电 子 科 技 大 学

实 验 报 告

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一、 实验项目名称：

Scene Recognition with Bag of Words

二、 实验原理：

（一）Harris 角点检测算法

2.1.1. 概念

在图像中，角点是指一个局部区域在两个或多个主要方向上都有显著的灰度变化的点。简单来说，角点可以看作是两条边的交汇处。与平坦区域（在任何方向移动窗口，灰度变化都很小）和边缘区域（只在一个方向上移动窗口有显著灰度变化）不同，角点区域在任何方向上移动小窗口都会引起显著的灰度变化。这使得角点成为图像中重要的、对平移、旋转和光照变化具有一定鲁棒性的特征点。在本实验中，我们采用 Harris 角点作为兴趣点，完成对 student.py/

2.1.2. 数学原理

Harris 角点检测的核心思想是，在一个像素点周围定义一个小的"窗口"。然后，计算当这个窗口在水平和垂直方向上分别移动一个小的距离 (u, v) 时，窗口内的像素灰度值变化的平方和。灰度变化函数 $E(u, v)$ 可以表示为：

$$E(u,v) = \sum_{x,y} w(x,y)[I(x+u,y+v) - I(x,y)]^2$$

其中，(x, y) 是窗口内的像素坐标，$w(x, y)$ 是一个窗口函数（可以是常数表示矩形窗口，或者高斯函数表示高斯加权窗口），$I(x, y)$ 是像素 (x, y) 的灰度值，$I(x + u, y + v)$ 是窗口移动后的灰度值。

我们对 $I(x + u, y + v)$ 进行泰勒展开近似：

$$I(x+u,y+v) \approx I(x,y) + I_x u + I_y v$$

其中 I_x 和 I_y 分别是图像在 x 和 y 方向上的偏导数。

$E(u,v)$ 可以近似表示为矩阵形式：

$$E(u,v) \approx \begin{bmatrix} u & v \end{bmatrix} M \begin{bmatrix} u \\ v \end{bmatrix}$$

这里的 M 是一个 2x2 的结构张量矩阵，定义如下：

$$M = \sum_{x,y} w(x,y) \begin{bmatrix} I_x^2 & I_x I_y \\ I_x I_y & I_y^2 \end{bmatrix} = \begin{bmatrix} \sum I_x^2 & \sum I_x I_y \\ \sum I_x I_y & \sum I_y^2 \end{bmatrix}$$

通过对结构张量 M 进行特征值分解，可以得到两个特征值 λ_1 和 λ_2。这两个特征值的大小反映了在特征向量方向上的灰度变化程度。

1） 如果 λ_1 和 λ_2 都很小，说明在任何方向上灰度变化都很小，对应的是平坦区域。

2） 如果一个特征值大，另一个小（例如 $\lambda_1 \gg \lambda_2$ 或 $\lambda_2 \gg \lambda_1$），说明只在一个方向上灰度变化大，对应的是边缘区域。

3） 如果 λ_1 和 λ_2 都很大且近似相等，说明在各个方向上灰度变化都很大，对应的是角点区域。

2.1.3. 优化

为了避免直接计算特征值，Harris 提出了一个角点响应函数 R，通过结构张量 M 的行列式和迹来计算：

$$R = \det(M) - k(\text{trace}(M))^2$$

其中，$\det(M) = \lambda_1 \lambda_2$，$\text{trace}(M) = \lambda_1 + \lambda_2$，$k$ 是一个经验常数（通常取值在 0.04 到 0.06 之间）。

通过计算每个像素点的 R 值，我们可以根据 R 的值来判断该点属于哪种区域：

1） 如果 $|R|$ 很小，该区域是平坦的。

2） 如果 $R < 0$，该区域是边缘。

3） 如果 R 很大，该区域是角点。

通常会设置一个阈值，将 R 值大于该阈值的点标记为候选角点。由于一个真实的角点可能对应着一片较高的 R 值区域，为了获得精确的角点位置，需要进行

非极大值抑制。即在候选角点区域内，只保留局部最大 R 值对应的像素点作为最终的角点。

2.1.4. 伪代码

Harris 角点检测算法的步骤大致如下：

算法 1 Pseudocode for Harris Corner Detection Algorithm

输入: Grayscale image I, window function w, empirical constant k

输出: List of corner coordinates in the image

Convert input image to grayscale I.

