do not represent the ground truth distribution well, but rather a weakly correlated cloud of datapoints. GMM: For small training sets, the generated distribution looks very sharp (in case a component fit to two points) and pointy (when a component fit to only one point). The more training samples there are, the better the generated samples align with the ground truth. **KDE:** For small training sets, the generated distributions look a bit clumped, which smoothens out for larger training sets. **MMD** In [43]: # Implement the maximum mean discrepancy (MMD) metric with squared exponential and inverse multi-quadra tic kernels for evaluation. def squared exponential kernel(x1, x2, h=1): **return** np.exp(-np.sum((x1 - x2) \*\* 2) / (2 \* h)) def inverse multi quadratic kernel(x1, x2, h): return 1 / np.sqrt(np.sum((x1 - x2) \*\* 2) / h + 1) def mmd2(X\_true, X\_pred, kernel): N = X true.shape[0]M = X pred.shape[0]repulsive = 1 / (M + (M-1)) \* np.sum([kernel(X\_pred[i], X\_pred[j], 1) for i in range(M) for j in [k for k in range(M) if k != i]]) attractive = 2 / (M \* N) \* np.sum([kernel(X pred[i], X true[j], 1) for i in range(M) for j in range (N)]) return repulsive - attractive In [44]: from tqdm import tqdm import pandas as pd mmd results = { In [99]: kernel name: { model name: [ mmd2(X, model.sample(n\_samples), kernel) for X, model in tqdm(zip(X\_list, model\_list)) ] for model name, model list in zip(["hist", "gaussian", "GMM", "kde"], [hist list, gaussian li st, gmm list, kde list]) } for kernel\_name, kernel in zip( ["squared exponential", "inverse multi quadratic"], [squared exponential kernel, inverse multi quadratic kernel]) 5it [00:15, 3.15s/it] 5it [00:15, 3.14s/it] 5it [00:15, 3.15s/it] 5it [00:15, 3.13s/it] 5it [00:15, 3.17s/it] 5it [00:15, 3.15s/it] 5it [00:15, 3.17s/it] 5it [00:15, 3.17s/it] In [100]: | # Print the results in a pandas dataframe for each kernel for kernel name in mmd results: print(f"Kernel: {kernel name}") print(np.sqrt(pd.DataFrame.from dict(mmd results[kernel name], orient="index", columns=n samples li st))) print() Kernel: squared exponential 20 50 100 500 16.243284 15.903887 15.985504 15.901490 15.845968 gaussian 15.794292 16.268804 16.301880 16.248907 16.145385 15.746146 15.842532 15.878706 15.727855 15.888045 GMM 15.760532 15.657398 16.082515 15.792988 15.934068 kde Kernel: inverse\_multi\_quadratic 20 50 500 1000 100 18.333044 18.145060 18.132870 18.086046 18.094930 gaussian 18.044688 18.213901 18.485684 18.233271 18.316349 18.161287 18.113361 18.178472 18.123408 18.170503 GMM 18.009179 18.082094 18.138319 18.078386 18.202399 kde In [101]: # Visualize the results fig, ax = plt.subplots(1, 2, figsize=(20, 6))for i, kernel name in enumerate(["squared exponential", "inverse multi quadratic"]): for model name in ["hist", "gaussian", "GMM", "kde"]: ax[i].scatter(n samples list, np.sqrt(pd.DataFrame.from dict(mmd results[kernel name], orient= "index", columns=n samples list)).T[model name]) ax[i].plot(n\_samples\_list, np.sqrt(pd.DataFrame.from\_dict(mmd\_results[kernel\_name], orient="index", columns=n samples list)).T) ax[i].set xlabel("n samples") ax[i].set ylabel("MMD (lower is better)") ax[i].set\_title(f"Kernel: {kernel\_name}") ax[i].legend(["hist", "gaussian", "GMM", "kde"]) ax[i].grid() Kernel: squared\_exponential Kernel: inverse\_multi\_quadratic 16.3 gaussiar gaussian GMM GMM 16.2 16.1 (lower is better) (lower is better 18.3 16.0 15.9 18.1 15.7 18.0 1000 1000 **Observations: Histogram:** MMD decreases with larger