

1. Two-dimensional data

```
In [1]: import matplotlib.pyplot as plt
from sklearn.datasets import make_moons
from scipy.stats import multivariate_normal
import numpy as np
```

1. Two-dimensional Histogram

```
In [2]: class Histogram2D:
    def __init__(self, bins=20, range=None):
        self.bins = bins
        self.range = range

    def fit(self, X):
        hist, x_edges, y_edges = np.histogram2d(X[:,0], X[:,1],
                                                bins=self.bins,
                                                range=self.range)

        self.hist = hist / np.sum(hist)
        self.x_edges = x_edges
        self.y_edges = y_edges

        self.hx = x_edges[1] - x_edges[0]
        self.hy = y_edges[1] - y_edges[0]
        return self

    def sample(self, n_samples):
        probs = self.hist.flatten()
        probs /= np.sum(probs)

        idx = np.random.choice(len(probs), size=n_samples, p=probs)
        ix = idx // self.bins
        iy = idx % self.bins

        xs = self.x_edges[ix] + np.random.rand(n_samples) * self.hx
        ys = self.y_edges[iy] + np.random.rand(n_samples) * self.hy

        samples = np.stack([xs, ys], axis=1)
        return samples

    def score_samples(self, X):
        ix = np.searchsorted(self.x_edges, X[:,0], side='right') - 1
        iy = np.searchsorted(self.y_edges, X[:,1], side='right') - 1

        ix = np.clip(ix, 0, self.bins - 1)
        iy = np.clip(iy, 0, self.bins - 1)

        probs = self.hist[ix, iy]

        probs = np.maximum(probs, 1e-12)
        logp = np.log(probs)

        return logp
```

2. Single Gaussian

```
In [3]: class SingleGaussian:
    def __init__(self):
        self.mean = None
        self.cov = None

    def fit(self, X):
        self.mean = np.mean(X, axis=0)
        diff = X - self.mean
        self.cov = np.cov(diff.T, bias=True)
        return self

    def sample(self, n_samples):
        samples = np.random.multivariate_normal(self.mean, self.cov, size=n_samples)
        return samples

    def score_samples(self, X):
        # log p(x) = -1/2 [ (x-μ)^T Σ^{-1} (x-μ) + log|Σ| + D*log(2π) ]
        D = X.shape[1]
        diff = X - self.mean
        inv_cov = np.linalg.inv(self.cov)
        det_cov = np.linalg.det(self.cov)
        exp_term = np.einsum('ij,jk,ik->i', diff, inv_cov, diff)
        logp = -0.5 * (exp_term + np.log(det_cov) + D * np.log(2 * np.pi))

        return logp
```

3. GMM (Gaussian Mixture Model)

```
In [4]: class GMM:
    def __init__(self, n_components=3, max_iter=100, tol=1e-4, seed=0):
        self.K = n_components
        self.max_iter = max_iter
        self.tol = tol
        self.seed = seed

    def fit(self, X):
        rng = np.random.default_rng(self.seed)
        N, D = X.shape

        np.random.seed(0)
        self.pi = np.ones(self.K) / self.K
        self.mu = X[np.random.choice(N, self.K, replace=False)]
        self.sigma = np.array([np.cov(X.T) for _ in range(self.K)])

        log_likelihood_old = 0

        for step in range(self.max_iter):
            # E-step
            gamma = np.zeros((N, self.K))
            for k in range(self.K):
                rv = multivariate_normal(mean=self.mu[k], cov=self.sigma[k])
                gamma[:, k] = self.pi[k] * rv.pdf(X)
            gamma /= np.sum(gamma, axis=1, keepdims=True)

            # M-step
```

```

Nk = np.sum(gamma, axis=0)
self.pi = Nk / N
self.mu = (gamma.T @ X) / Nk[:, np.newaxis]
self.sigma = np.zeros((self.K, D, D))
for k in range(self.K):
    diff = X - self.mu[k]
    self.sigma[k] = (gamma[:, k][:, np.newaxis] * diff).T @ d
    self.sigma[k] = 0.5*(self.sigma[k] + self.sigma[k].T)
    self.sigma[k] += 1e-6*np.eye(D)

log_likelihood = np.sum(np.log(np.sum([
    self.pi[k] * multivariate_normal.pdf(X, self.mu[k], self.
        for k in range(self.K)
    ], axis=0))))
if abs(log_likelihood - log_likelihood_old) < self.tol:
    break
log_likelihood_old = log_likelihood
return self

def sample(self, n_samples):
    component = np.random.choice(self.K, size=n_samples, p=self.pi)
    samples = np.array([
        np.random.multivariate_normal(self.mu[k], self.sigma[k])
        for k in component
    ])
    return samples

def score_samples(self, X):
    pdf = np.sum([
        self.pi[k] * multivariate_normal.pdf(X, self.mu[k], self.sig
            for k in range(self.K)
    ], axis=0)
    return np.log(pdf + 1e-12)

```

4. KDE (Kernel Density Estimation) with a Gaussian Kernel

In [5]:

```

class GaussianKDE:
    def __init__(self, bandwidth=0.2):
        self.bandwidth = bandwidth
        self.X_train = None
        self.N = None
        self.D = None

    def fit(self, X):
        self.X_train = X
        self.N, self.D = X.shape
        return self

    def score_samples(self, X):
        h = self.bandwidth
        N, D = self.N, self.D
        Xq = X[:, None, :]
        Xtrain = self.X_train[None, :, :]

        diff = Xq - Xtrain
        dist2 = np.sum(diff**2, axis=2)

        kernel_vals = np.exp(-0.5 * dist2 / (h**2))

```

```

    norm_const = (2 * np.pi)**(D/2) * (h*D) * N
    p = np.sum(kernel_vals, axis=1) / norm_const

    return np.log(p + 1e-12)

def sample(self, n_samples):
    idx = np.random.choice(self.N, size=n_samples, replace=True)
    centers = self.X_train[idx]
    noise = np.random.randn(n_samples, self.D) * self.bandwidth
    return centers + noise

```

In [6]:

```

import numpy as np

def _pdist2(X, Y):
    XX = (X**2).sum(1, keepdims=True)
    YY = (Y**2).sum(1, keepdims=True).T
    d2 = XX + YY - 2 * X @ Y.T
    return np.maximum(d2, 0.0)

def mmd2_unbiased(X, Y, h=1.0, kernel='se'):
    n, m = len(X), len(Y)
    dxx = _pdist2(X, X)
    dyy = _pdist2(Y, Y)
    dxy = _pdist2(X, Y)

    if kernel == 'se':
        Kxx = np.exp(-dxx/(h*h))
        Kyy = np.exp(-dyy/(h*h))
        Kxy = np.exp(-dxy/(h*h))
    elif kernel == 'imq':
        Kxx = 1.0/np.sqrt(1.0 + dxx/(h*h))
        Kyy = 1.0/np.sqrt(1.0 + dyy/(h*h))
        Kxy = 1.0/np.sqrt(1.0 + dxy/(h*h))
    else:
        raise ValueError("kernel must be 'se' or 'imq'")

    np.fill_diagonal(Kxx, 0.0)
    np.fill_diagonal(Kyy, 0.0)

    term_x = Kxx.sum()/(n*(n-1))
    term_y = Kyy.sum()/(m*(m-1))
    term_xy = 2.0*Kxy.mean()
    return term_x + term_y - term_xy

def median_heuristic(X, max_n=800):
    idx = np.random.choice(len(X), size=min(max_n, len(X)), replace=False)
    Z = X[idx]
    d2 = _pdist2(Z, Z)
    med = np.median(d2[np.triu_indices_from(d2, k=1)])
    return np.sqrt(0.5*med)

```

In [7]:

```

def make_data(n, noise=0.1, seed=0):
    X, _ = make_moons(n_samples=n, noise=noise, random_state=seed)
    return X.astype(float)

X_test = make_data(2000, noise=0.1, seed=123)

train_sizes = [100, 200, 500, 1000]
hist_bins_list = [10, 20, 30, 50, 80]

```

```

K_list = [1, 2, 3, 5, 8, 12]
kde_bandwidth_list = [0.05, 0.1, 0.2, 0.3]

def plot_curves(results_dict, title):
    """
    results_dict: {label: {"x": list_sizes, "y": list_values}}
    """
    for label, d in results_dict.items():
        plt.plot(d["x"], d["y"], marker="o", label=label)
    plt.xlabel("Train size")
    plt.ylabel("MMD$^2$")
    plt.title(title)
    plt.legend()
    plt.tight_layout()
    plt.show()

def eval_hist_over_bins(train_size, bins_list, kernel="se", R=5, fixed_range=True):
    Xtr_list = [make_data(train_size, noise=0.1, seed=12345+r) for r in range(R)]
    mmds = []
    for b in bins_list:
        vals = []
        for r in range(R):
            X_train = Xtr_list[r]
            model = Histogram2D(bins=b, range=fixed_range).fit(X_train)
            X_gen = model.sample(2000)
            vals.append(mmd2_unbiased(X_test, X_gen, h=h_fixed, kernel=kernel))
        mmds.append(float(np.mean(vals)))
    return {"x": bins_list, "y": mmds, "label": f"n={train_size}", "kernel": kernel}

def plot_results_group_bins(group, title_prefix):
    for ker in ("se", "imq"):
        subset = [g for g in group if g["kernel"] == ker]
        results = {g["label"]: {"x": g["x"], "y": g["y"]} for g in subset}
        for label, d in results.items():
            plt.plot(d["x"], d["y"], marker="o", label=label)
        plt.xlabel("bins")
        plt.ylabel("MMD$^2$")
        plt.title(f"{title_prefix} - {ker.upper()} kernel")
        plt.legend()
        plt.tight_layout()
        plt.show()

