**Figure 1:** a) All hypothesized pathways in the initial path model for the effect of local- and landscape-level habitat and pollinator community characteristics on BQCV, DWV, and SBV prevalence within four focal pollinator host species: *Apis mellifera*, *Bombus impatiens*, *Lasioglossum* spp., and *Eucera pruinosa*. Dark gray arrows are modelled with linear regressions and light gray paths are modelled with GLMMs with binomial distributions. Double headed arrows indicate correlated errors included in the model. b) The final path model shows that habitat characteristics are directly linked with BQCV prevalence and indirectly linked with BQCV and DWV prevalence through pollinator species richness, but not combined *A. mellifera* and *B. impatiens* abundance. Significant negative (red) and positive (black) associations between linked variables are shown, but non-significant paths are not. Path thickness corresponds to the magnitude of the range standardized regression coefficients, which indicate the proportional shift in the response variable given a full shift in the predictor variable along its range. Full model statistics can be found in **Appendix S2: Table S3**.

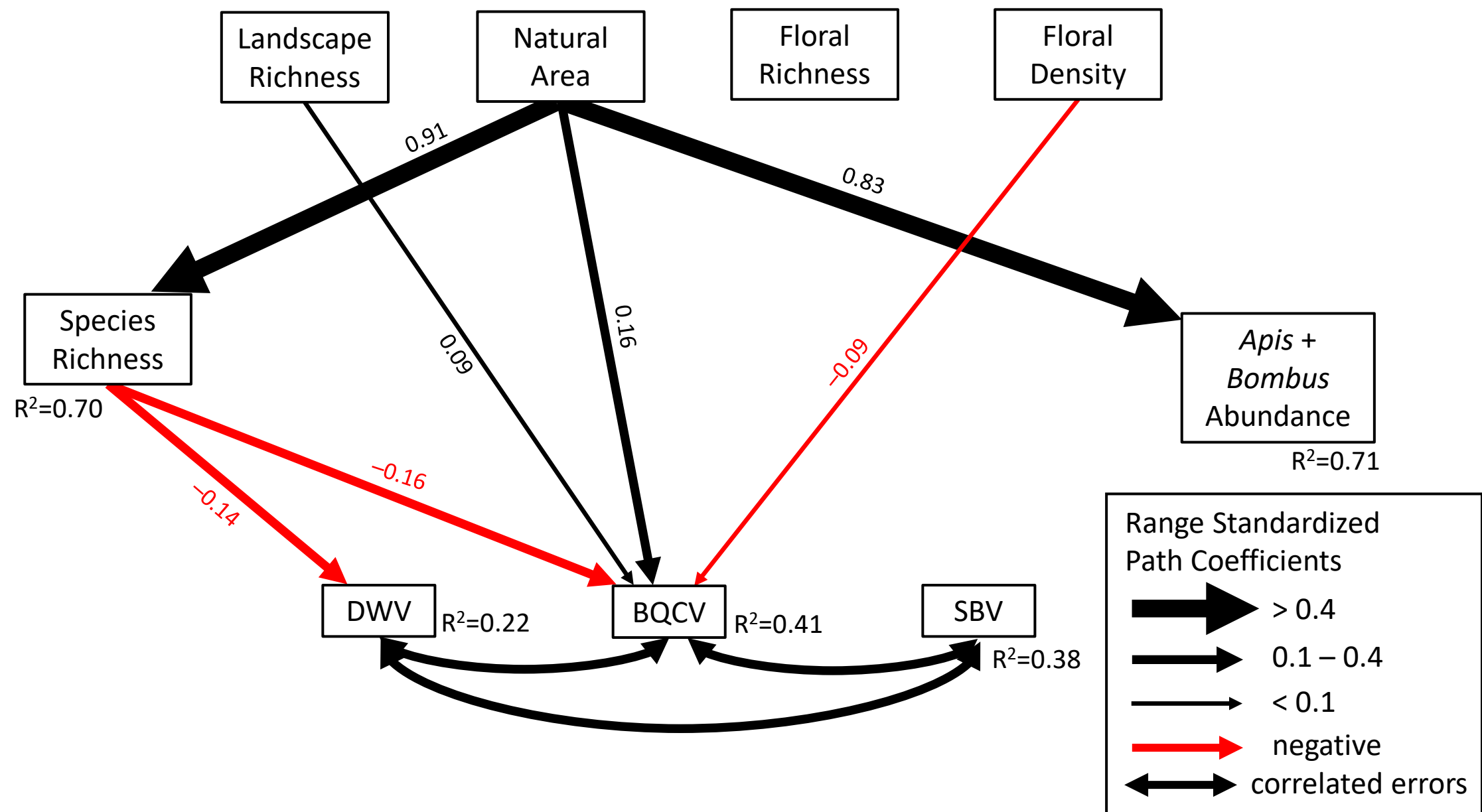a. **Hypothesized Pathways**
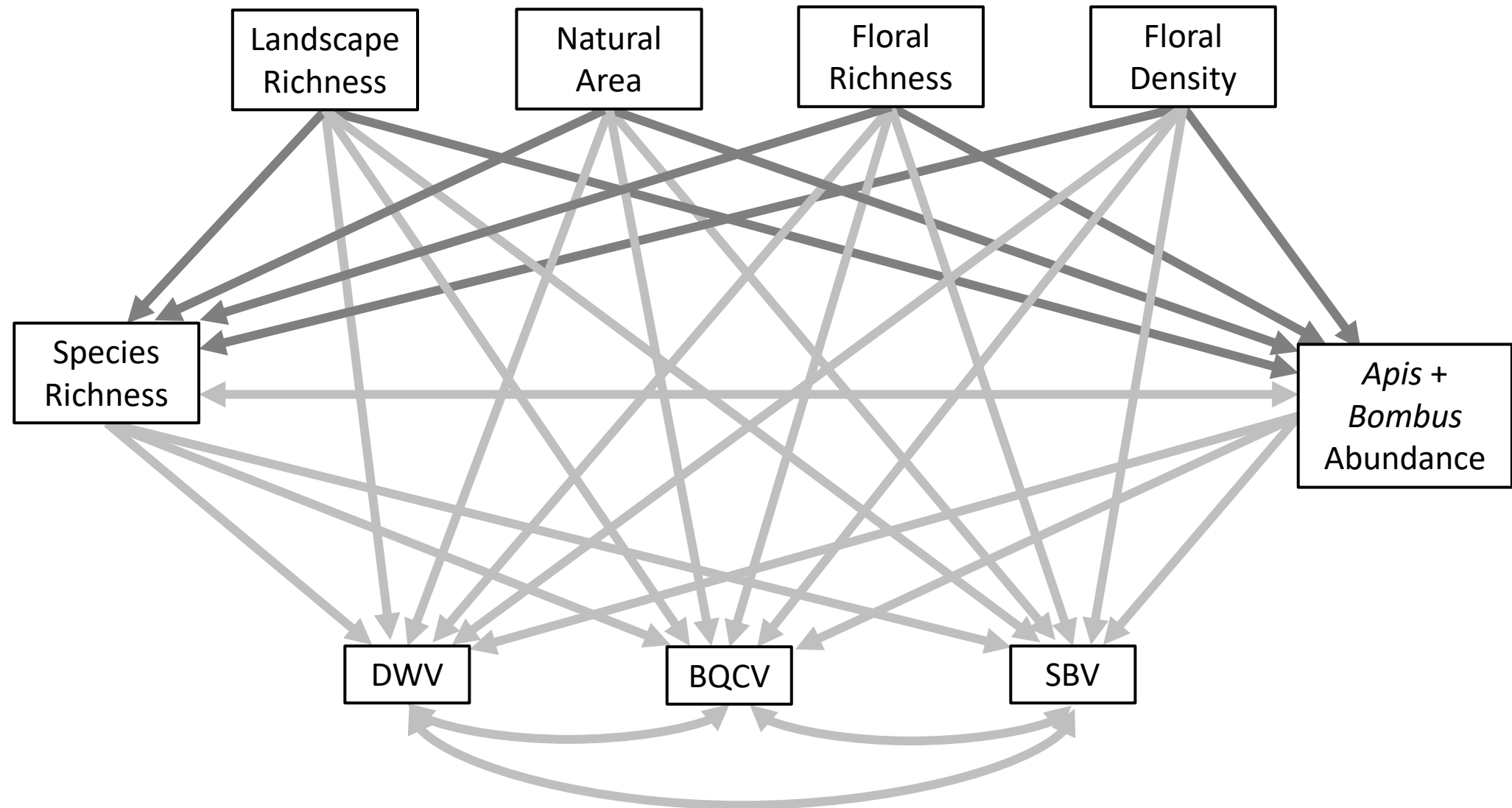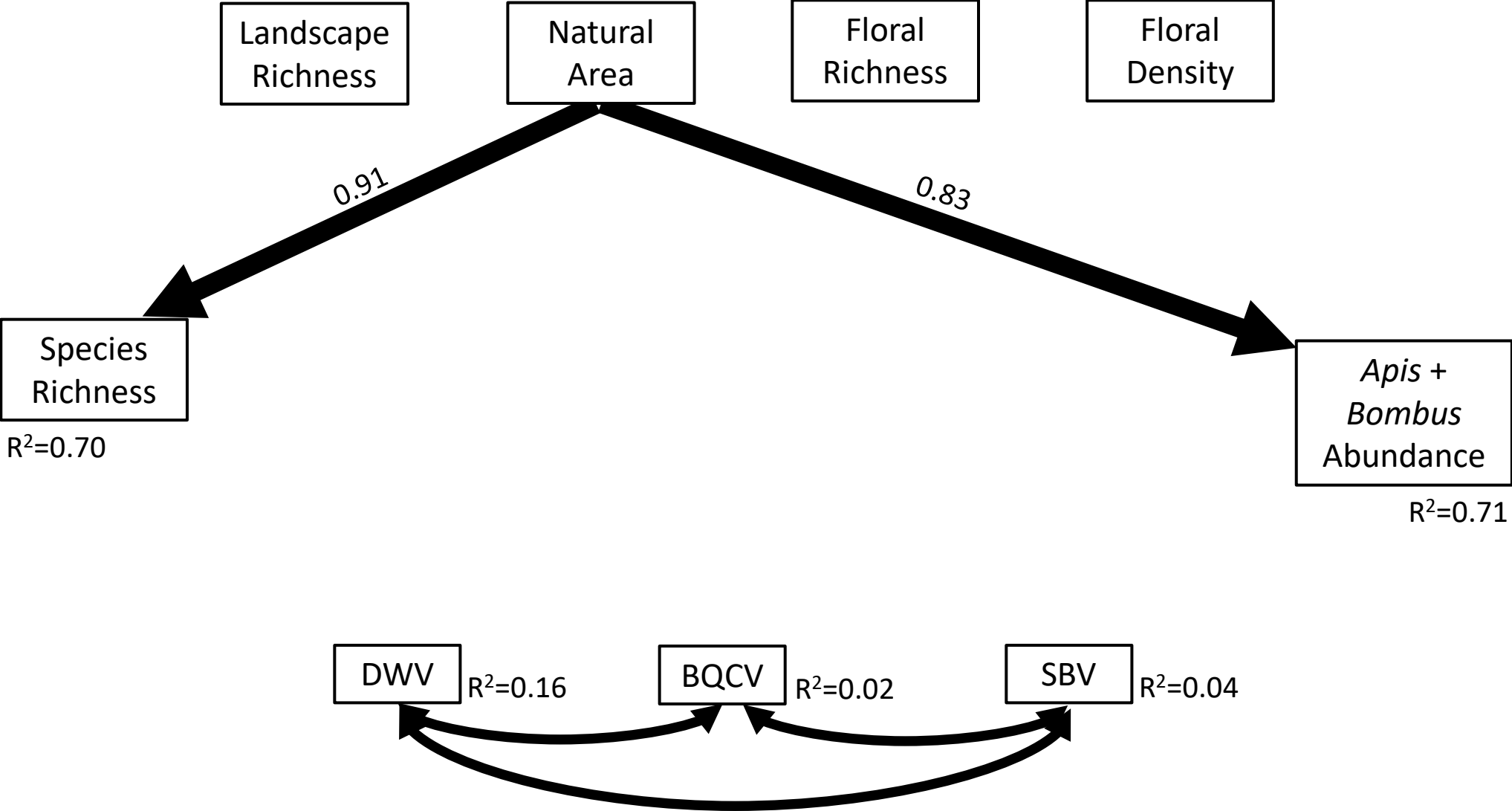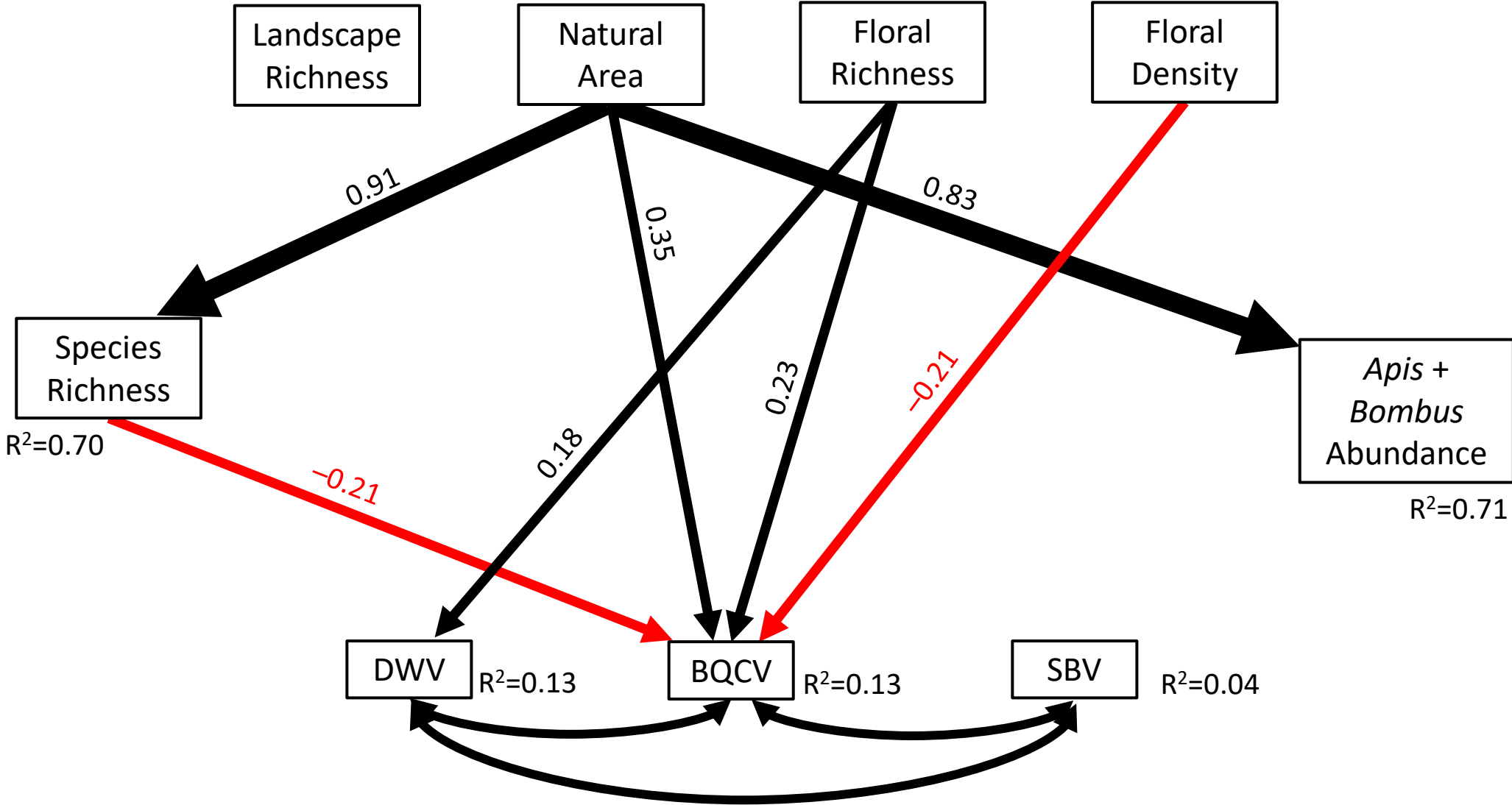
b. Final Path Model