training set. **Gaussian:** MMD increases with larger training set. This is expected, since the model does not profit from more data. **GMM:** MMD increases and then plateaus for larger training sets. **KDE**: MMD does not improve nor worsen reliably. Most changes happen in the range of 20 to 50 training samples. **Hyperparameters** n samples = 1000In [91]: In [92]: X = make moons(n samples=n samples, noise=0.1)[0] In [93]: hist bins list = [1, 5, 10, 20, 50]gmm components list = [1, 2, 5, 10, 20]kde bandwidth list = [0.01, 0.05, 0.1, 0.5, 1]In [94]: # Fit the models hist = {bins: Histogram(bins=(bins, bins)).fit(X) for bins in tqdm(hist bins list)} gmm = {components: GMM(L=components).fit(X, max iter=100) for components in tqdm(gmm components list)} kde = {bandwidth: KDE(bandwidth=bandwidth).fit(X) for bandwidth in tqdm(kde bandwidth list)} | 5/5 [00:00<00:00, 450.94it/s] 100%| 5/5 [00:00<00:00, 22.97it/s] | 5/5 [00:00<00:00, 149796.57it/s] 100%| In [95]: # Compute the MMD mmd\_results\_hyper = { kernel name: { model name: [ mmd2(X, model.sample(n samples), kernel) for model in tqdm(model list) ] for model\_name, model\_list in zip(["hist", "gmm", "kde"], [hist.values(), kde.values(), gmm.v alues()]) } for kernel name, kernel in zip( ["squared exponential", "inverse multi quadratic"], [squared exponential kernel, inverse multi quadratic kernel]) 100% 5/5 [00:23<00:00, 4.73s/it] 4.73s/it] 100%| 5/5 [00:23<00:00, 100%| 5/5 [00:23<00:00, 4.73s/it] 5/5 [00:23<00:00, 4.75s/it] 100% 100%| | 5/5 [00:23<00:00, 4.74s/it] 100%| | 5/5 [00:23<00:00, 4.78s/it] In [96]: # Print the results in a pandas dataframe for each kernel for kernel name in mmd results hyper: print(f"Kernel: {kernel name}") print(np.sqrt(pd.DataFrame.from\_dict(mmd\_results\_hyper[kernel\_name], orient="index"))) Kernel: squared exponential 0 1 2 hist 14.677911 15.449488 15.670949 15.692174 15.875053 15.877567 15.729625 15.664891 14.206359 11.149662 kde 16.157561 15.844109 15.946050 15.805962 15.608165 Kernel: inverse multi quadratic 0 hist 17.444086 17.832204 18.029457 18.066019 18.195827 18.102013 18.117604 18.113399 17.163230 15.517855 gmm 18.410015 18.177891 18.170217 18.218007 18.087590 kde In [97]: fig, ax = plt.subplots(1, 3, figsize=(20, 5))for i, (model\_name, model\_name\_nice, hyperparameters, hyper\_name) in enumerate(zip( ["hist", "gmm", "kde"], ['Histogram', 'GMM', 'KDE'], [hist bins list, gmm components list, kde bandwidth list], ["bins", "n\_components", "bandwidth"])): for j, kernel name in enumerate(["squared exponential", "inverse multi quadratic"]): ax[i].scatter(hyperparameters, np.sqrt(pd.DataFrame.from dict(mmd results hyper[kernel name], o rient="index")).T[model name], label=kernel name) ax[i].plot(hyperparameters, np.sqrt(pd.DataFrame.from\_dict(mmd\_results\_hyper[kernel\_name], orie nt="index")).T[model\_name]) ax[i].set xlabel(hyper name) ax[i].set ylabel("MMD (lower is better)") ax[i].set\_title(model\_name\_nice) ax[i].legend() ax[i].grid() Histogram GMM KDE 18.5 squared\_exponential 18 18.0 inverse multi quadratio 18.0 17.5 is better) 16 petter) 17.5 17.0 squared\_exponential 16.5 17.0 () inverse\_multi\_quadratic ≜ 14 16.0 ₩ 16.5 15.5 16.0 12 15.0 squared\_exponentia inverse\_multi\_quadratio 15.5 10 2.5 5.0 10.0 12.5 15.0 17.5 0.2 n\_components **Observations: Histogram:** Performance drops with more bins, which is unexpected. **GMM:** Significantly profits from more components. **KDE:** Does not profit from more bins. 2 Higher-dimensional data In [106]: from