```

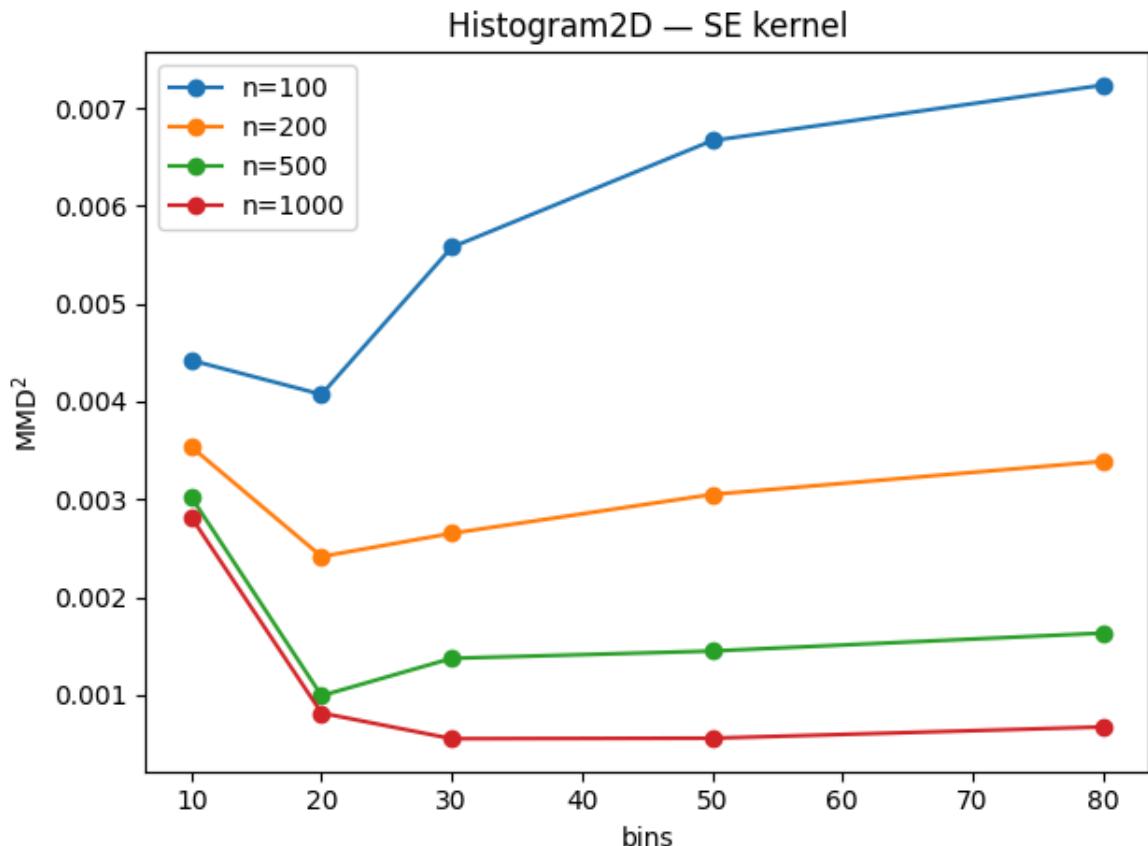
```

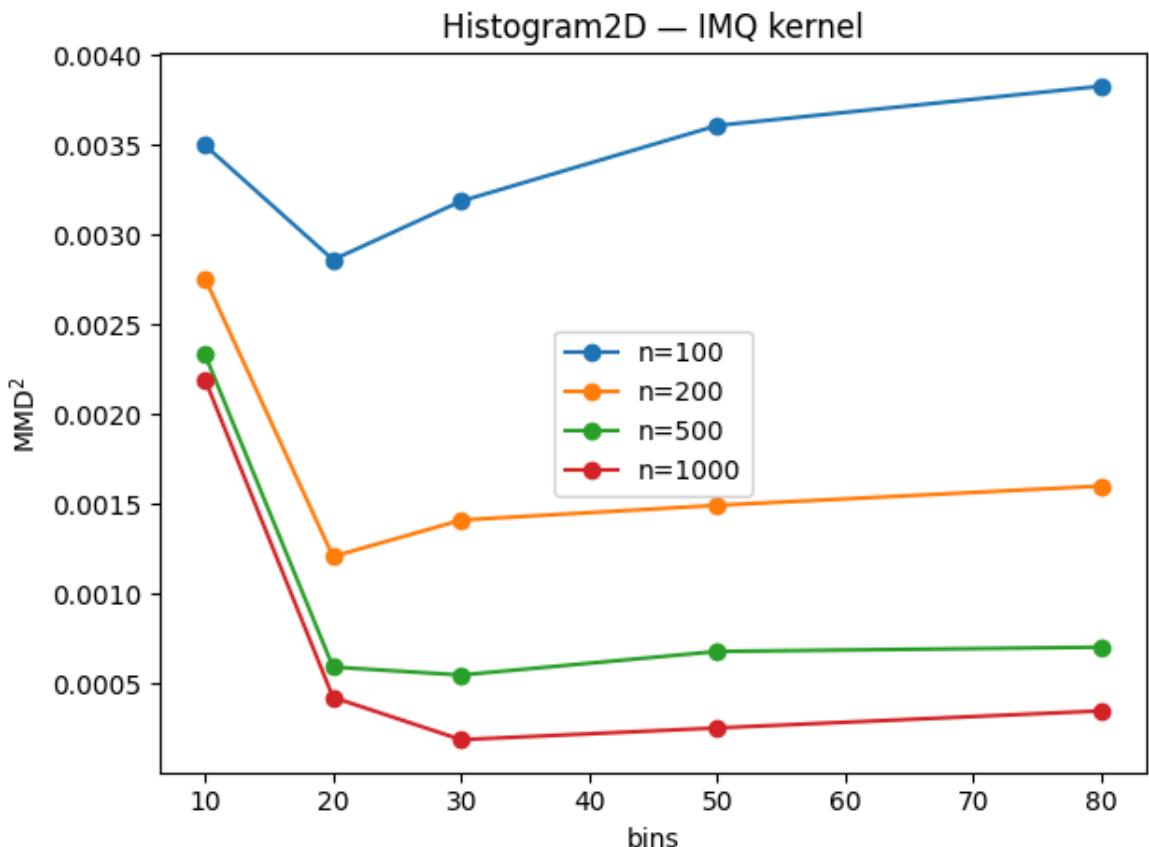
In [8]: h_fixed = 0.12
pad = 0.2
fixed_range = [(X_test[:,0].min()-pad, X_test[:,0].max()+pad),
                (X_test[:,1].min()-pad, X_test[:,1].max()+pad)]

all_hist = []
for n in train_sizes:
    all_hist.append(eval_hist_over_bins(n, hist_bins_list, kernel="se",
                                        fixed_range=fixed_range, h_fixed=h_fixed))
    all_hist.append(eval_hist_over_bins(n, hist_bins_list, kernel="imq",
                                        fixed_range=fixed_range, h_fixed=h_fixed))
plot_results_group_bins(all_hist, "Histogram2D")

```

```
/var/folders/jq/_3nxnjcd16nb8qvqvyf92n7r0000gn/T/ipykernel_8940/222114344
1.py:6: RuntimeWarning: divide by zero encountered in matmul
d2 = XX + YY - 2 * X @ Y.T
/var/folders/jq/_3nxnjcd16nb8qvqvyf92n7r0000gn/T/ipykernel_8940/222114344
1.py:6: RuntimeWarning: overflow encountered in matmul
d2 = XX + YY - 2 * X @ Y.T
/var/folders/jq/_3nxnjcd16nb8qvqvyf92n7r0000gn/T/ipykernel_8940/222114344
1.py:6: RuntimeWarning: invalid value encountered in matmul
d2 = XX + YY - 2 * X @ Y.T
```





Histogram2D — SE kernel

For all training sizes, MMD^2 drops markedly when we move from 10 to 20 bins and then increases again as the grid gets finer (30–80). Larger training sets consistently achieve lower MMD^2 across the entire range.

The initial improvement ($10 \rightarrow 20$ bins) reflects reduced bias: a very coarse grid cannot capture the curved “two-moons” structure. Beyond 20 bins, variance dominates: many bins become sparsely populated or empty, so the histogram sample generator picks bins that do not represent the test distribution well, which pushes MMD^2 up. With more data, the variance penalty is smaller, hence the shallower increase.

Histogram2D — IMQ kernel

The overall pattern matches the SE plot: a clear drop between 10 and 20 bins, followed by a mild increase as the grid is refined. Absolute MMD^2 values are smaller than with SE.

The IMQ kernel weights larger pairwise distances more heavily and is less sensitive to very local misalignments than SE. Consequently, the variance introduced by many tiny bins hurts slightly less in IMQ, hence the lower scale.

```
In [9]: def eval_gmm_over_components(train_size, k_list, kernel="se",
                               R=5, h_fixed=None, seed_base=24680, ngen=200
                               Xtr_list = [make_data(train_size, noise=0.1, seed=seed_base + r) for
```

```

mmds = []
for K in k_list:
    vals = []
    for r in range(R):
        X_train = Xtr_list[r]
        model = GMM(n_components=K, seed=0).fit(X_train)
        X_gen = model.sample(ngen)
        h = h_fixed if h_fixed is not None else median_heuristic(np.var(vals))
        vals.append(mmd2_unbiased(X_test, X_gen, h=h, kernel=kernel))
    mmds.append(float(np.mean(vals)))
return {"x": k_list, "y": mmds, "label": f"n={train_size}", "kernel": kernel}

def plot_results_group_components(group, title_prefix):
    for ker in ("se", "imq"):
        subset = [g for g in group if g["kernel"] == ker]
        results = {g["label"]: {"x": g["x"], "y": g["y"]} for g in subset}
        for label, d in results.items():
            plt.plot(d["x"], d["y"], marker="o", label=label)
        plt.xlabel("n_components (K)")
        plt.ylabel("MMD$^2$")
        plt.title(f"{title_prefix} - {ker.upper()} kernel")
        plt.legend()
        plt.tight_layout()
        plt.show()

h_fixed = median_heuristic(X_test)

all_gmm = []
for n in train_sizes:
    all_gmm.append(eval_gmm_over_components(n, K_list, kernel="se", R=5,
                                             all_gmm.append(eval_gmm_over_components(n, K_list, kernel="imq", R=5,
                                             plot_results_group_components(all_gmm, "GMM"))

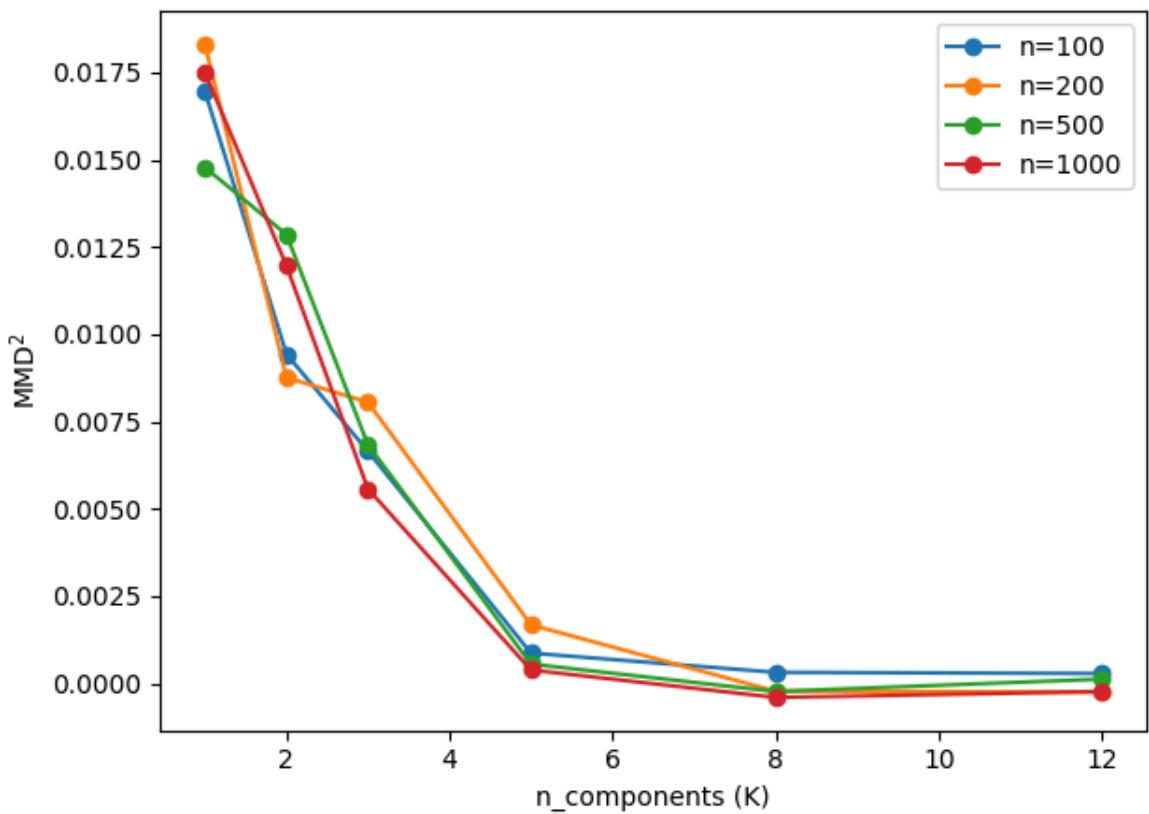
```

```

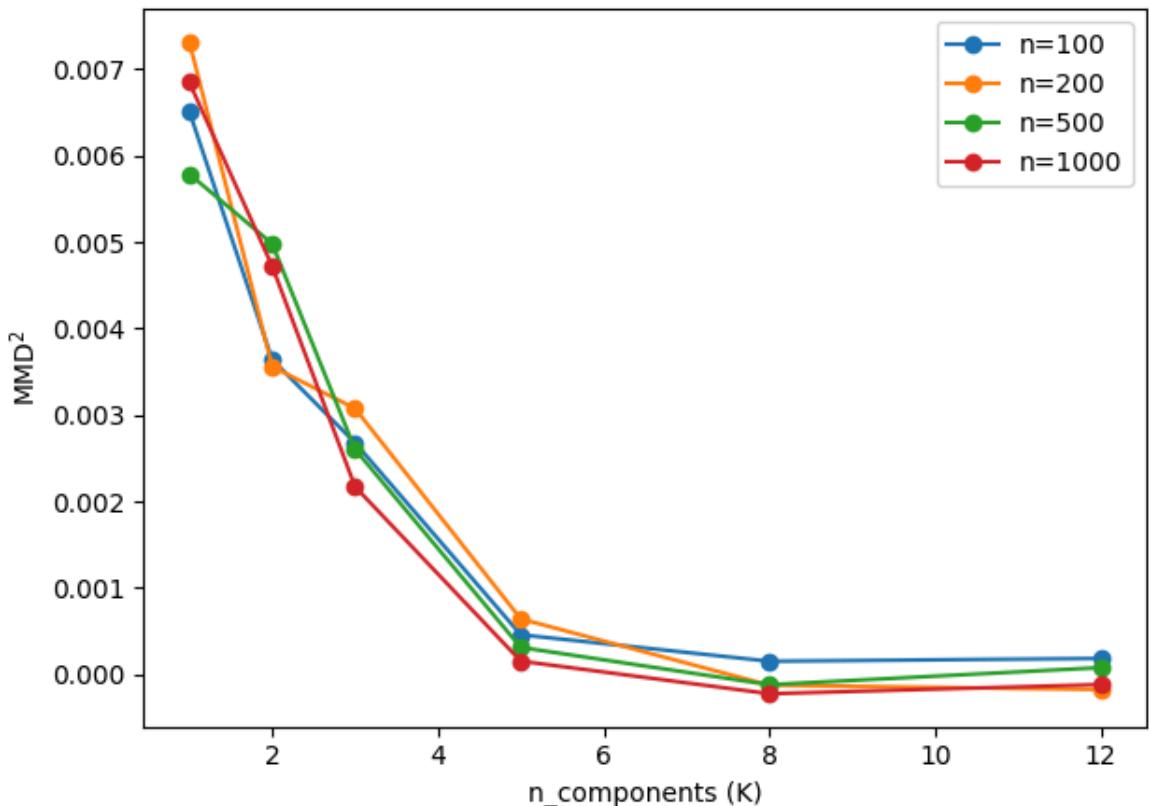
/var/folders/jq/_3nxnjcd16nb8qvqvyf92n7r0000gn/T/ipykernel_8940/222114344
1.py:6: RuntimeWarning: divide by zero encountered in matmul
  d2 = XX + YY - 2 * X @ Y.T
/var/folders/jq/_3nxnjcd16nb8qvqvyf92n7r0000gn/T/ipykernel_8940/222114344
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  d2 = XX + YY - 2 * X @ Y.T
/var/folders/jq/_3nxnjcd16nb8qvqvyf92n7r0000gn/T/ipykernel_8940/222114344
1.py:6: RuntimeWarning: invalid value encountered in matmul
  d2 = XX + YY - 2 * X @ Y.T
/var/folders/jq/_3nxnjcd16nb8qvqvyf92n7r0000gn/T/ipykernel_8940/335894962
3.py:30: RuntimeWarning: divide by zero encountered in matmul
  self.mu = (gamma.T @ X) / Nk[:, np.newaxis]
/var/folders/jq/_3nxnjcd16nb8qvqvyf92n7r0000gn/T/ipykernel_8940/335894962
3.py:30: RuntimeWarning: overflow encountered in matmul
  self.mu = (gamma.T @ X) / Nk[:, np.newaxis]
/var/folders/jq/_3nxnjcd16nb8qvqvyf92n7r0000gn/T/ipykernel_8940/335894962
3.py:30: RuntimeWarning: invalid value encountered in matmul
  self.mu = (gamma.T @ X) / Nk[:, np.newaxis]