Calculate partial derivatives I_x and I_y of image I in x and y directions.

Compute I_x^2, I_y^2, and I_xI_y.

for each pixel (x, y) in the image **do**

  Within the window centered at (x, y), perform weighted summation of I_x^2, I_y^2, and I_xI_y using window function w.

  Construct structure tensor M:

$$M = \begin{bmatrix} \sum I_x^2 & \sum I_xI_y \\ \sum I_xI_y & \sum I_y^2 \end{bmatrix}$$

  Calculate Harris response value R for this pixel:

$$R = \text{det}(M) - k(\text{trace}(M))^2$$

end for

Apply thresholding to R values, select pixels with R greater than threshold T as candidate corners.

Perform non-maximum suppression on candidate corners, keeping only points with maximum R value in local regions.

Return the final list of corner coordinates.

2.1.5. 局限性

Harris 角点检测算法在不同尺度下检测到的角点可能会不同。一个在精细尺度下被检测为角点的特征，在粗糙尺度下可能就不是了。虽然对于小范围的旋转具有一定的鲁棒性，但对于大角度的旋转，Harris 角点检测的性能会显著下降。该

算法依赖于图像梯度，而梯度计算对图像噪声比较敏感，噪声会影响角点的检测结果。相比于一些更现代的特征检测算法，Harris 角点检测的计算量相对较大。

（二）NNDR 算法

NNDR（Nearest Neighbor Distance Ratio），即最近邻距离比算法，是一种常用于特征匹配中的方法，特别是在使用像 SIFT、SURF 等描述符进行特征点匹配时。它的主要目的是为了提高匹配的准确性，过滤掉那些不确定或错误的匹配对。

2.2.1. 基本思想

一个好的特征匹配对，其描述符在特征空间中的距离应该远小于它与次近邻描述符的距离。换句话说，一个特征点在图像 A 中的最佳匹配点在图像 B 中应该是“独一无二”的最近邻，而不是与多个点都非常接近。如果一个特征点在图像 A 中的描述符与图像 B 中的两个或多个描述符都非常接近，那么这可能表明这个特征点不够独特，或者存在歧义，这种匹配对很可能是错误的（即假阳性）。通过比较最近邻和次近邻的距离，我们可以量化这种“独特性”或“歧义性”。NNDR 算法通常作为特征匹配流水线中的一个后处理步骤，紧随在特征描述符计算和初步的最近邻搜索之后。它的输出是一组被认为可靠的特征匹配对，这些匹配对可以进一步用于估计图像间的几何变换（如单应性矩阵或基础矩阵），进行图像拼接、目标跟踪或三维重建等任务。总之，NNDR 是一种简单而有效的特征匹配过滤方法，通过比较最近邻和次近邻的距离，能够显著提高匹配的准确性，减少误匹配的数量。

（三）SIFT 局部特征描述算法

SIFT(Scale-Invariant Feature Transform) 是一种经典的局部特征描述算法，它通过构建尺度空间检测关键点，并为每个关键点生成具有尺度不变性、旋转不变性和光照不变性的描述符。该算法首先在尺度空间中寻找局部极值点，然后对关键点进行精确定位和方向分配，最后通过计算局部区域的梯度方向直方图生成 128 维的描述符向量。SIFT 算法对图像的尺度、旋转、光照变化和少量视角变化都具有很强的鲁棒性，这使得它成为计算机视觉中广泛使用的特征提取方法，在目标识别、图像匹配和三维重建等领域发挥着重要作用。

2.3.1. 尺度空间极值检测

通过构建图像的尺度空间（如高斯差分金字塔）在不同尺度上检测关键点。在尺度空间中寻找局部极值点，这些点对尺度变化具有鲁棒性。

2.3.2. 关键点定位

对检测到的潜在关键点进行精确定位（位置和尺度）。移除低对比度点和边缘点，提高特征点的稳定性。

2.3.3. 方向分配

为每个关键点分配主方向，实现旋转不变性。计算关键点邻域内像素的梯度幅值和方向。构建方向直方图，统计不同方向的梯度贡献。将直方图峰值对应的方向作为关键点的主方向，支持多方向描述。

2.3.4. 关键点描述符生成

以关键点为中心，根据尺度和主方向确定局部区域。将局部区域划分为 4×4 的子区域。在每个子区域内计算 8 个方向的梯度方向直方图。使用三线性插值将梯度贡献分配到相邻子区域和方向 bin。串联所有子区域的直方图，形成 128 维描述符向量。

