

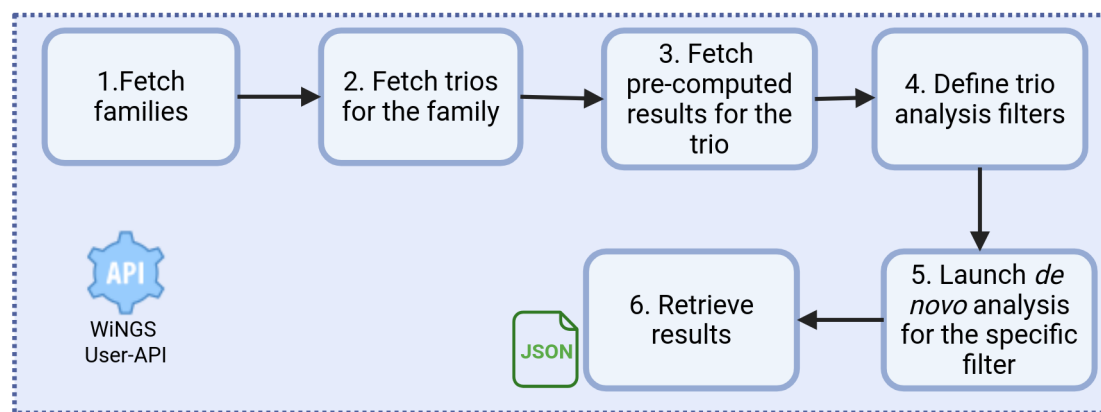


Fig. S5. SV trio analysis workflow

1. Families are returned based on the user access level. 2. Trios available for the family are listed. 3. Pre-computed segregation indicates the counts of variants shared between the family members based on different inheritance patterns. 4. Define filters for trio analysis 5. Launch a request to filter the *de novo* variants based on the created filter conditions. 6. Retrieve results for the specific request.