```

GMM — SE kernel



GMM — IMQ kernel



GMM — SE kernel

MMD² decreases steeply as the number of components grows from 1 to 5, then flattens around zero (and even dips slightly below zero) for K ≥ 6–12. Larger training sets yield slightly better optima.

A single Gaussian cannot model the two-moon geometry. Increasing K reduces bias by allowing a multi-modal approximation; after 5 components the mixture is flexible enough to closely match the target, and additional components bring diminishing returns. Tiny negative values are again consistent with an unbiased MMD² estimate around the optimum.

GMM — IMQ kernel

Same qualitative behavior as with SE, at a smaller numerical scale. The optimum is reached around K≈6–8, after which the curve is essentially flat.

IMQ's heavier tail makes it slightly more tolerant to local overfitting; hence the very low (sometimes negative) MMD² once K is sufficient.

```
In [10]: def eval_kde_over_bandwidth(train_size, bw_list, kernel="se",
                                R=5, seed_base=31415, ngen=2000,
                                h_mmd_fixed=None):
    Xtr_list = [make_data(train_size, noise=0.1, seed=seed_base + r) for
                mmds = []
                for h_kde in bw_list:
                    vals = []
                    for r in range(R):
                        X_train = Xtr_list[r]
                        model = GaussianKDE(bandwidth=h_kde).fit(X_train)
                        X_gen = model.sample(ngen)
                        h_mmd = h_mmd_fixed if h_mmd_fixed is not None else median_he
                        vals.append(mmd2_unbiased(X_test, X_gen, h=h_mmd, kernel=kern
                        mmds.append(float(np.mean(vals)))
    return {"x": bw_list, "y": mmds, "label": f"n={train_size}", "kernel": kernel}

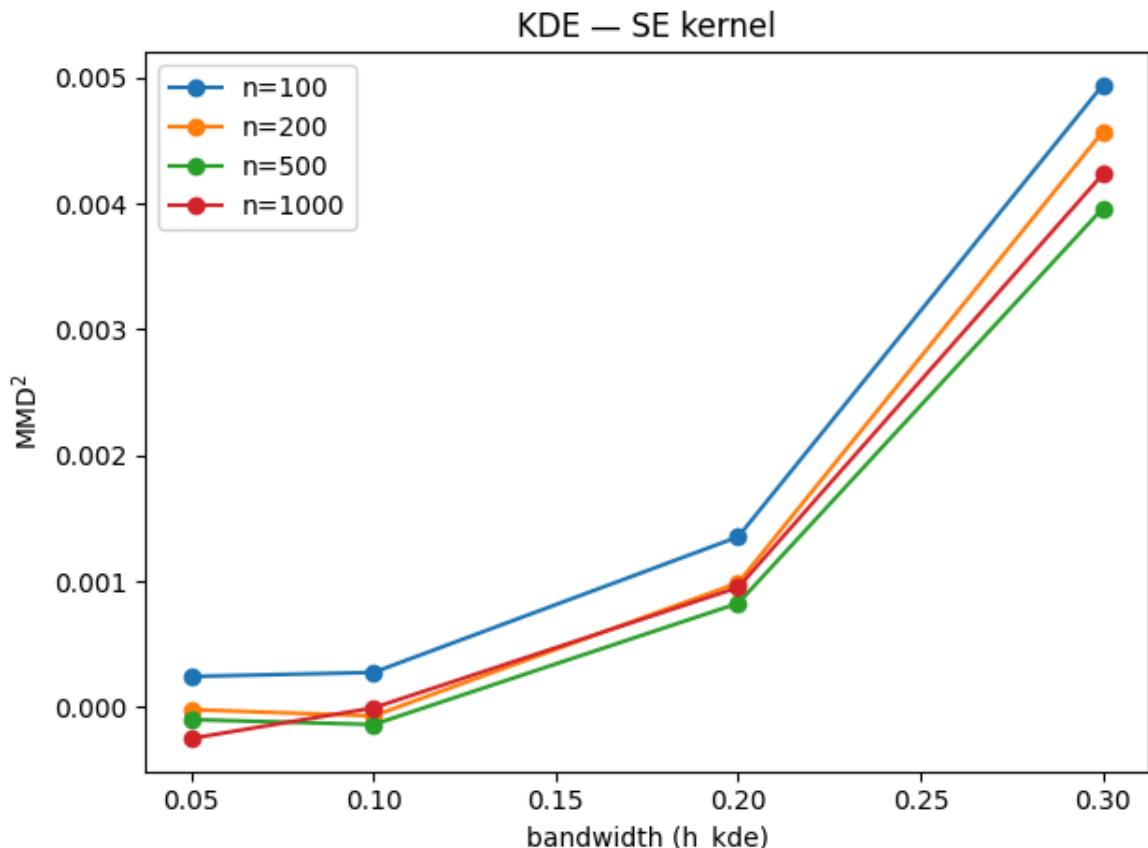
def plot_results_group_bandwidth(group, title_prefix):
    for ker in ("se", "imq"):
        subset = [g for g in group if g["kernel"] == ker]
        results = {g["label"] : {"x": g["x"], "y": g["y"]} for g in subset}
        for label, d in results.items():
            plt.plot(d["x"], d["y"], marker="o", label=label)
        plt.xlabel("bandwidth (h_kde)")
        plt.ylabel("MMD$^2$")
        plt.title(f"{title_prefix} - {ker.upper()} kernel")
        plt.legend()
        plt.tight_layout()
        plt.show()

bw_list = kde_bandwidth_list
h_mmd_fixed = median_heuristic(X_test)

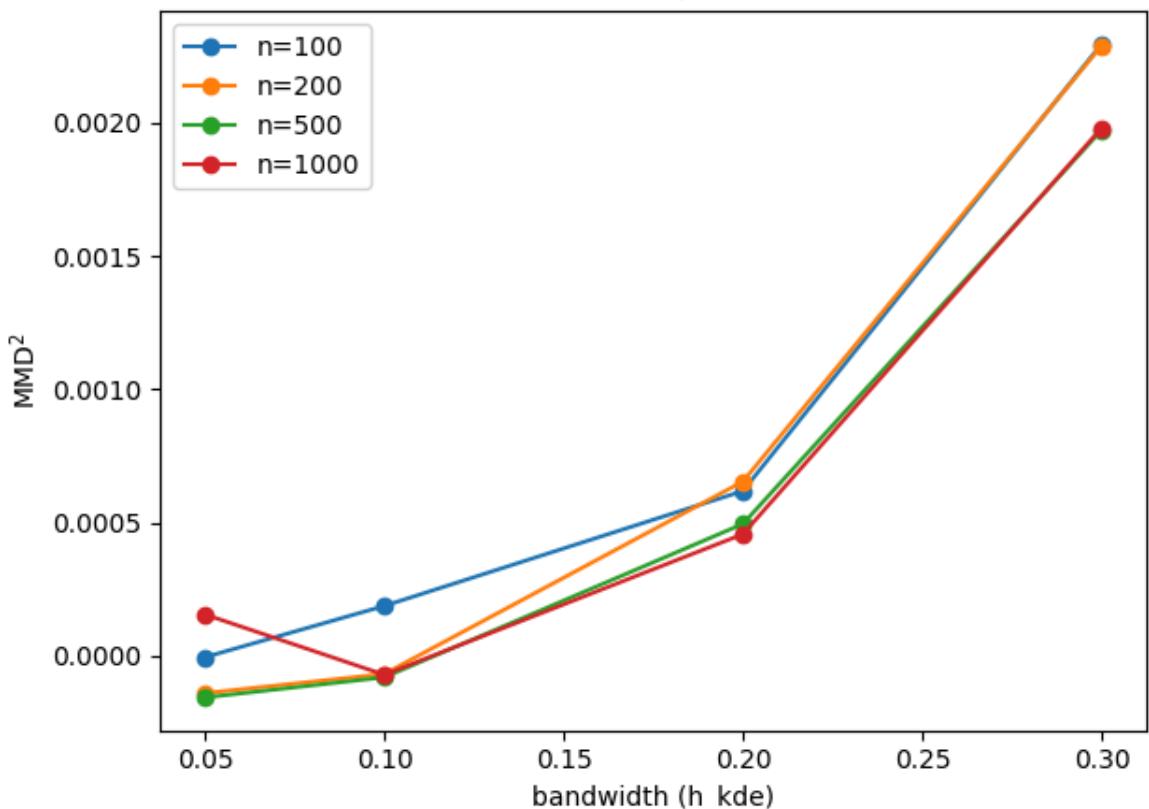
all_kde = []
for n in train_sizes:
    all_kde.append(eval_kde_over_bandwidth(n, bw_list, kernel="se", R=5,
                                            h_mmd_fixed=h_mmd_fixed))
    all_kde.append(eval_kde_over_bandwidth(n, bw_list, kernel="imq", R=5,
                                            h_mmd_fixed=h_mmd_fixed))

plot_results_group_bandwidth(all_kde, "KDE")
```

```
/var/folders/jq/_3nxnjcd16nb8qvqvyf92n7r0000gn/T/ipykernel_8940/222114344
1.py:6: RuntimeWarning: divide by zero encountered in matmul
d2 = XX + YY - 2 * X @ Y.T
/var/folders/jq/_3nxnjcd16nb8qvqvyf92n7r0000gn/T/ipykernel_8940/222114344
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/var/folders/jq/_3nxnjcd16nb8qvqvyf92n7r0000gn/T/ipykernel_8940/222114344
1.py:6: RuntimeWarning: invalid value encountered in matmul
d2 = XX + YY - 2 * X @ Y.T
```



KDE — IMQ kernel



KDE — SE kernel

MMD^2 increases monotonically with the bandwidth h ($0.05 \rightarrow 0.30$). The best region is at the smallest bandwidths; larger n helps but does not invert the trend.