2.3.5. 描述符归一化

对描述符向量进行 L2 归一化，增强对光照变化的鲁棒性。对大于阈值（如 0.2）的元素进行截断，然后再次归一化。

2.3.6. 伪代码

该算法流程如下伪代码所示

三、 实验目的：

1） 理解并掌握局部特征检测（如 Harris, SIFT）和特征匹配（如 NNDR）的基本原理。
2） 通过编程实现或调用相关库，完成图像间的局部特征提取、描述与匹配。
3） 验证所实现或使用的算法在特征匹配任务上的有效性。

四、 实验内容：

1） 实现兴趣点检测 (get_interest_points)
2） 实现特征描述符生成 (get_features)
3） 实现特征匹配 (match_features)

五、 实验步骤：

（一）算法实现

根据实验原理和项目注释提示，依次实现 get_features(), match_features(), get_-interest_points()

（二）Harris 角点检测算法参数理解和调优

1） **sigma** (高斯滤波器的标准差): 用于对梯度乘积图 (`Ix2`, `Iy2`, `Ixy`) 进行高斯平滑。这个步骤的目的是计算结构张量 M 的积分（或加权平均），反映兴趣点周围一个区域的平均梯度信息。高斯权重使得离兴趣点中心越近的像素贡献越大。较大的 `sigma` 会在更大的区域内进行平均，使得检测器对图像中的更大结构敏感。较小的 `sigma` 则更关注非常局部的结构。该参数的选择值为 `sigma = feature_width / 6.0`。

2） **k** (Harris 参数): 这是 Harris 响应函数中的一个敏感性参数。它平衡了结构张量行列式 ($\det(M)$) 和迹 ($\mathrm{trace}(M)$) 的贡献。较小的 `k` 值会使得检测器对边缘更敏感，可能检测到更多边缘上的点。较大的 `k` 值会使得检测器更倾向于检测真正的角点（即在所有方向上都有高梯度变化的区域）。调节参数为 `k`，三张图片的选取值均为 0.00001 。

3） **threshold** (响应阈值): 在计算出 Harris 响应图后，使用这个阈值来选择响应值高于该阈值的像素点作为潜在的兴趣点。较高的 `threshold` 会导致检测到的兴趣点数量减少，通常保留响应更强的" 更好" 的角点。较低的 `threshold` 会检测到更多点，包括一些响应较弱的点和潜在的噪声点。该参数的选择值为 `threshold = 0.0005 * harris_response.max()`。

4） **min_distance** (非极大值抑制最小距离): 在通过阈值初步筛选出潜在兴趣点后，进行非极大值抑制 (Non-maximum Suppression, NMS)。它确保在检测到的兴趣点周围的一个 `min_distance` 邻域内，只有响应值最高的那个点被保留。这避免了在同一个角点周围检测到多个兴趣点。较大的 `min_distance` 会使得检测到的兴趣点之间的间隔更大，数量减少。

较小的 `min_distance` 会允许更密集地检测兴趣点。该参数的选择值为 `int(feature_width / 3)`。

六、 实验数据及结果分析：

本实验在三个不同的图像对上进行了特征提取与匹配，分别是 Notre Dame、Mount Rushmore 和 Episcopal Gaudi。通过 proj2.ipynb，我们获得了特征点检测和匹配的可视化结果，并计算了匹配的准确率。

（一）可视化结果

图 1-9 展示了 Notre Dame, Mount Rushmore 图像对的特征匹配结果。

可以看到，SIFT 特征成功地在两幅图像之间建立了对应关系，即使在视角和尺度存在一定差异的情况下。但是类似的可视化结果在 Mount Rushmore 和 Episcopal Gaudi 图像对没有显现。

