Technical Update Documentation

Function Name: `SpreadDisease`

Overview of Updates

1. **Previous Functionality**:
   - The `SpreadDisease` function simulated the spread of a single disease in a forest with a single tree species.
2. **New Functionality**:
   - The function has been updated to support multi-species forests. It can now simulate the spread of a single disease in forests containing multiple tree species.

Interface Changes

Previous Interface

```
def SpreadDisease(forest_state, age_list,
infection_time, p_spread):
    ...
```

Updated Interface

```
def SpreadDisease(forest_state, age_list,
infection_time, p_spread, tree_species=None,
spread_matrix=None):
```

```
    """
    Simulates disease spread in a forest with multiple
tree species.

    Parameters:
    - forest_state (np.ndarray): N x N matrix
representing the forest state.
        - `1`: Infected tree
        - `-1`: Healthy tree
        - `0`: Empty cell
    - age_list (np.ndarray): N x N matrix representing
tree ages.
    - infection_time (np.ndarray): N x N matrix
recording infection times for infected trees.
    - p_spread (float): Base probability of disease
spread.
    - tree_species (np.ndarray, optional): N x N matrix
indicating the species of each tree. 0 for empty cell.
    - spread_matrix (np.ndarray, optional): S x 1 matrix
where S is the number of species, representing species-
specific spread probabilities. Note that the first row
must be 0.

    Returns:
    - updated_forest_state (np.ndarray): N x N matrix
with the updated forest state.
    """
```

Changes Summary

- **Added two optional parameters**:
    1. `tree_species` : A matrix representing the species of each
       tree in the forest.
    2. `spread_matrix` : A vector(for now) specifying the base
       spread probabilities for each tree species.
- **Backward Compatibility**:

- If `tree_species` and `spread_matrix` are not provided, the function defaults to the single-species forest logic.

Implementation Details

Logic for Multi-Species Forests

1. **Species-Specific Spread Probabilities**:
   - If `tree_species` and `spread_matrix` are provided, each tree's spread probability is adjusted based on its species.
   - Example:
     - `spread_matrix = [[0],[0.3],[0.7]]`
     - For trees of species 1, the probability that they get infected is 0.3
     - For trees of species 2, the probability that they get infected is 0.7

Key Notes

1. **Input Validation**:
   - `tree_species` must have the same shape as `forest_state`.
   - If `spread_matrix` is provided, the number of its rows must equal to $1+$ maximum value in `tree_species`.
     - For instance, there are 3 kinds of tree, then `spread_matrix` should have 4 rows. Because of the 0 for empty cells.

Example

My process of initializing `tree_species` and `spread_matrix`:

```python
random_values = np.random.randint(1, 3, size=(N, N))
test_tree_species = np.zeros((N, N))
test_tree_species[(initial_forest != 0)] = random_values[(initial_forest != 0)]
test_tree_species = test_tree_species.astype(int)
test_spread_matrix = np.random.rand(3, 1)
test_spread_matrix[0, 0] = 0
```

IMPORTANT! THE FIRST ROW OF SPREAD_MATRIX MUST BE 0!