The moons distribution has thin, curved structures. Small bandwidths capture these manifolds; large bandwidths oversmooth and fill the gap between the moons, producing samples that deviate from the test set, hence larger MMD^2 . With more data, even small h remains stable (variance drops), so the curves for larger n stay low near $h=0.05\text{--}0.10$.

KDE — IMQ kernel

The same monotone increase with bandwidth appears, with slightly smaller magnitudes than SE. For $n=1000$ and small h the estimates hover around zero and can be marginally negative.

Identical to the SE case: oversmoothing harms alignment with the moon geometry; IMQ's wider sensitivity range lowers the overall scale and masks some local discrepancies.

```
In [11]: def sanity_check_sg_vs_gmm1(train_sizes, h_fixed=None, R=5, ngen=2000, ke
      if h_fixed is None:
          h_fixed = median_heuristic(X_test)
      diffs = []
      for n in train_sizes:
          vals = []
          for r in range(R):
```

```

        X_train = make_data(n, noise=0.1, seed=10_000*n + r)
        sg = SingleGaussian().fit(X_train)
        g1 = GMM(n_components=1).fit(X_train)
        XgA = sg.sample(ngen); mmdA = mmd2_unbiased(X_test, XgA, h=h)
        XgB = g1.sample(ngen); mMDB = mmd2_unbiased(X_test, XgB, h=h)
        vals.append(abs(mmdA - mMDB))
    diffss.append((n, float(np.mean(vals))))
return diffss

print(sanity_check_sg_vs_gmm1(train_sizes, kernel="se"))
print(sanity_check_sg_vs_gmm1(train_sizes, kernel="imq"))

```

```

/var/folders/jq/_3nxnjcd16nb8qvqvyf92n7r0000gn/T/ipykernel_8940/222114344
1.py:6: RuntimeWarning: divide by zero encountered in matmul
d2 = XX + YY - 2 * X @ Y.T
/var/folders/jq/_3nxnjcd16nb8qvqvyf92n7r0000gn/T/ipykernel_8940/222114344
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d2 = XX + YY - 2 * X @ Y.T
/var/folders/jq/_3nxnjcd16nb8qvqvyf92n7r0000gn/T/ipykernel_8940/222114344
1.py:6: RuntimeWarning: invalid value encountered in matmul
d2 = XX + YY - 2 * X @ Y.T
[(100, 0.0006686948435117301), (200, 0.0010291972593730492), (500, 0.00130
59714436334247), (1000, 0.00031216550074530947)]
[(100, 0.00027353478721581226), (200, 0.00038382705668977836), (500, 0.000
23641252889725629), (1000, 0.00021200474914424562)]

```

```

In [12]: def make_grid(X, n=150, pad=0.2):
    lo = X.min(axis=0) - pad
    hi = X.max(axis=0) + pad
    xs = np.linspace(lo[0], hi[0], n)
    ys = np.linspace(lo[1], hi[1], n)
    GX, GY = np.meshgrid(xs, ys)
    G = np.column_stack([GX.ravel(), GY.ravel()])
    return xs, ys, GX, GY, G

def visualize_model(model, X_train, n_gen=1000, title="Model"):
    xs, ys, GX, GY, G = make_grid(np.vstack([X_train, X_test]))
    Z = np.exp(model.score_samples(G)).reshape(GX.shape)

    plt.contourf(GX, GY, Z, levels=20)
    plt.colorbar()
    plt.scatter(X_train[:, 0], X_train[:, 1], s=6, alpha=0.6)
    plt.axis("equal")
    plt.title(f"{title}: density (score_samples) + train pts")
    plt.tight_layout()
    plt.show()

    X_gen = model.sample(n_gen)
    plt.scatter(X_gen[:, 0], X_gen[:, 1], s=6, alpha=0.6, label="generate")
    plt.scatter(X_test[:, 0], X_test[:, 1], s=6, alpha=0.6, label="test")
    plt.axis("equal")
    plt.legend()
    plt.title(f"{title}: generated vs test")
    plt.tight_layout()
    plt.show()

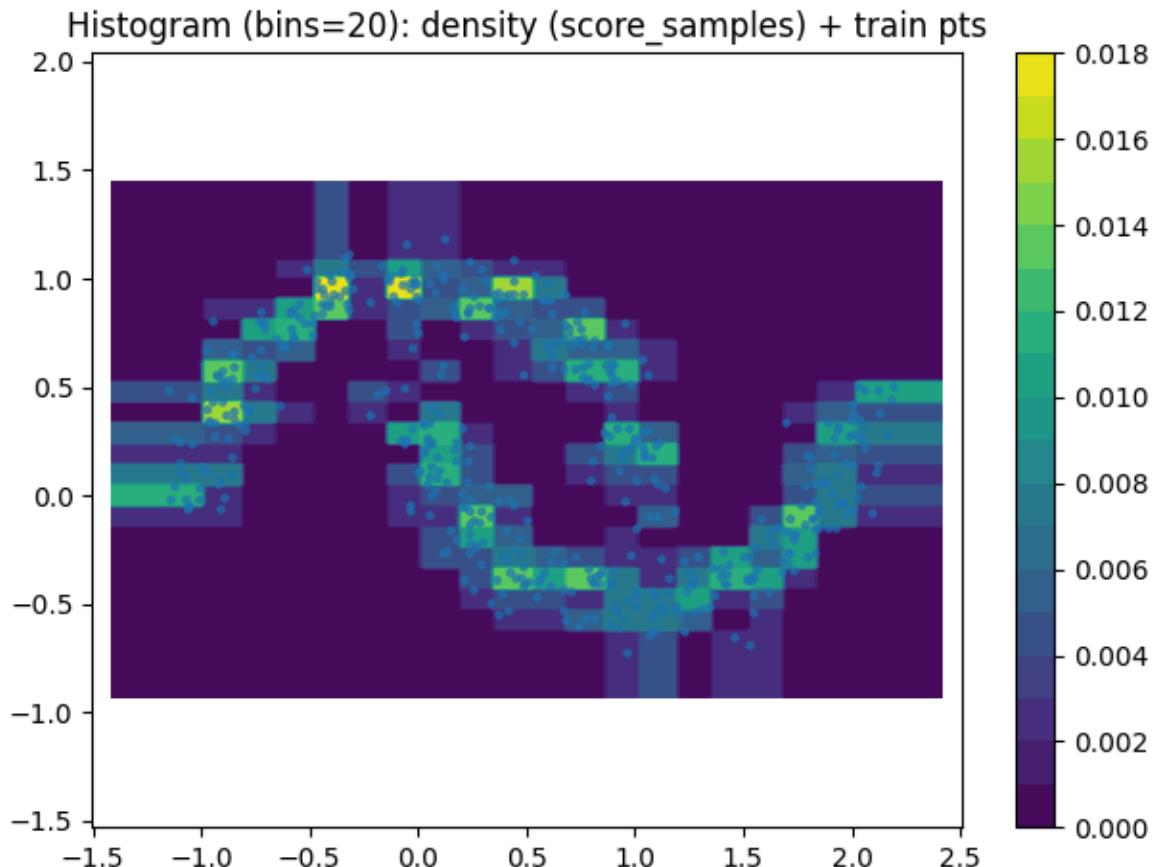
X_tr = make_data(500, noise=0.1, seed=7)

models_show = [

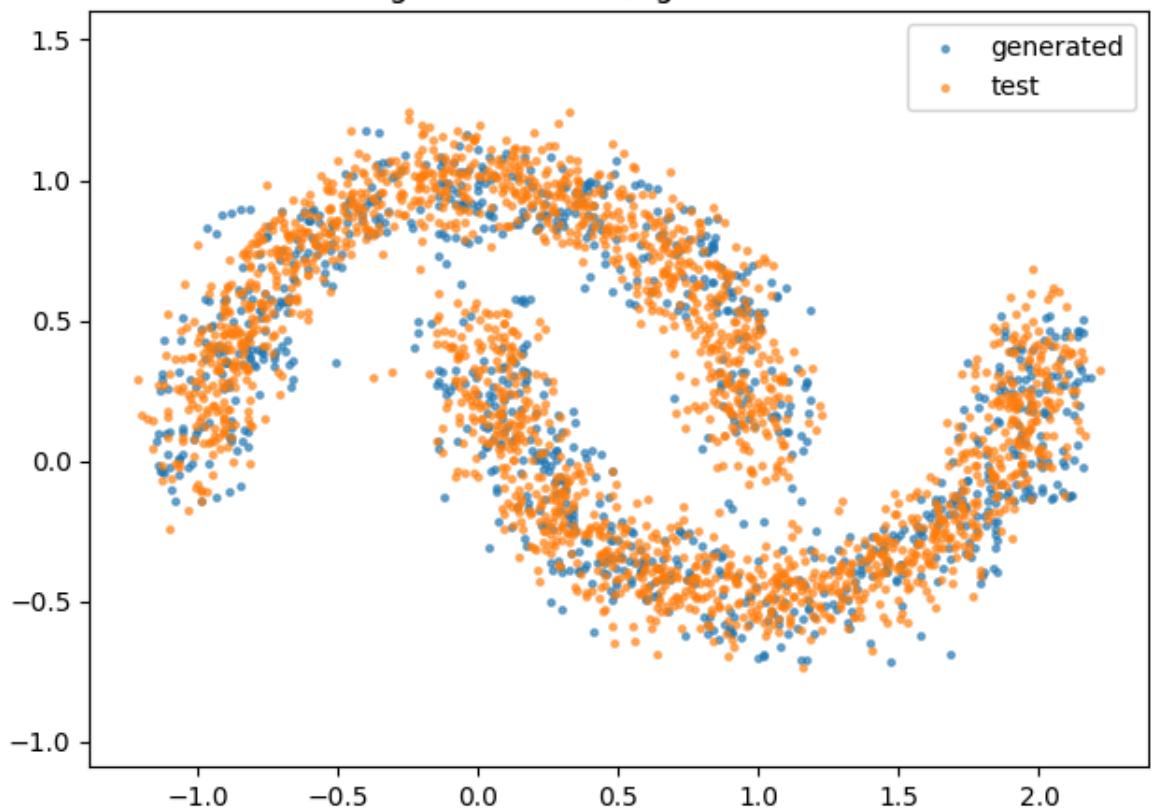
```

```
("Histogram (bins=20)", Histogram2D(bins=20).fit(X_tr)),
("Single Gaussian", SingleGaussian().fit(X_tr)),
("GMM (K=4)", GMM(n_components=4, seed=0).fit(X_tr)),
("KDE (h=0.15)", GaussianKDE(bandwidth=0.15).fit(X_tr)),
]

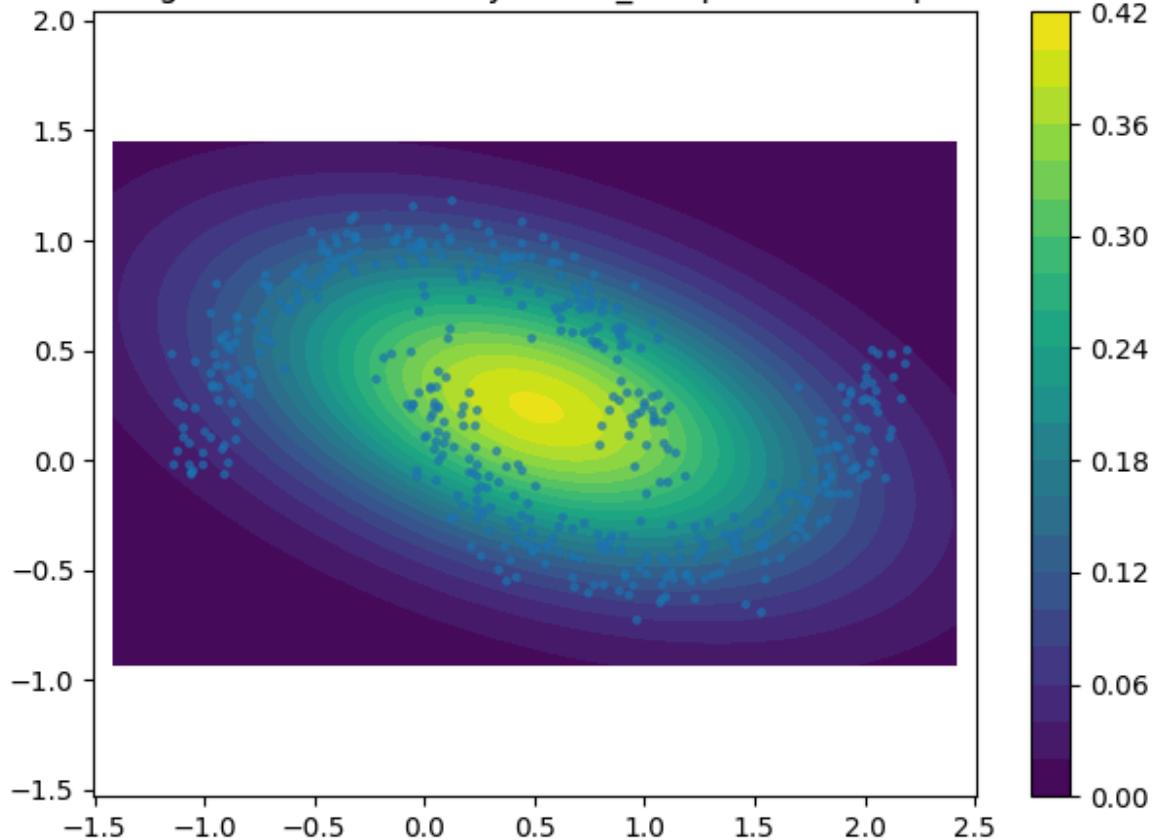
for name, mdl in models_show:
    visualize_model(mdl, X_tr, title=name)
```



