**Diabetic Complications MVP Gamma – Hypoglycemia Taskforce**

Monday September 9th at 1 PM EST

VANTS 1-800-767-1750, code 87945#

**Attendees:**

* Lauren Costa
* Larry Phillips
* Brian Charest
* Mary Rhee
* Peter Reaven
* Yan Sun

**Minutes:**

1. Hypoglycemia Controls- Confirm definition (including sensitivity analysis)
   1. **Proposed Approach 1:**  Define controls as the sum of rows 2-8, which is 84,948 individuals (94,324 – 9,376).  This includes anyone who had a PCP visit in every calendar year since Diabetes Dx, OR had a glucose reading in every calendar year since Diabetes Dx.  Use Row 8 (N=29,138) in a sensitivity analysis.
   2. **Proposed Approach 2:**  Define controls as the sum of rows 2, 4, 6, and 8, which is 55,275 individuals.  This includes anyone who had a glucose reading in every calendar year since Diabetes Dx.  Use Row 8 (N=29,138) in a sensitivity analysis.
   3. **Discussion:**
      1. Improved definition of controls, without suffering from sample size, can be more beneficial for a genetic analysis.
      2. However if you’re a case, you at somepoint had a low outpatient glucose reading. We didn’t consider requiring regular PCP/glucose readings. So why implement this for controls?
         1. It’s a matter of if one glucose reading ever is enough to call it a control
         2. Can start large and then narrow in
         3. In agreement that those with NO outpatient glucose measurements should be excluded.
            1. Then everything else should be a sensitivity analysis
         4. To be clear, case definition: After diabetes diagnosis, glucose reading <70 OR ED visit with hypoglycemia code at visit (VA ER)
      3. Start with running CHIP GWAS (more manageable) to compare top findings between the 2 different analyses to determine if there is a big difference when using different control definitions (broad vs. more strict) – would be much faster. Then can discuss preferred plan.
      4. Make sure these phenotype files are in Genisis- can have two definitions as we discussed today. Then consider the preliminary analyses.
         1. Brian will provide files with flags to provide flexibility to genetic analysts
         2. Largest, most inclusive definition: Remove those who NEVER had a glucose reading after diabetes dx and include all others
         3. More inclusive: glucose reading every year/more than 1 fill ever
         4. Covariates: age, sex
         5. Will focus on just European ancestry to start
            1. In the future: include some measure of comorbidity (Ex. Elixhauser)

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| --- | --- | --- | --- |
| **>=1 Insulin or Sulfonyurea fill any time after Diabetes Dx** | **PCP Visit in every calendar year since Diabetes Dx** | **Glucose reading in every calendar year since Diabetes Dx** | **# of Patients** |
| 0 | 0 | 0 | 9,376 |
| 0 | 0 | 1 | 2,009 |
| 0 | 1 | 0 | 4,752 |
| 0 | 1 | 1 | 21,235 |
| 1 | 0 | 0 | 16,646 |
| 1 | 0 | 1 | 2,893 |
| 1 | 1 | 0 | 8,275 |
| 1 | 1 | 1 | 29,138 |
|  |  | **Overall Total:** | **94,324** |

**Action Items:**

* Brian will create phenotyping files with flags based on different control definition criteria
* Brian to compare distribution of glucose/PCP measurements between cases/controls
* Sridharan to put Leslie and Yan in touch to discuss effort for hypo genetic analyses