**PPIE on community and patient-specific QV files**

**Community QV files are like reference genomes: they are agreed standards that everyone can use, versioned and stable across projects. Patient-specific QV files are custom layers that sit on top of these standards. They can contain the person’s own notes, preferences, and consent, and they import the community QV files rather than changing them. This way a pipeline can run with just the community QV set for general research, or with the patient wrapper for an individual case. It keeps the science consistent while also respecting what matters to each patient.**

**Here are some examples of the input that different patients provide:**

**1. “Please only tell me about genetic results where something can be done, like a treatment, prevention, or regular checks. I don’t want to get results that I can’t act on.”**

**2. “I do not want to hear about extra findings that are not related to my current condition, unless they are directly useful for my health.”**

**3. “I would like to know if I carry something that could affect my children in the future, even if it does not affect me now.”**

**4. “Please do not give me results that could cause unnecessary worry if nothing can be done about them. If in doubt, I would prefer the doctor to decide what is important.”**

**5. “In my family, my brother had similar symptoms, and my mother had unexplained health problems. Please take this into account when looking at my results.”**

**6. “I would like the results in simple, everyday language that I can understand, with the option to also get a detailed medical report if needed.”**

**7. “Our child has epilepsy. We have tried levetiracetam and valproate, which were not effective. Side effects included severe sleep disturbance and mood changes. Ketogenic diet was very effective in reducing seizure frequency. Please consider this when matching results to treatment options. There is a family history: the child’s uncle also had seizures in childhood that improved with age.”**

**8. “None”.**

**These examples are represented in structured YAML fields, as shown in file "example\_list\_of\_ PPIE\_yaml.txt".**

**An example of a specific patient’s private custom wrapper QV file (patient 1) is shown in file "custom\_patient\_wrapper\_QV\_yaml.txt" which import's two community shared QV disease panels (disease\_x\_panel\_v1 and acmg\_sf\_v3.3).**