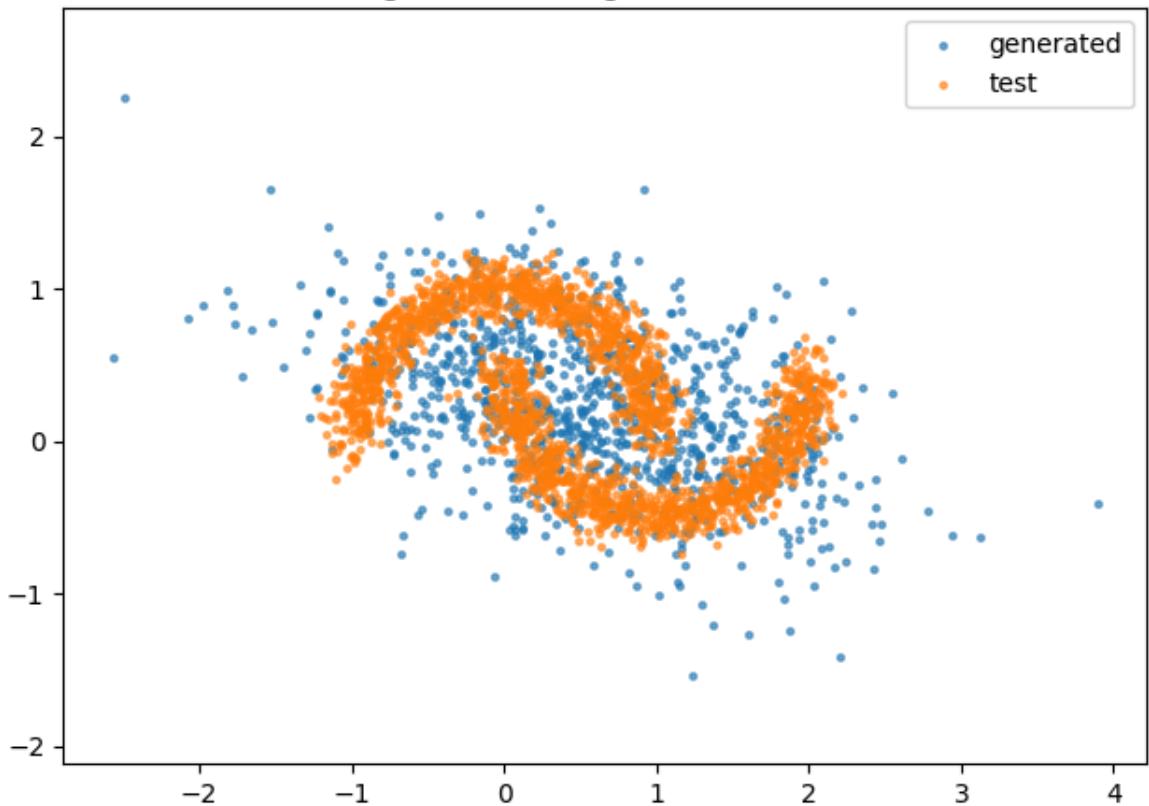
Histogram (bins=20): generated vs test



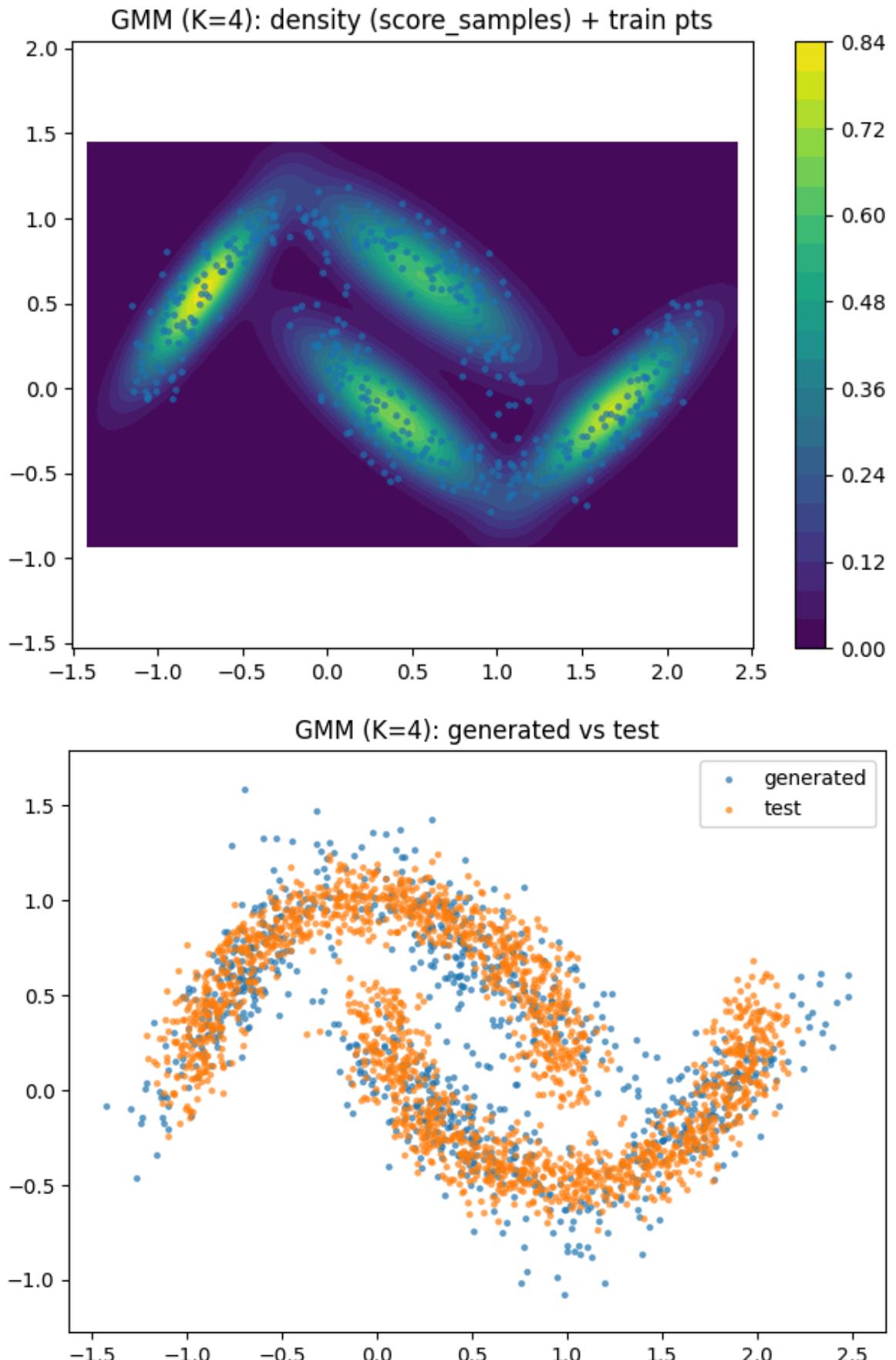
Single Gaussian: density (score_samples) + train pts

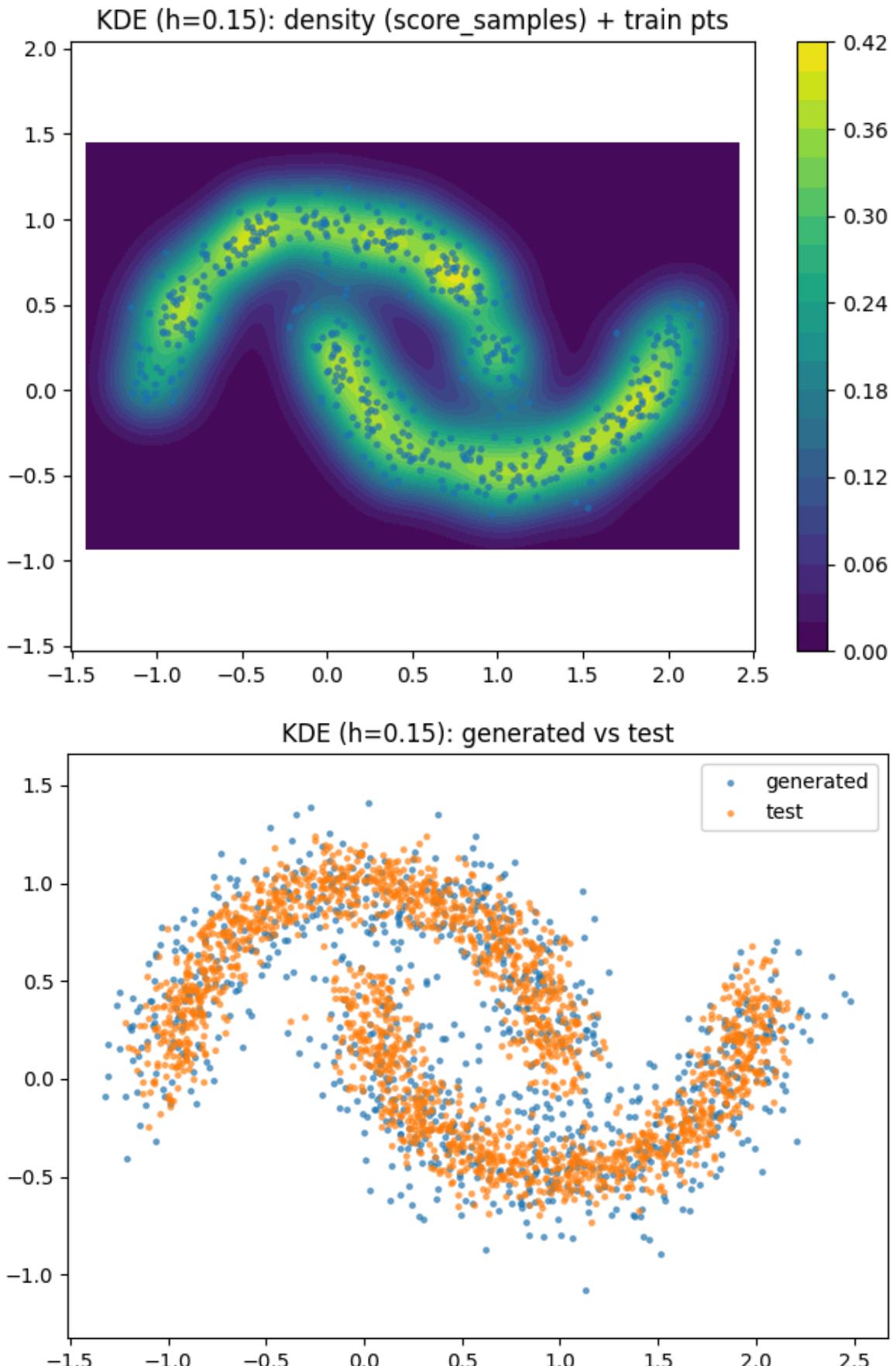


Single Gaussian: generated vs test



```
/Users/xinyi/Desktop/node2/node2/lib/python3.13/site-packages/scipy/stats/_covariance.py:630: RuntimeWarning: divide by zero encountered in matmul
      return x @ self._LP
/Users/xinyi/Desktop/node2/node2/lib/python3.13/site-packages/scipy/stats/_covariance.py:630: RuntimeWarning: overflow encountered in matmul
      return x @ self._LP
/Users/xinyi/Desktop/node2/node2/lib/python3.13/site-packages/scipy/stats/_covariance.py:630: RuntimeWarning: invalid value encountered in matmul
      return x @ self._LP
```





Histogram (bins=20): density (score_samples) + train points

The piecewise-constant nature of the 2D histogram is visible: density blocks align with grid cells and create jagged boundaries. Still, the model captures the two arcs

fairly well at this resolution.