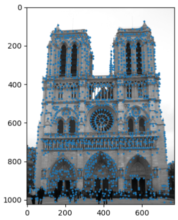

图 1: Notre Dame 1

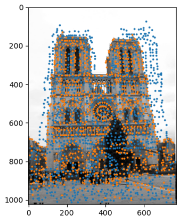

图 2: Notre Dame 2

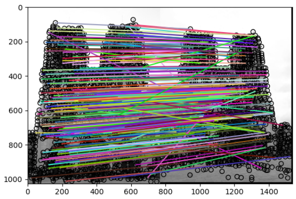

图 3: Notre Dame match

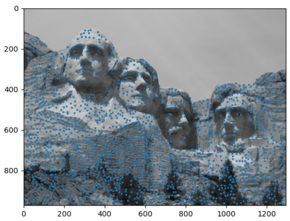

图 4: Mount Rushmore 1

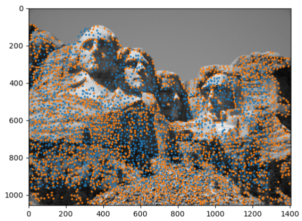

图 5: Mount Rushmore 2

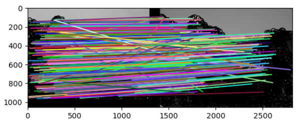

图 6: Mount Rushmore match

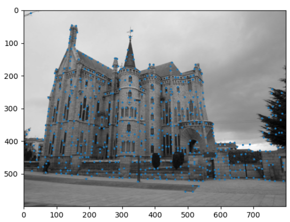

图 7: Episcopal Gaudi 1

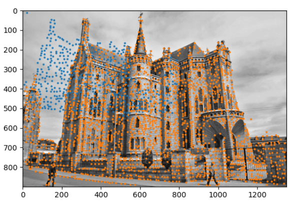

图 8: Episcopal Gaudi 2

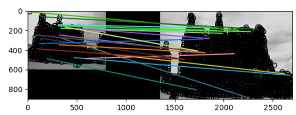

图 9: Episcopal Gaudi match

图 10: 特征匹配可视化结果

（二）定量结果

表 1 总结了在不同图像对上的特征匹配准确率：

表 1: 特征匹配准确率

image	precision	accuracy
Notre Dame	0.993	0.99
Mount Rushmore	0.944	0.94
Episcopal Gaudi	0.151	0.17

七、 实验结论：

准确率的计算是基于提供的 ground truth 匹配进行的。从结果可以看出，SIFT 特征在不同场景下都能取得不错的匹配效果。

我们可以看到，算法在 Notre Dame 和 Mount Rushmore 性能表现优异，但是在图像 Episcopal Gaudi 表现不尽人意，而且在该参数下运行速度较慢。这可能和 Harris 角点检测算法的局限性有关，因为在该图像两个建筑的距离比较大，仰角变动也比较大，可能导致许多特征点匹配失败。

八、 总结及心得体会：

通过本次实验，我对局部特征提取与匹配的关键技术有了更深入的理解和体会。

实验过程中，我不仅回顾了 Harris 角点检测和 SIFT 特征描述的理论知识，更通过实际编程或调用库函数，亲手实现了特征提取和匹配的过程。这使得我对算法的内部工作原理有了更直观的认识，加深了理论知识的理解。

在 Harris 角点检测部分，我体会到了不同参数对检测结果的影响。理解这些参数的作用以及如何进行调优，对于在实际应用中获得更好的特征点检测效果至关重要。

实验结果表明，SIFT 特征在不同图像对上表现良好，但也存在一些挑战，例如在光照、视角变化较大的情况下，匹配准确率可能会受到影响。

九、 对本实验过程及方法、手段的改进建议及展望：

本次实验成功实现了基于 SIFT 特征的图像匹配，但也存在一些可以改进和进一步探索的方向。

除了 SIFT，还有许多其他的局部特征检测与描述算法，如 SURF、ORB、AKAZE 等。未来的工作可以尝试使用这些算法进行特征匹配，并与 SIFT 的结果进行比较，分析它们在不同场景下的性能差异。