sklearn.datasets import load digits from sklearn.model selection import train test split digits = load digits() X = digits.dataY = digits.target X\_train, X\_test, y\_train, y\_test = train\_test\_split(X, Y, test\_size=0.33, random\_state=42) In [121]: from sklearn.neighbors import KernelDensity from sklearn.mixture import GaussianMixture from sklearn.ensemble import RandomForestClassifier from sklearn.neighbors import KDTree In [235]: # Fit the models kde = KernelDensity(bandwidth=0.1).fit(X train) gmm = GaussianMixture(n components=64).fit(X train) kdtree = KDTree(X train) In [236]: n\_samples = X\_test.shape[0] print(n samples) 594 In [237]: | kde samples = kde.sample(n samples) gmm samples = gmm.sample(n samples)[0] # Shuffle the gmm samples np.random.shuffle(gmm samples) kdtree samples = X train[kdtree.query(X test, k=1)[1].flatten()] In [238]: # Compute the MMD mmd results high  $d = {$ kernel name: { model name: mmd2(X test, model samples, kernel) for model name, model samples in zip(["kde", "gmm", "kdtree"], [kde samples, gmm samples, kdtre e samples]) } for kernel name, kernel in zip( ["squared\_exponential", "inverse multi quadratic"], [squared exponential kernel, inverse multi quadratic kernel]) In [239]: | pd.DataFrame.from dict(mmd results high d, orient="index") Out[239]: kde gmm kdtree **squared\_exponential** 0.146513 7.602031e-13 0.363943 inverse\_multi\_quadratic 6.478762 6.303493e+00 6.804585 In [240]: # Show some samples fig, ax = plt.subplots(10, 3, figsize=(3, 10))for j, (model\_name, model\_samples) in enumerate(zip(["kde", "gmm", "kdtree"], [kde\_samples, gmm\_samples , kdtree samples])): for i in range (10): ax[i, j].imshow(model\_samples[i].reshape(8, 8), cmap="gray") **if** i == 0: ax[i, j].set title(model name) ax[i, j].axis("off") kde kdtree gmm In [266]: n samples = int(1e5) In [267]: kde samples = kde.sample(n samples) gmm samples = gmm.sample(n samples)[0] # Shuffle the gmm samples np.random.shuffle(gmm samples) kdtree samples = X train[kdtree.query(X test, k=1)[1].flatten()] In [268]: rf = RandomForestClassifier(n\_estimators=100).fit(X\_train, y\_train) # Print its score print(f"Random forest score: {rf.score(X\_test, y\_test):.3f}") Random forest score: 0.976

| In [270]: | <pre># For each generated sample, predict the label with the random forest y_pred_samples = {     model_name: rf.predict(model_samples) for model_name, model_samples in zip(["kde", "gmm", "kdtree"] }, [kde_samples, gmm_samples, kdtree_samples])  # Show the distribution of the predicted labels y_pred_distributions = {     model_name: np.bincount(y_pred_samples[model_name], minlength=10) / n_samples_model for model_name,     n_samples_model in zip(y_pred_samples, [n_samples, n_samples, X_test.shape[0]]) }  # Show the results fig, ax = plt.subplots(1, 3, figsize=(20, 5)) for i, model_name in enumerate(["kde", "gmm", "kdtree"]):     ax[i].bar(np.arange(10), y_pred_distributions[model_name], zorder=2)     ax[i].set_title(model_name)     ax[i].set_xlabel("Label")</pre> |
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|           | ax[i].set_vticks(np.arange(10)) ax[i].set_xticks(np.arange(10)) ax[i].grid(zorder=-1, axis="y")   Observations:  KDE and GMM result in similar, rather uniform distributions with less generated samples for digits 4, 5 and 9. Meanwhile, the KDTree tends   |
|           | to generate more digits of classes 4, 5 and 9 and is less uniform and has more digit-to-digit variation.  |
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