Histogram (bins = 20): generated vs test

Generated samples broadly follow the moons and match the global shape. Small clumps near bin edges and a few tiny gaps reflect uniform sampling inside selected bins.

Single Gaussian: density (score_samples) + train points

Contours are elliptical and fill the central gap, which contradicts the bimodal curved structure of the moons. This shows strong model bias: a single Gaussian cannot represent the non-elliptical, multi-modal geometry.

Single Gaussian: generated vs test

Samples concentrate in the middle and spill between the two arcs, clearly misaligning with the test set. This is a bad model and explains the large MMD² obtained for K=1 vs the moons.

GMM (K = 4): density (score_samples) + train points

Multiple elongated components start to trace the arcs and carve out the low-density gap. Some leakage remains between the moons and at the tips, but the global pattern is largely correct. Increasing K typically tightens the fit.

GMM (K = 4): generated vs test

Generated points align closely with the test set. In the MMD² curves the optimum appears around K≈6–8, where these residual errors further diminish.

KDE (h = 0.15): density (score_samples) + train points

Gaussian KDE produces a smooth density that follows the curved manifolds and maintains the central gap. With this bandwidth the bias-variance trade-off is favorable.

KDE (h = 0.15): generated vs test

Generated samples are almost indistinguishable from the test points. Among the four models, KDE with a small h gives the best visual match.

2. Higher-dimensional data

In [13]:

```
from sklearn.datasets import load_digits
from sklearn.mixture import GaussianMixture
from sklearn.neighbors import KernelDensity
```

```

from sklearn.ensemble import RandomForestClassifier
from joblib import Parallel, delayed

In [14]: rng = np.random.RandomState(42)
digits = load_digits()
X_train, y_train = digits.data, digits.target
n_features = X_train.shape[1]
test_size = 2000

gmm_components = [1, 2, 3, 4, 5, 7, 10, 15, 20, 30, 50, 100]
kde_bandwidths = [0.001, 0.002, 0.005, 0.0075, 0.01, 0.02, 0.05, 0.075, 0
n_mins = [5, 10, 20, 50, 100, 200]

mmd_results = {
    'GMM': {'parameters': [], 'mmd_se': [], 'mmd_imq': [], 'model': []},
    'KDE': {'parameters': [], 'mmd_se': [], 'mmd_imq': [], 'model': []},
    'DF' : {'parameters': [], 'mmd_se': [], 'mmd_imq': [], 'model': []}
}

import numpy as np
from joblib import Parallel, delayed

class Node:
    pass

class DensityTree:
    def __init__(self, n_min=10):
        ''' n_min: minimum required number of instances in leaf nodes
        '''
        self.n_min = n_min
        self.bins = {
            'count': [],
            'mean': [],
            'cov': []
        }

    def fit(self, features, D_try=None):
        '''
        features: the feature matrix of the training sets
        '''
        N, D = features.shape

        if D_try is None:
            D_try = int(np.sqrt(D)) # number of features to consider for

        # initialize the root node
        self.root = Node()
        self.root.features = features

        # build the tree
        stack = [self.root]
        while len(stack):
            node = stack.pop()
            active_indices = self.select_active_indices(D, D_try)
            left, right = self.make_split_node(node, active_indices)
            if left is None: # no split found
                self.make_leaf_node(node)
            else:
                stack.append(left)

from sklearn.ensemble import RandomForestClassifier
from joblib import Parallel, delayed

```

```

        stack.append(right)

    self.weights_ = np.array(self.bins['count'])
    self.weights_ = self.weights_ / self.weights_.sum()
    self.means_ = np.array(self.bins['mean'])
    self.covariances_ = np.array(self.bins['cov'])
    self.n_components = self.weights_.shape[0]

    return self

def make_split_node(self, node, indices):
    """
    node: the node to be split
    indices: a numpy array of length 'D_try', containing the feature
             indices to be considered for the present split

    return: None, None -- if no suitable split has been found, or
            left, right -- the children of the split
    """

    # find best feature j_min (among 'indices') and best threshold t_
    l_min = float('inf') # upper bound for the loss, later the loss
    j_min, t_min = None, None

    for j in indices:
        thresholds = self.find_thresholds(node, j)

        # compute loss for each threshold
        for t in thresholds:
            loss = self.compute_loss_for_split(node, j, t)

            # remember the best split so far
            # (the condition is never True when loss = float('inf'))
            if loss < l_min:
                l_min = loss
                j_min = j
                t_min = t

    if j_min is None: # no split found
        return None, None

    # create children for the best split
    left, right = self.make_children(node, j_min, t_min)

    # turn the current 'node' into a split node
    # (store children and split condition)
    node.left = left
    node.right = right
    node.split_index = j_min
    node.threshold = t_min

    return left, right

def select_active_indices(self, D, D_try):
    """
    return a 1-D array with D_try randomly selected indices from
    """
    return np.random.choice(range(D), size=D_try, replace=False)

def find_thresholds(self, node, j):
    """
    return: a 1-D array with all possible thresholds along featur

```

```

    ...
    if node.features.shape[0] / 2 < self.n_min:
        return []
    sort = np.sort(node.features[:,j])
    t = (sort[:-1] + sort[1:]) / 2
    if self.n_min > 1:
        t = t[(self.n_min-1):(-self.n_min+1)]
    return t

def make_children(self, node, j, t):
    ''' execute the split in feature j at threshold t

        return: left, right -- the children of the split, with feature
        properly assigned according to the split
    '''
    left = Node()
    right = Node()

    left.features = node.features[node.features[:,j] <= t]
    right.features = node.features[node.features[:,j] > t]

    return left, right

def entropy_gaussian(self, features):
    ''' calculate the differential entropy of a d-variate Gaussian distribution

        features: a numpy array
        return: entropy
    '''
    if features.shape[0] == 1:
        print(features)
    sigma = np.linalg.det(np.cov(features.T))
    entropy = np.multiply(np.power((2 * np.pi * np.e), features.shape[1]), -np.log(sigma) / 2)
    if entropy <= 0:
        return 0
    if np.isnan(entropy):
        entropy = np.inf
    return entropy

def compute_loss_for_split(self, node, j, t):
    # return the loss if we would split the instance along feature j
    # or float('inf') if there is no feasible split
    l_response = node.features[node.features[:,j] <= t]
    r_response = node.features[node.features[:,j] > t]
    if len(l_response) <= 1 or len(r_response) <= 1:
        return float('inf')

    loss = self.entropy_gaussian(l_response) + self.entropy_gaussian(r_response)
    return loss

def make_leaf_node(self, node):
    # turn node into a leaf node
    self.bins['count'].append(node.features.shape[0])
    self.bins['mean'].append(node.features.mean(0))
    self.bins['cov'].append(np.cov(node.features.T) + 1e-6 * np.eye(node.features.shape[1]))

def sample(self, n_samples):
    samples = []

```

```

# Choose the components of samples
component_choices = np.random.choice(self.n_components, size=n_sa

    for k in range(self.n_components):
        # Compute the numbers of samples of the component k
        n_k = np.sum(component_choices == k)
        if n_k > 0:
            # Generate the samples from the normal distribution with
            samples_k = np.random.multivariate_normal(mean=self.means
                                                        cov=self.covari
                                                        size=n_k)
            samples.append(samples_k)

    # Combine samples
    samples = np.vstack(samples)

    # Shuffle samples
    np.random.shuffle(samples)

    return samples

def bootstrap_sampling(features):
    '''return a bootstrap sample of features
    ...
    N = features.shape[0]
    inds = np.random.choice(N, N, replace=True)
    return features[inds]

class DensityForest():
    ...
    This class implements a random forest for density estimation, i.e. a
    collection of density trees according to the method described in
    Criminisi, Shotton & Konukoglu (2011): Decision Forests, Chapter 5
    https://www.microsoft.com/en-us/research/wp-content/uploads/2016/02/C

    Each tree performs a recursive subdivision of the training domain
    into adaptive bins. For the trees to differ from one another, this
    is randomized in the usual way (i.e. each tree only sees a bootstrap
    sample of the training set, and only a random subset of the features
    is considered in each split decision).
    The bins of the trees contain a Gaussian fit to the instances within
    bin -- this works much better than a uniform distribution over the bi

    To sample from the forest, first a tree is selected uniformly at rand
    Then a bin in that tree is selected according to the probability of e
    bin, i.e. using the discrete distribution over the fraction of instan
    located in each bin. Finally, a sample is generated from the Gaussian
    the selected bin.

    Usage:
    from density_forest import DensityForest

    Xtrain = ... # load/create the training set
    min_samples_per_bin = 5

    model = DensityForest(n_min=min_samples_per_bin)
    model.fit(Xtrain)

```

```

samples = model.sample(n_samples=20)
...
def __init__(self, n_trees=10, n_min=1):
    self.n_trees = n_trees
    self.trees = [DensityTree(n_min) for _ in range(self.n_trees)]

def fit(self, features):
    self.trees = Parallel(n_jobs=-1)(delayed(self.fit_tree))(tree, fea)

def fit_tree(self, tree, features):
    bootstrap_features = bootstrap_sampling(features)
    tree.fit(bootstrap_features)
    return tree

def sample(self, n_samples):
    samples = []

    # Choose the trees of samples
    tree_choices = np.random.choice(self.n_trees, size=n_samples)

    for k in range(self.n_trees):
        # Compute the numbers of samples of the tree k
        n_k = np.sum(tree_choices == k)
        if n_k > 0:
            # Generate the samples from the tree k
            samples_k = self.trees[k].sample(n_k)
            samples.append(samples_k)

    # Combine samples
    samples = np.vstack(samples)

    # Shuffle samples
    np.random.shuffle(samples)

    return samples

```

In [15]:

```

for n_comp in gmm_components:
    gmm = GaussianMixture(n_components=n_comp, init_params='k-means++', r
    gmm.fit(X_train)
    samples, _ = gmm.sample(test_size)
    mmd_se = mmd2_unbiased(samples, X_train, h=1.0, kernel='se')
    mmd_imq = mmd2_unbiased(samples, X_train, h=1.0, kernel='imq')
    mmd_results['GMM']['parameters'].append(n_comp)
    mmd_results['GMM']['mmd_se'].append(float(mmd_se))
    mmd_results['GMM']['mmd_imq'].append(float(mmd_imq))
    mmd_results['GMM']['model'].append(gmm)

for bw in kde_bandwidths:
    kde = KernelDensity(kernel='gaussian', bandwidth=bw)
    kde.fit(X_train)
    samples = kde.sample(test_size, random_state=42)
    mmd_se = mmd2_unbiased(samples, X_train, h=1.0, kernel='se')
    mmd_imq = mmd2_unbiased(samples, X_train, h=1.0, kernel='imq')
    mmd_results['KDE']['parameters'].append(bw)
    mmd_results['KDE']['mmd_se'].append(float(mmd_se))
    mmd_results['KDE']['mmd_imq'].append(float(mmd_imq))
    mmd_results['KDE']['model'].append(kde)

for n_min in n_mins:
    df = DensityForest(n_trees=10, n_min=n_min)