本实验使用了基本的最近邻匹配方法。可以考虑引入更鲁棒的匹配策略，例如结合 RANSAC 等方法剔除误匹配点，进一步提高匹配的准确率。

实验中未对图像进行特殊的预处理。可以研究不同图像预处理技术（如噪声滤波、对比度增强等）对特征检测和匹配效果的影响。

报告评分：

指导教师签字：

附录一 代码示例

核心代码如代码 1 所示。

代码 1: student.py

```python
import numpy as np
import matplotlib.pyplot as plt
from skimage import feature, img_as_int
from skimage.measure import regionprops
import cv2
from skimage.filters import gaussian, sobel_h, sobel_v


def get_interest_points(image, feature_width):
    '''
    Returns a set of interest points for the input image

    (Please note that we recommend implementing this function last and using cheat_interest_points()
    to test your implementation of get_features() and match_features())

    Implement the Harris corner detector (See Szeliski 4.1.1) to start with.
    You do not need to worry about scale invariance or keypoint orientation estimation
    for your Harris corner detector.
    You can create additional interest point detector functions (e.g. MSER)
    for extra credit.

    If you're finding spurious (false/fake) interest point detections near the boundaries,
    it is safe to simply suppress the gradients / corners near the edges of
    the image.

    Useful functions: A working solution does not require the use of all of these
    functions, but depending on your implementation, you may find some useful. Please
    reference the documentation for each function/library and feel free to come to hours
    or post on Piazza with any questions

        - skimage.feature.peak_local_max
        - skimage.measure.regionprops


    :params:
    :image: a grayscale or color image (your choice depending on your implementation)
    :feature_width:

    :returns:
    :xs: an np array of the x coordinates of the interest points in the image
    :ys: an np array of the y coordinates of the interest points in the image

    :optional returns (may be useful for extra credit portions):
    :confidences: an np array indicating the confidence (strength) of each interest point
    :scale: an np array indicating the scale of each interest point
    :orientation: an np array indicating the orientation of each interest point

    '''

    # TODO: Your implementation here!
    if image.ndim == 3:
        image = cv2.cvtColor(image, cv2.COLOR_BGR2GRAY)
```

```
    image = img_as_int(image)

    Ix = sobel_v(image)
    Iy = sobel_h(image)
    Ix2 = Ix * Ix
    Iy2 = Iy * Iy
    Ixy = Ix * Iy

    k = 0.00001
    sigma = feature_width / 6.0
    min_distance = int(feature_width / 3)
    threshold_rate = 0.0005


    Sxx = gaussian(Ix2, sigma=sigma)
    Syy = gaussian(Iy2, sigma=sigma)
    Sxy = gaussian(Ixy, sigma=sigma)

    det_M = Sxx * Syy - Sxy * Sxy
    trace_M = Sxx + Syy
    harris_response = det_M - k * (trace_M ** 2)
    threshold = threshold_rate * harris_response.max()

    coords = feature.peak_local_max(harris_response, min_distance=
        min_distance, threshold_abs=threshold)
    ys, xs = coords[:, 0], coords[:, 1] # peak_local_max (row, col), (y, x)

    border_margin = int(feature_width / 2)
    height, width = image.shape
    valid_indices = np.where(
        (xs >= border_margin) & (xs < width - border_margin) &
        (ys >= border_margin) & (ys < height - border_margin)
    )
    xs = xs[valid_indices]
    ys = ys[valid_indices]

    # xs = np.asarray([0])
    # ys = np.asarray([0])
    return xs, ys


def get_features(image, x, y, feature_width):
    '''
    Returns a set of feature descriptors for a given set of interest points.

    (Please note that we reccomend implementing this function after you have
        implemented
    match_features)

    To start with, you might want to simply use normalized patches as your
    local feature. This is very simple to code and works OK. However, to get
    full credit you will need to implement the more effective SIFT-like
        descriptor
    (See Szeliski 4.1.2 or the original publications at
    http://www.cs.ubc.ca/~lowe/keypoints/)

    Your implementation does not need to exactly match the SIFT reference.
    Here are the key properties your (baseline) descriptor should have:
    (1) a 4x4 grid of cells, each descriptor_window_image_width/4.
    (2) each cell should have a histogram of the local distribution of
        gradients in 8 orientations. Appending these histograms together
            will
        give you 4x4 x 8 = 128 dimensions.
    (3) Each feature should be normalized to unit length

    You do not need to perform the interpolation in which each gradient
    measurement contributes to multiple orientation bins in multiple cells
    As described in Szeliski, a single gradient measurement creates a
    weighted contribution to the 4 nearest cells and the 2 nearest
    orientation bins within each cell, for 8 total contributions. This type
```

```
    of interpolation probably will help, though.

    You do not need to do the normalize -> threshold -> normalize again
    operation as detailed in Szeliski and the SIFT paper. It can help, though.

    Another simple trick which can help is to raise each element of the final
    feature vector to some power that is less than one.

