**Problem summary**

**Given:** Six positive integers. The integers correspond to the number of couples in a population possessing each genotype pairing for a given factor. In order, the six given integers represent the number of couples having the following genotypes:

**1. AA-AA**

**2. AA-Aa**

**3. AA-aa**

**4. Aa-Aa**

**5. Aa-aa**

**6. aa-aa**

**Return:** The expected number of offspring displaying the dominant phenotype in the next generation, under the assumption that every couple has exactly two offspring.

**Algorithm idea**

Consider the offspring possible for each couple. Any couple with a homozygous dominant member will produce offspring with at least one dominant allele. So, all offspring generated by the first three types of couples will have a dominant allele. The probability of passing a dominant allele for the next two can be easily found using Punnet squares (3/4 and 1/2, respectively). Thus the answer can be expressed as

E=2∗(v+w+x)+3/2∗y+zE=2∗(v+w+x)+3/2∗y+z

Where EE is the expected number of offspring displaying the dominant genotype, and vv, ww, xx, yy, and zz are the first through fifth given couple populations.

**Complexity analyses and correctness**

The algorithm requires constant time.