```

```
df.fit(X_train)
samples = df.sample(test_size)
mmd_se = mmd2_unbiased(samples, X_train, h=1.0, kernel='se')
mmd_imq = mmd2_unbiased(samples, X_train, h=1.0, kernel='imq')
mmd_results['DF']['parameters'].append(n_min)
mmd_results['DF']['mmd_se'].append(float(mmd_se))
mmd_results['DF']['mmd_imq'].append(float(mmd_imq))
mmd_results['DF']['model'].append(df)
```

```
/Users/xinyi/Desktop/node2/node2/lib/python3.13/site-packages/sklearn/util
s/extmath.py:203: RuntimeWarning: divide by zero encountered in matmul
    ret = a @ b
/Users/xinyi/Desktop/node2/node2/lib/python3.13/site-packages/sklearn/util
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1.py:6: RuntimeWarning: divide by zero encountered in matmul
    d2 = XX + YY - 2 * X @ Y.T
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    current_pot = closest_dist_sq @ sample_weight
/Users/xinyi/Desktop/node2/node2/lib/python3.13/site-packages/sklearn/cluster/_kmeans.py:237: RuntimeWarning: invalid value encountered in matmul
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```



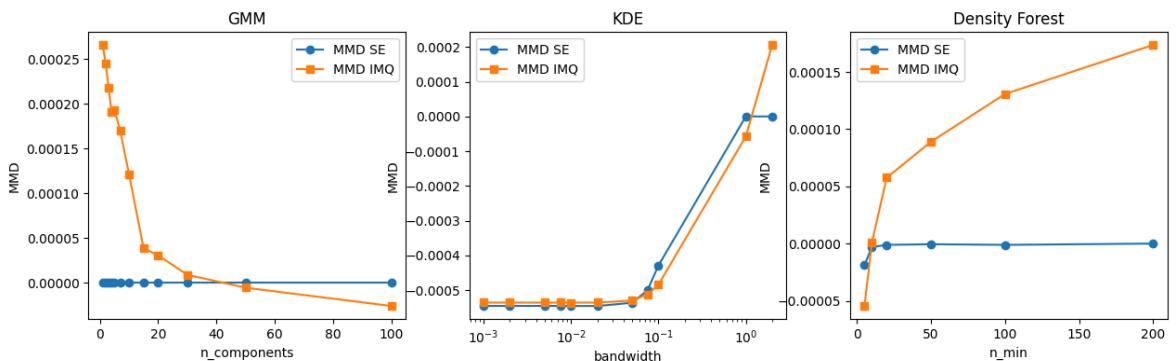
```
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```

```
In [16]: fig, axes = plt.subplots(1, 3, figsize=(15, 4))

ax = axes[0]
ax.plot(mmd_results['GMM']['parameters'], mmd_results['GMM']['mmd_se'],
        ax.plot(mmd_results['GMM']['parameters'], mmd_results['GMM']['mmd_imq'],
        ax.set_xlabel('n_components'); ax.set_ylabel('MMD'); ax.set_title('GMM');

ax = axes[1]
ax.plot(mmd_results['KDE']['parameters'], mmd_results['KDE']['mmd_se'],
        ax.plot(mmd_results['KDE']['parameters'], mmd_results['KDE']['mmd_imq'],
        ax.set_xscale('log'); ax.set_xlabel('bandwidth'); ax.set_ylabel('MMD'); a

ax = axes[2]
ax.plot(mmd_results['DF']['parameters'], mmd_results['DF']['mmd_se'],
        ax.plot(mmd_results['DF']['parameters'], mmd_results['DF']['mmd_imq'],
        ax.set_xlabel('n_min'); ax.set_ylabel('MMD'); ax.set_title('Density Fore
plt.show()
```



Digits is 64-D with pixel values $\approx 0\text{--}16$. With the SE kernel and $h=1.0$, off-diagonal kernel values are ~ 0 , so SE-MMD² stays near zero (tiny negatives are unbiased-estimator noise). The IMQ kernel decays slower, hence it's informative.

GMM:

As n_components increases, flexibility improves \rightarrow IMQ-MMD² decreases and plateaus. SE stays ~ 0 due to the bandwidth issue.

KDE:

Very small bandwidth \rightarrow lowest MMD². Increasing bandwidth oversmooths \rightarrow IMQ-MMD² rises sharply. SE shows the same trend but compressed near zero.

Density Forest:

Larger n_min \rightarrow larger leaves \rightarrow higher bias \rightarrow IMQ-MMD² increases with n_min. SE remains 0 (same reason).

```
In [17]: def select_models(res, model_name):
    mmd_scores = (np.array(res[model_name]['mmd_se']) + np.array(res[model_name]['mmd_imq']))
    best_idx = np.argmin(mmd_scores); worst_idx = np.argmax(mmd_scores)
    return (res[model_name]['model'][best_idx], res[model_name]['model'][worst_idx],
            res[model_name]['parameters'][best_idx], res[model_name]['parameters'][worst_idx])

gmm_good, gmm_bad, K_good, K_bad = select_models(mmd_results, 'GMM')
kde_good, kde_bad, h_good, h_bad = select_models(mmd_results, 'KDE')
df_good, df_bad, nmin_good, nmin_bad = select_models(mmd_results, 'DF')

def gen_samples(model, kind, n=test_size):
    if kind == 'GMM':
        s, _ = model.sample(n); return s
    elif kind == 'KDE':
        return model.sample(n, random_state=42)
    else:
        return model.sample(n)

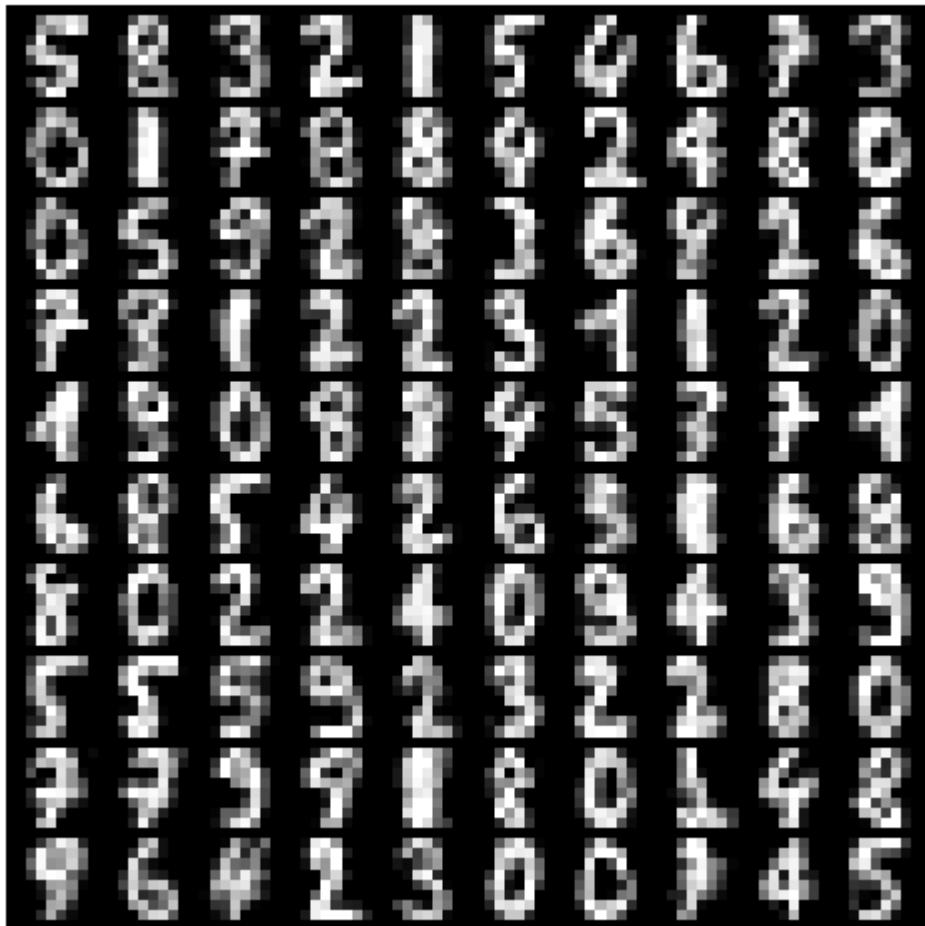
samples_gmm_good = gen_samples(gmm_good, 'GMM')
samples_gmm_bad = gen_samples(gmm_bad, 'GMM')
samples_kde_good = gen_samples(kde_good, 'KDE')
samples_kde_bad = gen_samples(kde_bad, 'KDE')
```

```
samples_df_good = gen_samples(df_good, 'DF')
samples_df_bad = gen_samples(df_bad, 'DF')
```

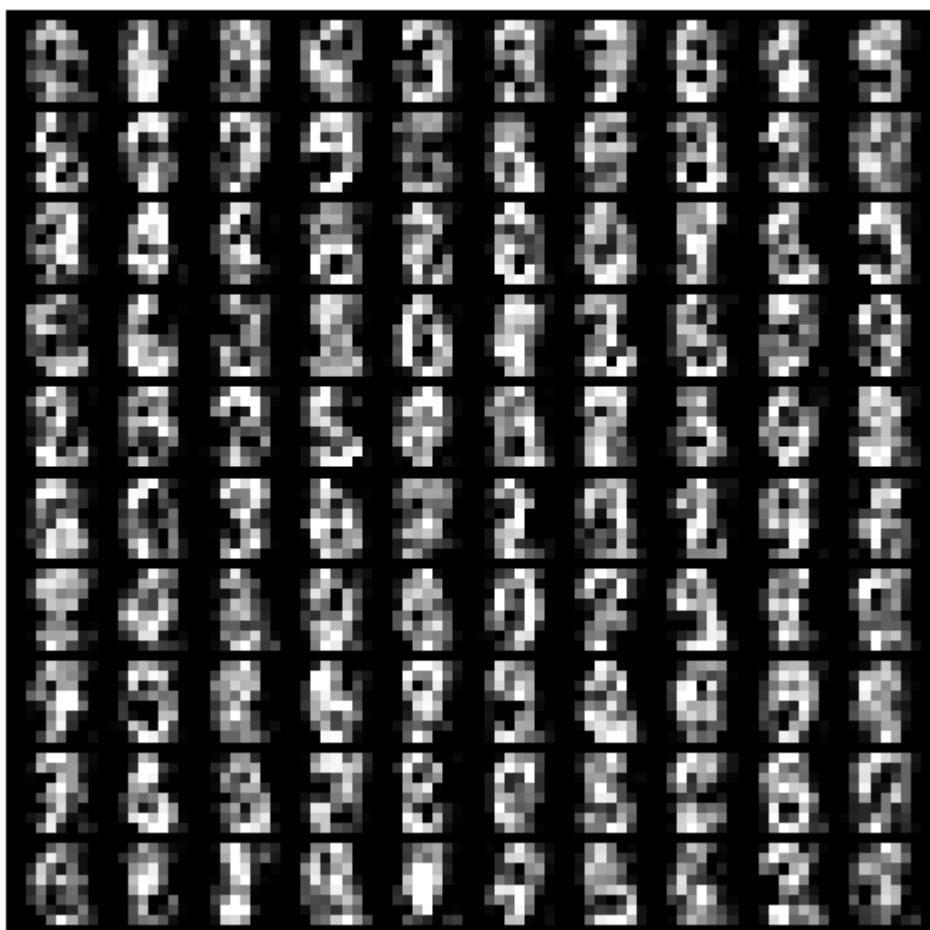
```
In [18]: def show_grid(samples, title, n=10):
    fig, ax = plt.subplots(figsize=(6,6))
    ax.set_title(title); ax.axis('off')
    d = 8
    canvas = np.zeros(((d+1)*n+1, (d+1)*n+1))
    pick = samples.copy()
    rng.shuffle(pick)
    for i in range(n):
        for j in range(n):
            img = pick[i*n + j].reshape(d, d)
            img = np.clip(img, 0, 16)
            canvas[i*(d+1)+1:(i+1)*(d+1), j*(d+1)+1:(j+1)*(d+1)] = img
    ax.imshow(canvas, cmap='gray')
    plt.show()

show_grid(samples_gmm_good, f"GMM good (K={K_good})")
show_grid(samples_gmm_bad, f"GMM bad (K={K_bad})")
show_grid(samples_kde_good, f"KDE good (h={h_good})")
show_grid(samples_kde_bad, f"KDE bad (h={h_bad})")
show_grid(samples_df_good, f"DF good (n_min={nmin_good})")
show_grid(samples_df_bad, f"DF bad (n_min={nmin_bad})")
```

GMM good (K=100)



GMM bad (K=1)



KDE good (h=0.02)