    Useful functions: A working solution does not require the use of all of these
    functions, but depending on your implementation, you may find some useful. Please
    reference the documentation for each function/library and feel free to come to hours
    or post on Piazza with any questions

        - skimage.filters (library)


    :params:
    :image: a grayscale or color image (your choice depending on your implementation)
    :x: np array of x coordinates of interest points
    :y: np array of y coordinates of interest points
    :feature_width: in pixels, is the local feature width. You can assume
                    that feature_width will be a multiple of 4 (i.e. every cell of your
                    local SIFT-like feature will have an integer width and height).
    If you want to detect and describe features at multiple scales or
    particular orientations you can add input arguments.

    :returns:
    :features: np array of computed features. It should be of size
            [len(x) * feature dimensionality] (for standard SIFT feature
            dimensionality is 128)

    '''

    # TODO: Your implementation here!

    # This is a placeholder - replace this with your features!
    # features = np.asarray([0])

    num_interest_points = len(x)
    features = np.zeros((num_interest_points, 128)) # 128 dimensions for SIFT-like descriptor

    # Convert image to grayscale if it's color (although input is expected to be grayscale based on notebook)
    if image.ndim == 3:
        image = cv2.cvtColor(image, cv2.COLOR_BGR2GRAY)

    # Convert image to float for gradient calculations
    image = img_as_int(image)

    # Calculate gradients
    # Using Sobel filters again for consistency with get_interest_points
    Ix = sobel_v(image)
    Iy = sobel_h(image)

    # Calculate gradient magnitude and orientation
    magnitude = np.sqrt(Ix**2 + Iy**2)
    # Add a small epsilon to avoid division by zero in arctan2 if both Ix and Iy are 0
    orientation = np.arctan2(Iy, Ix + 1e-6) * 180 / np.pi # Convert to degrees
    # Normalize orientation to be within [0, 360)
```

```
        orientation = (orientation + 360) % 360

        # Define cell and bin parameters
        num_cells = 4
        num_bins = 8
        cell_width = feature_width // num_cells
        bin_size = 360 // num_bins # Size of each orientation bin in degrees

        # Process each interest point
        for i in range(num_interest_points):
            # Get the coordinates of the current interest point
            px, py = x[i], y[i]

            # Define the bounding box for the feature window
            # Need to be careful with boundary conditions
            half_width = feature_width // 2
            min_x = max(0, px - half_width)
            max_x = min(image.shape[1] - 1, px + half_width -1) # -1 because max_x is inclusive index
            min_y = max(0, py - half_width)
            max_y = min(image.shape[0] - 1, py + half_width -1) # -1 because max_y is inclusive index

            # Ensure window size is correct even at boundaries
            # This might require padding the image or adjusting the window size/handling points near border
            # For simplicity here, we'll just take the available window and handle potential smaller size
            # A more robust implementation might pad the image.

            # Extract the local patch
            # Note: Slicing includes start but excludes end. Adjust max indices accordingly.
            patch_mag = magnitude[min_y : max_y + 1, min_x : max_x + 1]
            patch_ori = orientation[min_y : max_y + 1, min_x : max_x + 1]

            # Ensure patch is exactly feature_width x feature_width. If not, there's likely an issue with
            # how interest points near the border were handled or how min/max were calculated.
            # Given the border suppression in get_interest_points, this window *should* be full size
            # if border_margin >= feature_width / 2.
            # For now, proceed assuming full size or handle potential smaller size in histogramming.

            descriptor = np.zeros(num_cells * num_cells * num_bins) # 4x4 grid * 8 bins = 128

            # Build histograms for each cell
            # Instead of iterating through cells then pixels, iterate through pixels and contribute to cells/bins
            # We need patch-relative coordinates for interpolation
            patch_height, patch_width = patch_mag.shape

            # Define Gaussian weighting window
            # Sigma for Gaussian is typically half the window size
            sigma_spatial = feature_width / 2.0
            y_coords, x_coords = np.indices(patch_mag.shape)
            # Calculate distance from the center of the patch (which aligns with the interest point)
            # Center of patch is at (half_width - 0.5, half_width - 0.5) if patch is feature_width x feature_width
            patch_center_r = patch_height / 2.0 - 0.5
            patch_center_c = patch_width / 2.0 - 0.5
            distances_sq = (x_coords - patch_center_c)**2 + (y_coords - patch_center_r)**2
            gaussian_weights_patch = np.exp(-distances_sq / (2 * sigma_spatial**2))