Figure 3. Separate path models including viral prevalence within only A) *Apis mellifera*, B) *Bombus impatiens*, C) *Lasioglossum* spp., and D) *Eucera pruinosa* hosts. SBV is extremely rare in *Lasioglossum* spp. and *E. pruinosa*, therefore the SBV component model was removed from the path models for those species. Each model included all possible links between habitat characteristics, pollinator community characteristics, and each virus, but only significant paths are shown in the figure. Red and black paths denote significant negative and positive associations between linked variables, respectively, and path thickness corresponds to the magnitude of the range standardized coefficients. Double headed arrows indicate correlated errors included in the model. Model statistics can be found in **Appendix S3**.
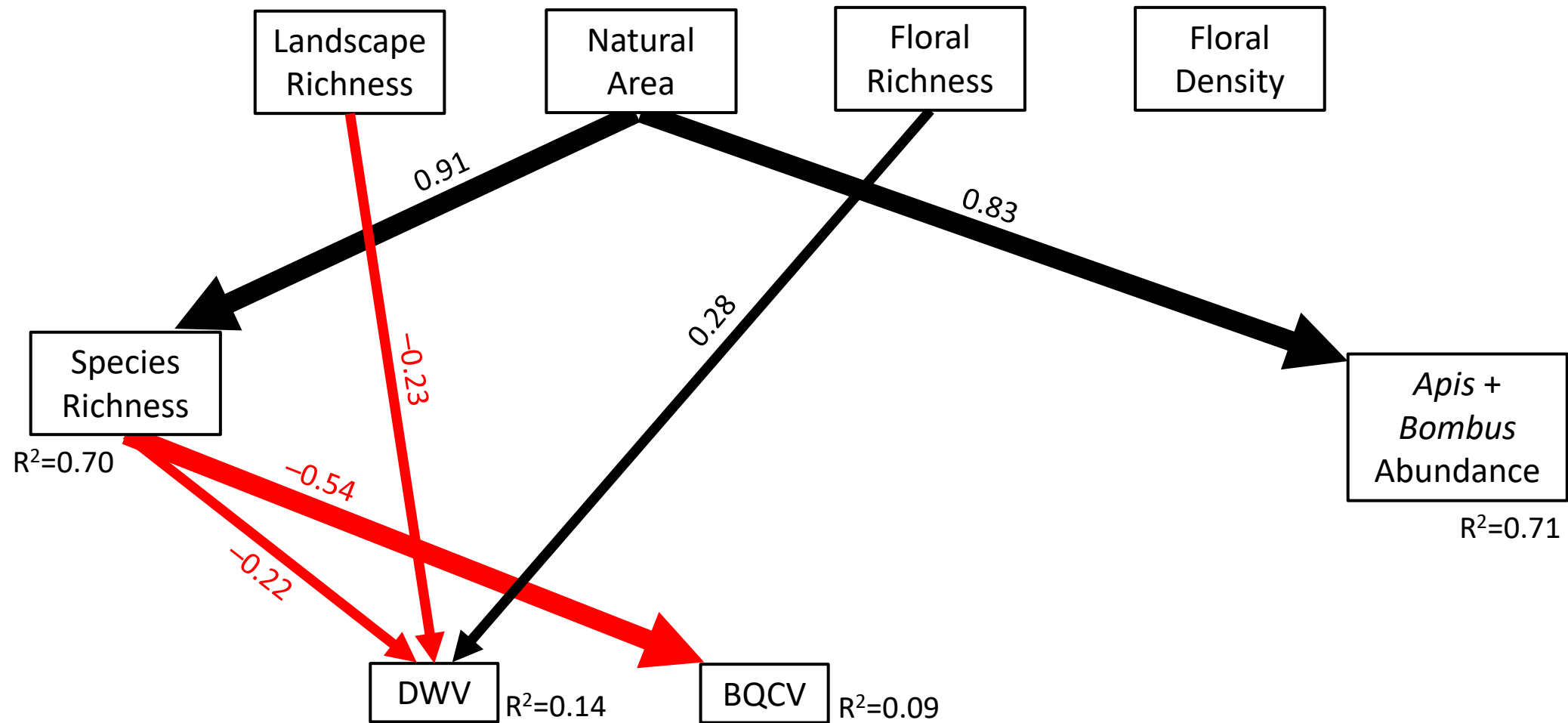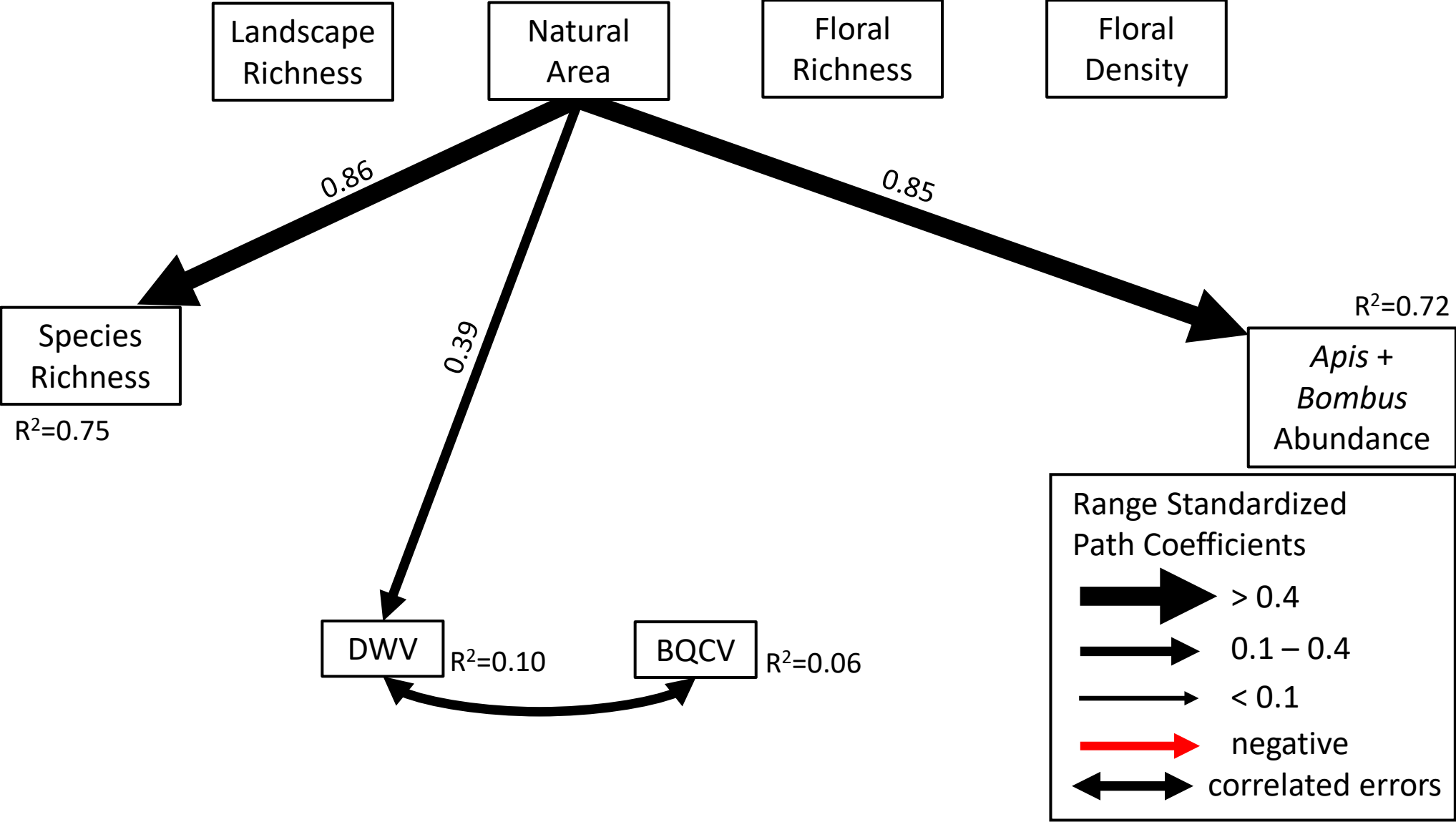
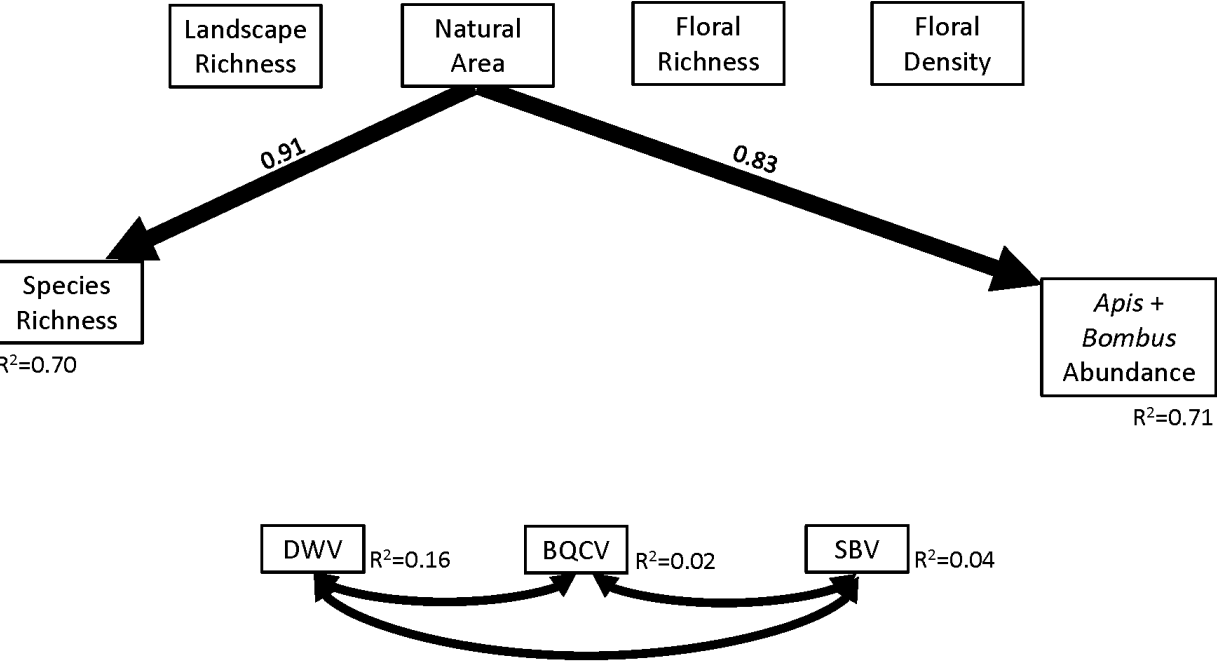## a. *Apis mellifera*
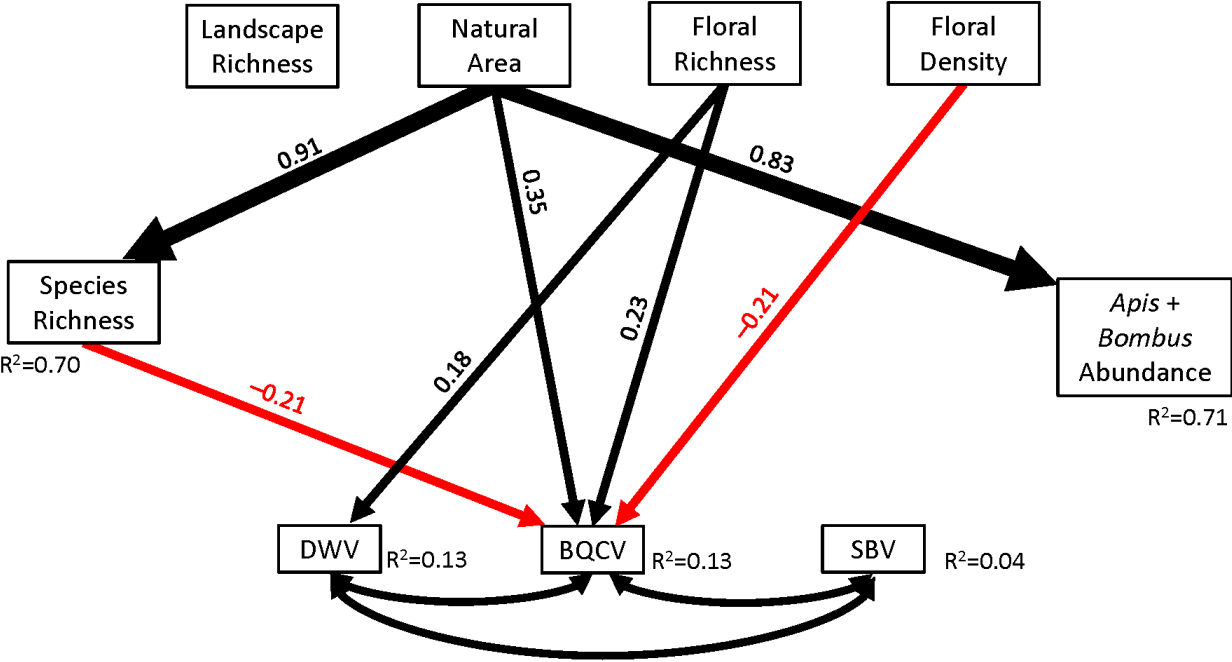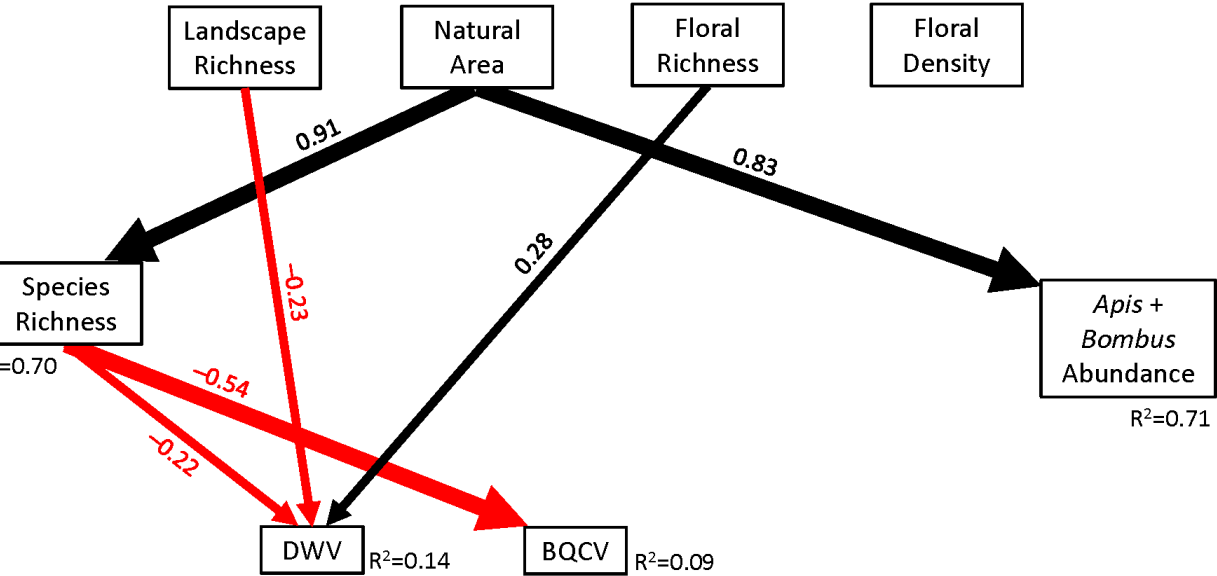
b. *Bombus impatiens*

