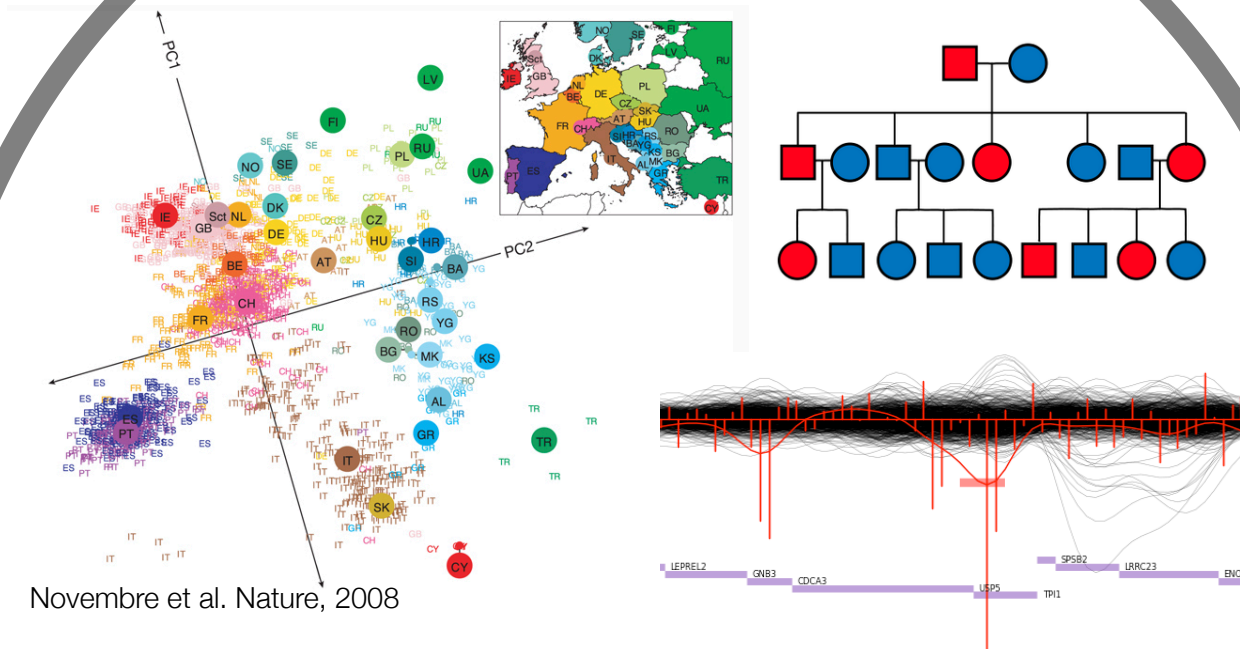
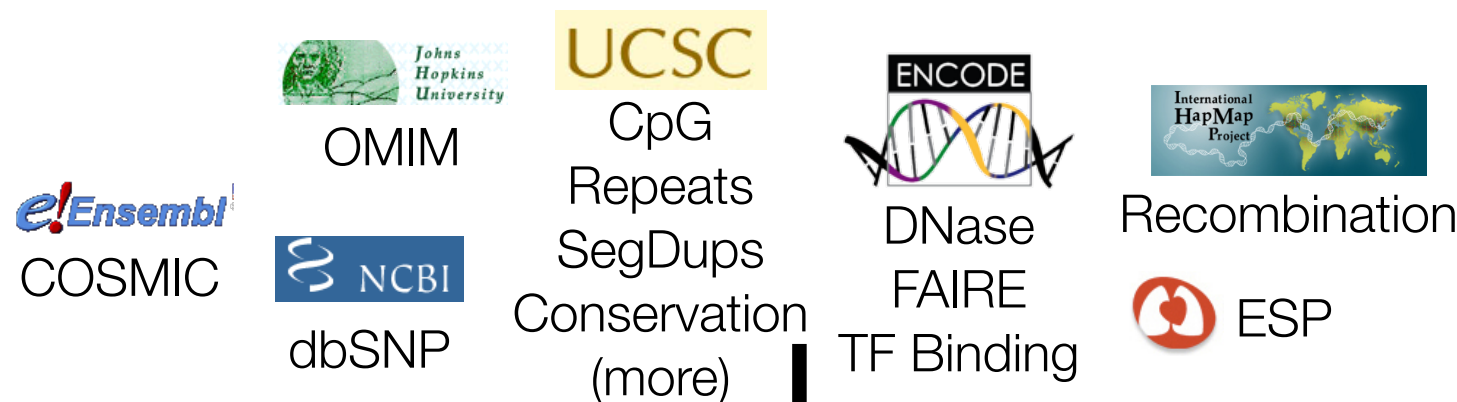


