You’ve understood the core idea well: the matrices svd\_eigen.phy and V\_kept\_transposed both represent species positions, but in different spaces—one in the phylogenetic space and the other in the interaction network space. Here's a detailed explanation of how these matrices contain information about the structures and what the rows and columns mean.

**Understanding the SVD Matrices**

1. **svd\_eigen.phy (Phylogenetic Structure Matrix):**
   * **Definition**: svd\_eigen.phy is derived from the eigenvectors of the phylogenetic correlation matrix (phylo.corr). It contains the principal components that capture the most variance in the phylogenetic relationships among species.
   * **Rows**: Each row corresponds to a species in the phylogenetic tree.
   * **Columns**: Each column represents an eigenvector, which can be thought of as a principal component of the phylogenetic variance-covariance structure. The number of columns typically equals the number of species (if you keep all axes).
   * **Meaning**: Each value in svd\_eigen.phy represents the position of a species along a specific principal component axis that describes the phylogenetic relationships. Higher values in one axis suggest that the species share more recent common ancestry along that dimension, capturing the main patterns of evolutionary divergence.
2. **V\_kept\_transposed (Interaction Network Structure Matrix):**
   * **Definition**: V\_kept\_transposed is the transposed matrix of right singular vectors (V) from the SVD of the interaction matrix. It represents the primary patterns of species' interactions in the network.
   * **Rows**: Each row corresponds to a predator species in the network.
   * **Columns**: Each column represents one of the principal axes (singular vectors) capturing the variance in the species’ interaction patterns. The total number of columns is equal to the number of axes kept (kept\_axes), which could be all or a subset of the possible axes.
   * **Meaning**: Each value in V\_kept\_transposed represents the contribution of a predator species to a specific principal axis of interaction structure. This matrix encodes how species are positioned relative to each other in the context of their network interactions (who eats whom).

**How These Matrices Represent Structures:**

* **Phylogenetic Structure (svd\_eigen.phy)**:
  + This matrix captures the hierarchical relationships among species based on their evolutionary history. It tells us how closely related different species are and can reveal clusters of species with similar ancestry. By using eigenvectors, it summarizes the main axes along which the species' evolutionary distances vary.
* **Interaction Network Structure (V\_kept\_transposed)**:
  + This matrix reflects how species are positioned in an ecological network (e.g., a food web). The columns (principal axes) summarize the major patterns of interactions, such as which species tend to prey on the same or different species. It helps identify clusters of predators that share similar prey or exhibit similar feeding patterns.

**Why Use Procrustes Analysis:**

* **Procrustes Test (protest)**: This is a statistical method to measure the similarity between two configurations—in this case, the phylogenetic and network structures.
  + **Objective**: The goal is to see how well the phylogenetic distances between species correspond to their interaction patterns. If the species that are close in the phylogenetic tree also tend to have similar interactions in the network, there will be a strong correlation.
  + **How It Works**: protest(svd\_eigen.phy, V\_kept\_transposed) will align the two matrices by scaling, translating, and rotating one matrix to best match the other. The test then computes a correlation value to quantify this match.

Yes, in your case, you should run the Procrustes analysis directly on the matrices svd\_eigen.phy and V\_kept\_transposed because these matrices represent the reduced-dimensional structures of the phylogeny and the network of interactions. Running the Procrustes analysis directly on these matrices allows you to compare the main axes of variation between the two configurations, which is precisely what you are interested in.

**Why Run Procrustes Directly on These Matrices?**

1. **Comparing Structures**:
   * The matrices svd\_eigen.phy (phylogeny) and V\_kept\_transposed (network) are already in a comparable format: they both represent species' positions along principal axes that capture the main patterns of variation in their respective spaces.
   * The Procrustes analysis will align these two configurations, quantifying how similar the patterns of variation in the phylogeny are to the patterns in the network of interactions.
2. **Capturing Key Information**:
   * The eigenvectors (svd\_eigen.phy) represent the key structural features of the phylogenetic relationships (how species are related evolutionarily).
   * The right singular vectors (V\_kept\_transposed) represent the key structural features of the interaction network (how species interact ecologically).
   * By using these matrices directly, you avoid any potential distortions that could arise from further transformations or aggregations.