c. *Lasioglossum* spp.

d. *Eucera pruinosa*

a. *Apis mellifera*

Landscape Richness · Natural Area · Floral Richness · Floral Density

Species Richness R²=0.70

0.91

0.83

Apis + Bombus Abundance R²=0.71

DWV R²=0.16 · BQCV R²=0.02 · SBV R²=0.04

b. *Bombus impatiens*

Landscape Richness · Natural Area · Floral Richness · Floral Density

Species Richness R²=0.70

0.91

0.83

0.35

0.23

0.18

−0.21

−0.21

Apis + Bombus Abundance R²=0.71

DWV R²=0.13 · BQCV R²=0.13 · SBV R²=0.04

c. *Lasioglossum* spp.

Landscape Richness · Natural Area · Floral Richness · Floral Density

Species Richness R²=0.70

0.91

0.83

0.28

−0.23

−0.54

−0.22

Apis + Bombus Abundance R²=0.71

DWV R²=0.14 · BQCV R²=0.09

d. *Eucera pruinosa*

Landscape Richness · Natural Area · Floral Richness · Floral Density

Species Richness R²=0.75

0.86

0.85

0.39

Apis + Bombus Abundance R²=0.72

DWV R²=0.10 · BQCV R²=0.06

Range Standardized Path Coefficients
- → > 0.4
- → 0.1 − 0.4
- → < 0.1
- → negative
- ↔ correlated errors