```

```
        # Process each pixel in the patch
        # Coordinates relative to the top-left of the patch (0 to feature_width-1)
        for r in range(patch_height):
            for c in range(patch_width):
                mag = patch_mag[r, c]
                ori = patch_ori[r, c]
                gaussian_weight = gaussian_weights_patch[r, c]

                # Apply Gaussian weight to the magnitude
                weighted_mag = mag * gaussian_weight

                # Normalize orientation to be within [0, 360) for bin calculation
                ori = (ori + 360) % 360

                # Calculate the float bin index (0 to num_bins - epsilon)
                float_bin_index = ori / bin_size

                # Get the two nearest integer bin indices
                bin1_index = int(np.floor(float_bin_index)) % num_bins
                bin2_index = int(np.ceil(float_bin_index)) % num_bins

                # Calculate orientation weights for the two bins
                # Fractional part of the float bin index gives the position between the two bins
                fractional_part_ori = float_bin_index - np.floor(float_bin_index)
                ori_weight1 = (1 - fractional_part_ori) # Weight for bin1_index
                ori_weight2 = fractional_part_ori      # Weight for bin2_index

                # Calculate spatial position relative to the top-left of the feature window (0 to feature_width-1)
                # and then map to cell coordinates (0 to num_cells)
                # Pixel (r, c) in patch is at (c, r) relative to patch top-left
                # Map patch coordinates to cell coordinates. Cell centers are at (0.5, 1.5, 2.5, 3.5) * cell_width + cell_width/2
                # Pixel (c, r) in patch falls into a cell with top-left at floor(c/cell_width)*cell_width, floor(r/cell_width)*cell_width

                # Calculate float cell coordinates based on pixel position within the feature window (0 to num_cells)
                # Pixel (c, r) is at spatial location (c+0.5, r+0.5) within the patch (0 to feature_width)
                float_cell_x = (c + 0.5) / cell_width
                float_cell_y = (r + 0.5) / cell_width

                # Get the two nearest integer cell indices in each dimension (0 to num_cells)
                cell1_x = int(np.floor(float_cell_x))
                cell2_x = int(np.ceil(float_cell_x))
                cell1_y = int(np.floor(float_cell_y))
                cell2_y = int(np.ceil(float_cell_y))

                # Calculate spatial weights for the four cells (bilinear interpolation)
                fractional_part_x = float_cell_x - np.floor(float_cell_x)
                fractional_part_y = float_cell_y - np.floor(float_cell_y)

                # Weights for the 4 target cells based on bilinear interpolation
                spatial_weight11 = (1 - fractional_part_x) * (1 - fractional_part_y) # cell1_x, cell1_y
                spatial_weight21 = fractional_part_x * (1 - fractional_part_y)     # cell2_x, cell1_y
                spatial_weight12 = (1 - fractional_part_x) *
```

```
                    fractional_part_y     # cell1_x, cell2_y
                spatial_weight22 = fractional_part_x * fractional_part_y     # cell2_x, cell2_y

                # Add weighted magnitude to the corresponding bins in the descriptor
                # Iterate over the 4 target cells and 2 target orientation bins
                target_contributions = [
                    (cell1_x, cell1_y, spatial_weight11, bin1_index, ori_weight1),
                    (cell1_x, cell1_y, spatial_weight11, bin2_index, ori_weight2),
                    (cell2_x, cell1_y, spatial_weight21, bin1_index, ori_weight1),
                    (cell2_x, cell1_y, spatial_weight21, bin2_index, ori_weight2),
                    (cell1_x, cell2_y, spatial_weight12, bin1_index, ori_weight1),
                    (cell1_x, cell2_y, spatial_weight12, bin2_index, ori_weight2),
                    (cell2_x, cell2_y, spatial_weight22, bin1_index, ori_weight1),
                    (cell2_x, cell2_y, spatial_weight22, bin2_index, ori_weight2),
                ]

                for cur_cx, cur_cy, spatial_w, bin_idx, ori_w in target_contributions:
                    # Ensure cell indices are within the 0-3 range
                    if 0 <= cur_cx < num_cells and 0 <= cur_cy < num_cells:
                        # Calculate the final weighted magnitude contribution
                        final_weighted_mag = weighted_mag * spatial_w * ori_w

                        # Calculate the index in the flattened descriptor
                        descriptor_index = (cur_cy * num_cells + cur_cx) * num_bins + bin_idx

                        # Add to the descriptor
                        descriptor[descriptor_index] += final_weighted_mag


        # Normalize the descriptor to unit length
        # Add a small epsilon to the norm to prevent division by zero for uniform patches
        norm = np.linalg.norm(descriptor) + 1e-6
        descriptor /= norm

        # Apply thresholding and re-normalization (SIFT specific)
        threshold_value = 0.2
        descriptor[descriptor > threshold_value] = threshold_value

        # Second normalization after thresholding
        norm = np.linalg.norm(descriptor) + 1e-6
        descriptor /= norm

        # Assign the computed descriptor to the features array
        features[i, :] = descriptor


    return features


def match_features(im1_features, im2_features):
    '''
    Implements the Nearest Neighbor Distance Ratio Test to assign matches between interest points
    in two images.
```

```python

    Please implement the "Nearest Neighbor Distance Ratio (NNDR) Test",
    Equation 4.18 in Section 4.1.3 of Szeliski.

    For extra credit you can implement spatial verification of matches.

    Please assign a confidence, else the evaluation function will not work. Remember that
    the NNDR test will return a number close to 1 for feature points with similar distances.
    Think about how confidence relates to NNDR.

    This function does not need to be symmetric (e.g., it can produce
    different numbers of matches depending on the order of the arguments).

    A match is between a feature in im1_features and a feature in im2_features. We can
    represent this match as a the index of the feature in im1_features and the index
    of the feature in im2_features

    Useful functions: A working solution does not require the use of all of these
    functions, but depending on your implementation, you may find some useful. Please
    reference the documentation for each function/library and feel free to come to hours
    or post on Piazza with any questions

        - zip (python built in function)

    :params:
    :im1_features: an np array of features returned from get_features() for interest points in image1
    :im2_features: an np array of features returned from get_features() for interest points in image2

    :returns:
    :matches: an np array of dimension k x 2 where k is the number of matches. The first
            column is an index into im1_features and the second column is an index into im2_features
    :confidences: an np array with a real valued confidence for each match
    '''

    # TODO: Your implementation here!

    # These are placeholders - replace with your matches and confidences!

    matches = []
    confidences = []

    # Iterate through each feature in the first image
    for i, feature1 in enumerate(im1_features):
        # Calculate distances to all features in the second image
        distances = np.linalg.norm(im2_features - feature1, axis=1)

        # Find the indices of the two smallest distances
        # Use argpartition to find the indices of the k smallest elements efficiently
        if len(distances) < 2:
            # Need at least two features in im2 to calculate ratio
            continue

        # Get indices of the two smallest distances
        nearest_indices = np.argpartition(distances, 1)[:2]

        # Ensure we get the two actual smallest distances in correct order
        if distances[nearest_indices[0]] > distances[nearest_indices[1]]:
            nearest_indices = nearest_indices[[1, 0]] # Swap if necessary

