Repeat regression analysis and summarize results.

Begin analysis of coefficient of variation using Lipson data.

REGRESSION ANALYSIS

*Fitness vs. lifespan*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Comparison** | **Medium** | **Multiple R2** | **p-value** | **Std. Dev.** |
| RLS | YPD | 0.02545 | 0.01499 | 10.240 |
| RLS | YPDGE | 0.02824 | 0.01034 | 12.393 |
| RLS | YPG | 0.03613 | 0.003657 | 10.145 |
| RLS | YPE | 0.0632 | 0.0001084 | 12.246 |
| RLS | YPL | 0.03474 | 0.004391 | 11.620 |

YPE gave the largest R2 value and the lowest p-value, thus YPE has the most significant relationship with replicative lifespan.

*Evolutionary distance vs. lifespan*

|  |  |  |  |
| --- | --- | --- | --- |
| **Species 1** | **Species 2** | **Multiple R2** | **p-value** |
| SCE | SPA | 0.002773 | 0.3758 |
| SCE | SMIK | 0.3482 | 0.386 |
| SCE | SBAY | 0.3646 | 0.8462 |

\*\*Add full names of yeast species

The large p-values (0.3758, 0.386, and 0.8462) show that there is no significant relationship between evolutionary distance and replicative lifespan in any of the yeast gene species.

*???????Genetic Interactions vs. lifespan*

|  |  |
| --- | --- |
| **Multiple R2** | **p-value** |
| 0.08851 | 0.0004161 |

Given small p-value (0.0004161) there is a correlation between the number of interactions and replicative life span. (Negative correlation, insert graph?)