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## "A Python Project about "Single Nucleotide Polymorphism"

**Definition of SNP**: A single nucleotide polymorphism (SNP) is a variation in a single nucleotide (A, T, C, or G) at a specific position in the DNA sequence among individuals of a species. For example, if a particular DNA sequence is normally represented as AAGCCTA in most individuals, but in some, it is AAGCTTA (where the "C" is replaced by "T"), this difference is considered an SNP.

In a **Python project** focused on SNPs, the goal might be to analyze large sets of genetic data to identify these variations and understand their potential impact. Using Python, scientists can process DNA sequences, search for SNPs, and analyze patterns or correlations with specific traits or conditions, making the findings easier to interpret and apply to real-world problems like Python enables efficient exploration of genetic diversity, contributing valuable insights into disease susceptibility, drug response, and population genetics, thus supporting advances in personalized medicine and genomic research.

## Python program coding of SNP analysis:

```
def find_snps(reference, variant):
    snps = []

# Ensure both sequences are the same length
    if len(reference) != len(variant):
        raise ValueError("Sequences must be of the same length.")

for i in range(len(reference)):
    if reference[i] != variant[i]:
        snps.append((i, reference[i], variant[i]))

return snps
```

```
def main():
  # Input reference and variant sequences
  reference sequence = input("Enter the reference sequence: ").strip().upper()
  variant_sequence = input("Enter the variant sequence: ").strip().upper()
  try:
    # Find SNPs
    snp_list = find_snps(reference_sequence, variant_sequence)
    # Output the SNPs found
    if snp_list:
      print("SNPs found:")
      for position, ref, var in snp_list:
         print(f"Position: {position}, Reference: {ref}, Variant: {var}")
    else:
      print("No SNPs found.")
  except ValueError as e:
    print(e)
if __name__ == "__main__":
  main()
```

## **Output Quotation for SNP Analysis Project:**

```
C:\Users\Tashpie\PycharmProjects\pythonProject5\.venv\Scripts\python.exe C:\Users\Tashpie\PycharmProjects\pythonProject5\snp.py

Enter the reference sequence: AGCTTAGCTA

Enter the variant sequence: AGCTTACCTA

SNPs found:

Position: 6, Reference: G, Variant: C

Process finished with evit code A
```