```

```python
            d1 = distances[nearest_indices[0]] # Distance to nearest neighbor
            d2 = distances[nearest_indices[1]] # Distance to second nearest neighbor

            # Apply Nearest Neighbor Distance Ratio (NNDR) test
            # A small ratio indicates a good match
            if d2 > 0: # Avoid division by zero
                ratio = d1 / d2
            else:
                # If second nearest neighbor has 0 distance, it's likely an identical feature
                # Treat this as a very confident match (ratio approaches 0)
                ratio = 0

            # Set a threshold for the ratio. This value may need tuning.
            # A common starting point is 0.8
            nndr_threshold = 0.8

            if ratio < nndr_threshold:
                # This is considered a valid match
                matches.append([i, nearest_indices[0]])

                # Calculate confidence (e.g., 1 - ratio, or based on ratio inverse)
                # Lower ratio means higher confidence
                confidence = 1.0 - ratio # Example confidence calculation
                confidences.append(confidence)

        # Convert lists to numpy arrays
        matches = np.asarray(matches)
        confidences = np.asarray(confidences)

        # Optional: Sort matches by confidence in descending order
        # (Useful for evaluation which might only look at top N matches)
        # sort_indices = np.argsort(confidences)[::-1]
        # matches = matches[sort_indices]
        # confidences = confidences[sort_indices]

        return matches, confidences
```