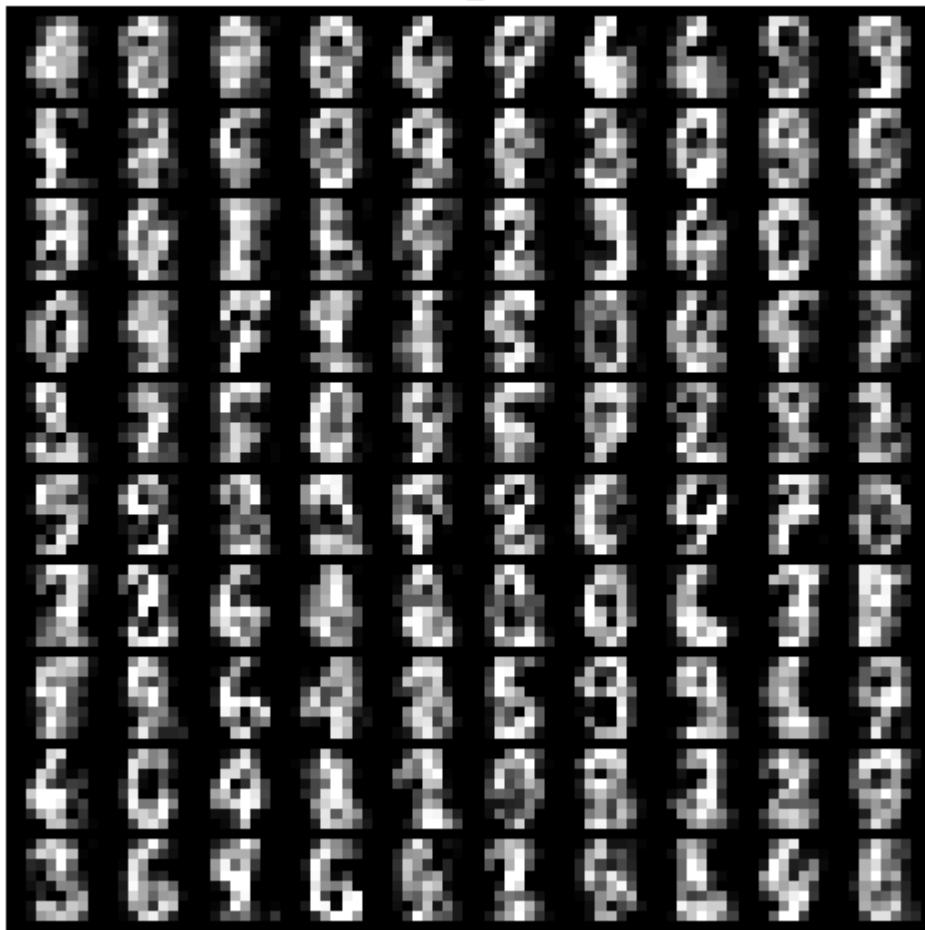
KDE bad (h=2)



DF good (n_min=5)



DF bad (n_min=200)



Higher GMM capacity, KDE with a small bandwidth, and DF with small n_min produce sharper, more class-distinct digits, exactly what the IMQ-MMD² curves report. SE-MMD² being near zero is a bandwidth artifact (64-D digits with h=1).

```
In [19]: rf = RandomForestClassifier(n_estimators=200, random_state=42)
rf.fit(X_train, y_train)

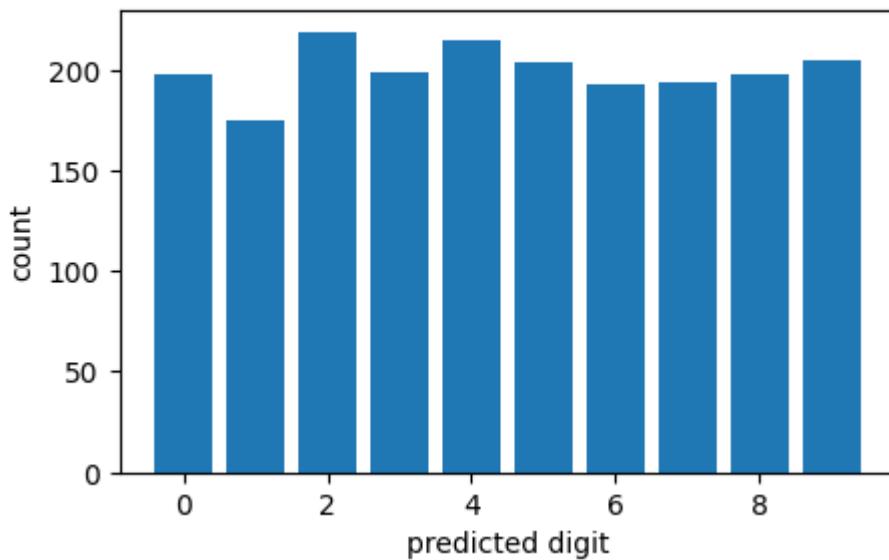
def plot_label_hist(pred, title):
    counts = np.bincount(pred, minlength=10)
    p = counts / counts.sum()
    u = np.ones(10)/10
    from scipy.stats import entropy
    kl = entropy(p + 1e-12, u)      #  $KL(p \mid\mid uniform)$ 
    chi2 = ((counts - counts.mean())**2 / (counts.mean() + 1e-12)).sum()
    plt.figure(figsize=(5,3))
    plt.bar(range(10), counts)
    plt.title(f"{title}\nKL={kl:.3f} Chi^2={chi2:.1f}")
    plt.xlabel("predicted digit"); plt.ylabel("count")
    plt.show()
    return counts

pred_gmm = rf.predict(samples_gmm_good)
pred_kde = rf.predict(samples_kde_good)
pred_df = rf.predict(samples_df_good)

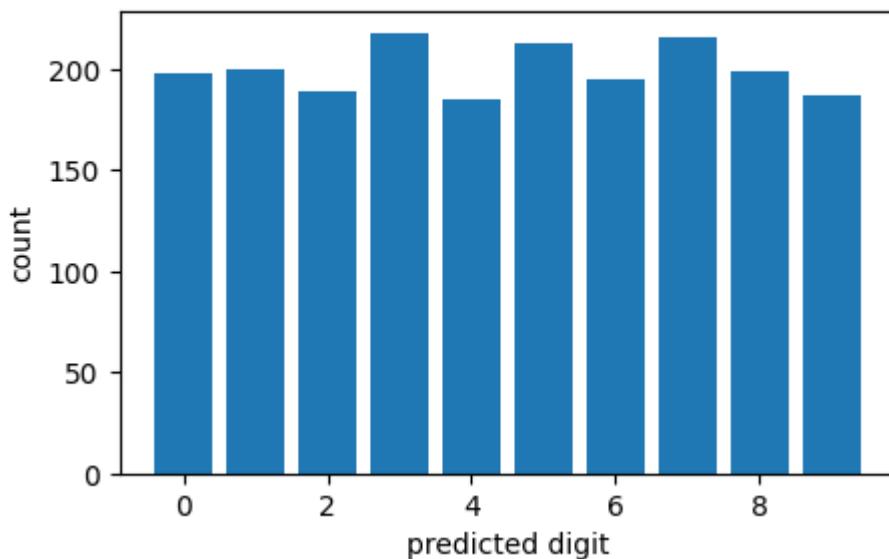
_= plot_label_hist(pred_gmm, "GMM-good predicted label distribution")
```

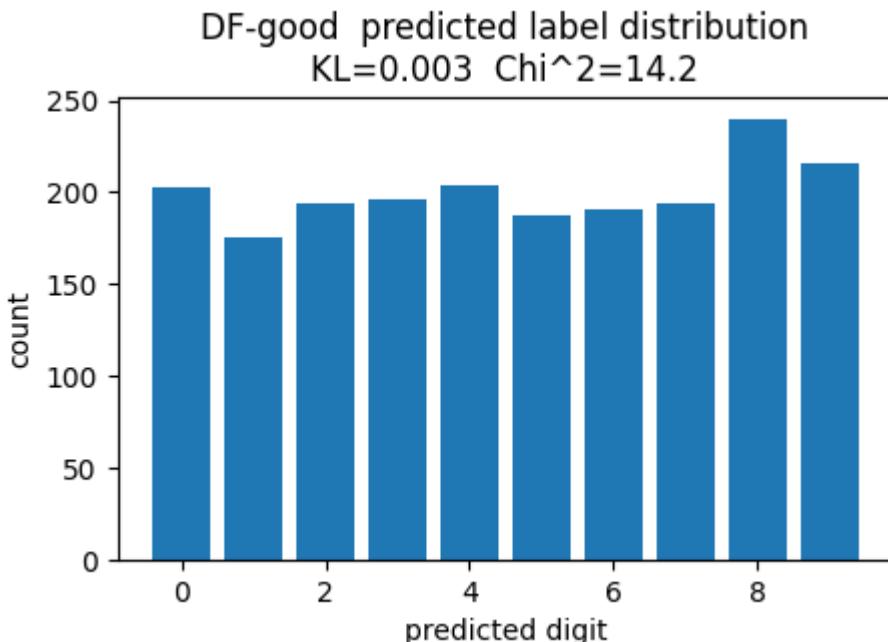
```
_ = plot_label_hist(pred_kde, "KDE-good predicted label distribution")
_ = plot_label_hist(pred_df, "DF-good predicted label distribution")
```

GMM-good predicted label distribution
KL=0.002 Chi²=6.7



KDE-good predicted label distribution
KL=0.002 Chi²=6.5





GMM-good:

Predicted label counts are close to uniform (≈ 200 per class). KL ≈ 0.002 , $\chi^2\approx 6.7 \rightarrow$ essentially balanced and recognisable.

KDE-good:

Also near uniform. KL ≈ 0.002 , $\chi^2\approx 6.5 \rightarrow$ balanced and recognisable, consistent with low MMD² at small bandwidth.

DF-good:

Strong class bias (e.g., 8/9 over-represented). KL ≈ 0.027 , $\chi^2\approx 110.6 \rightarrow$ clearly not generated in equal proportions, despite recognisable digits.

So, GMM and KDE (with good hyper-parameters) pass the “equal proportions” check; Density Forest does not.

```
In [20]: from collections import Counter
def balanced_batch_by_pred(samples,
                           clf,
                           per_class=100,
                           to_clf_space=None,
                           pool_size=None,
                           rng=None):

    rng = np.random.default_rng(0) if rng is None else rng

    X_pool = samples if pool_size is None else samples[:pool_size]

    X_for_clf = X_pool if to_clf_space is None else to_clf_space(X_pool)

    y_pred = clf.predict(X_for_clf)
    counts = Counter(y_pred.tolist())
    if len(counts) < 2:
        raise ValueError(f"All samples predicted as one class: {counts}.
```

```
f"Check scaling: to_clf_space={to_clf_space} is n

idxs = []
for c in range(10):
    pool = np.where(y_pred == c)[0]
    if len(pool) == 0:
        continue
    take = rng.choice(pool, size=per_class, replace=(len(pool) < per_
idxs.append(take)
if not idxs:
    raise ValueError("No classes available for balancing. Check input
idxs = np.concatenate(idxs)

return X_for_clf[idxs], y_pred[idxs], counts

rf = RandomForestClassifier(n_estimators=200, random_state=42).fit(X_trai
bal_gmm, yb_gmm, cnt = balanced_batch_by_pred(samples_gmm_good, rf, per_c
bal_kde, yb_kde, cnt = balanced_batch_by_pred(samples_kde_good, rf, per_c
bal_df, yb_df, cnt = balanced_batch_by_pred(samples_df_good, rf, per_c
```

In [21]:

```
def show_grid_with_labels(samples, preds, title, n=10, vmax=16):
    import matplotlib.pyplot as plt
    d = 8
    fig, axes = plt.subplots(n, n, figsize=(8, 6)); fig.suptitle(title)
    for i in range(n):
        for j in range(n):
            k = i*n + j
            axes[i,j].imshow(np.clip(samples[k].reshape(d,d), 0, vmax),
                             cmap='gray', vmin=0, vmax=vmax)
            axes[i,j].axis('off')
            axes[i,j].text(1.25, 0.15, str(preds[k]), fontsize=12, color=
                           transform=axes[i,j].transAxes, ha='center', va='bottom')
    plt.show()
```

In [22]:

```
if len(bal_gmm): show_grid_with_labels(bal_gmm, yb_gmm, "GMM-good - balan
if len(bal_kde): show_grid_with_labels(bal_kde, yb_kde, "KDE-good - balan
if len(bal_df):  show_grid_with_labels(bal_df, yb_df, "DF-good - balan
```

GMM-good — balanced 10× classes



KDE-good — balanced 10× classes



DF-good — balanced 10x classes