Genome annotations place variants in context

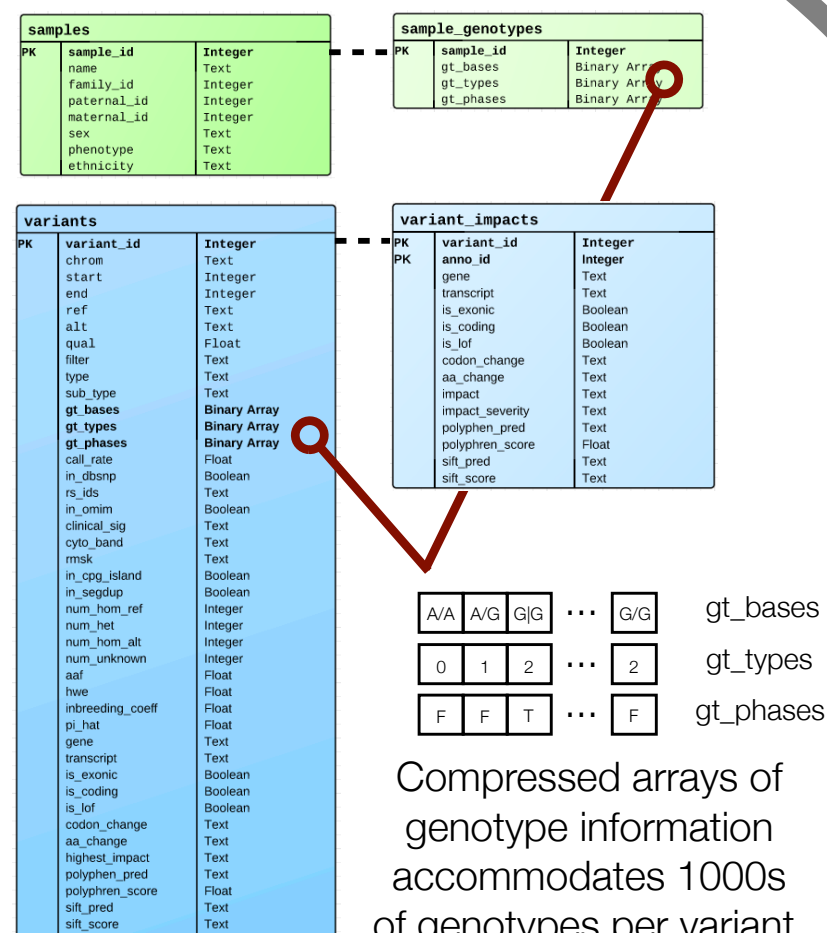


- Mendelian disorders
- Disease associations
- Family-based studies
- Cancer genomic studies

snpEff
VEP
VAT*

VCF file

PED+ file
(sample relationships)



```
# gemini imports
import gemini_utils as util

def my_tool(c, args):
    """
    Execute a query against the gemini database and
    conduct a custom analysis on the results
    """
    # build and execute the relevant query against the da
    query = "SELECT * FROM variants \\"
```