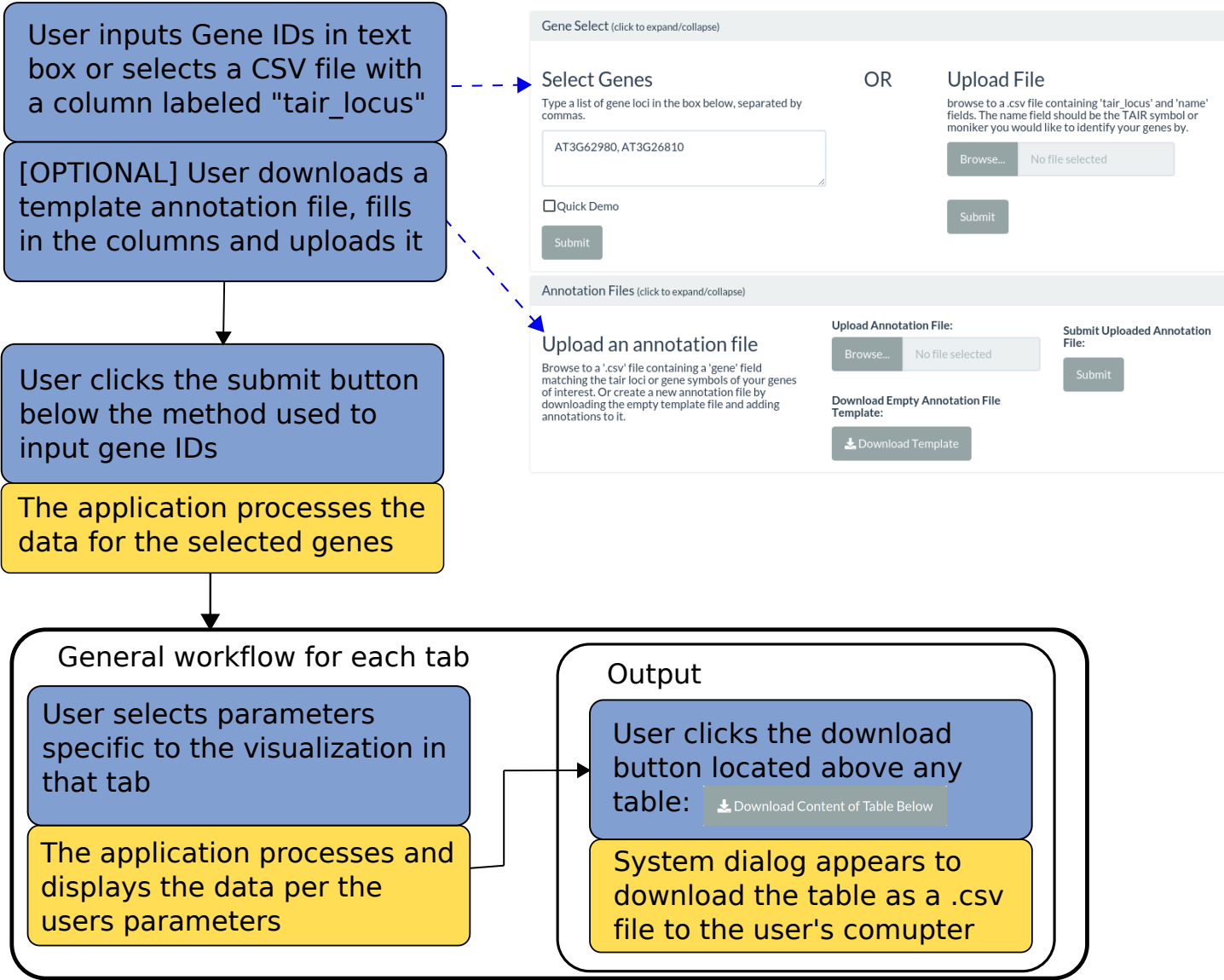


# a. ViVa workflow



## b. Mapping Tab parameters

**Select Genes and Filter Diversity Parameter**

Select one or more transcript IDs below and use the slider to select a minimum sitewise nucleotide diversity

☒ AFB2 (AT3G26810.1)

☒ TIR1 (AT3G62980.1)

Submit

**Log Nucleotide diversity filter limit**

**Type of SNP to mark**

☐ All

☐ Coding

☒ Missense

**Allele selection**

Select the alleles you want to see on the map by clicking the checkboxes

**select alleles to display**

☐ [ AT3G26810.1 | p.Arg204Lys/c.611G>A ]

☐ [ AT3G26810.1 | p.Asp176Glu/c.528C>A ]

☐ [ AT3G62980.1 | p.Thr154Ser/c.461C>G ]

☐ [ AT3G26810.1 | p.Lys368Asn/c.1104G>C ]

☐ [ AT3G62980.1 | p.Ile50Val/c.148A>G ]

Update Map

## c. Browser tab parameters

**Gene Select**

select one or more transcript IDs below

☐ AFB2 (AT3G26810.1)

☐ TIR1 (AT3G62980.1)

Submit

**Filters**

NOTE: all filters are combined by a logical AND. So for a row to be displayed, it must satisfy the requirements of ALL the filters.

☐ hide 0/0 genotypes?

**Filter 1**

column select: Gene\_Name

values to match:

Separate values with a comma followed by a space (ie. "a, b").

**Filter 2**

column select: Gene\_Name

values to match:

Separate values with a comma followed by a space (ie. "a, b").

**Filter 3 (Numeric)**

column select: Indiv

MIN:

MAX:

☐ keep rows with missing values?

**Filter 4 (Numeric)**

column select: Indiv

MIN:

MAX:

☐ keep rows with missing values?

Apply Filters