1. **Plasma Fasting Glucose, Serum C-peptide & Insulin (LAB10AM, L10AM\_B, L10AM\_C)** datasets

|  |  |  |  |
| --- | --- | --- | --- |
| **Feature** | **1999-2000 (LAB10AM)** | **2001-2002 (L10AM\_B)** | **2003-2004 (L10AM\_C)** |
| **Insulin Measurement** | RIA (Pharmacia) | RIA (Pharmacia) | Tosoh AIA-PACK IRI (11% lower values) |
| **Glycohemoglobin** | Not mentioned | Available for full sample | Available for full sample |
| **Plasma Glucose Range (mg/dL)** | 56.7 - 587.3 | 38.4 - 686.2 | 45.7 - 547.6 |
| **Subsample Weights** | WTSAF2YR, WTSAF4YR | WTSAF2YR, WTSAF4YR | WTSAF2YR only |
| **Limit of Detection (LOD)** | No mention | No mention | Introduced LOD for insulin (0.71 uU/mL) and C-peptide (0.021 nmol/L) |
| **Last Revision Date** | September 2009 | March 2007 | August 2016 |

 **If comparing insulin values across years (1999-2004)**, adjust **1999-2002 values** using the provided regression equations to match **2003-2004 values** (Tosoh method is ~11% lower).

* Use:  
  **Pharmacia-equivalent = 0.96006 × Tosoh + 3.23663**  
  **Tosoh-equivalent = 1.0027 × Pharmacia - 2.2934**

 **Use only plasma glucose (LBXGLU) values** for diabetes diagnosis, not serum glucose (LBXSGL).

 **Apply correct fasting sample weights**:

* **1999-2002**: Use **WTSAF4YR** for full 4-year analysis, **WTSAF2YR** for 2-year analysis.
* **2003-2004**: Use **WTSAF2YR** only.

 **If using insulin or C-peptide from 2003-2004**, account for **Limit of Detection (LOD)** values:

* **Insulin LOD** = **0.71 uU/mL**
* **C-peptide LOD** = **0.021 nmol/L**

 **Use appropriate linking variables (SEQN) to merge NHANES lab data with demographic or health data.**

2) Glycohemoglobin (HbA1c), follow these steps:

**1. Select Only the Required Years**

* Filter the dataframe to **only include the NHANES cycles you need** (e.g., **1999-2000, 2001-2002, 2003-2004**).
* Ensure you correctly **merge datasets** if using multiple years.

**2. Use the Correct Sample Weights**

* For **1999-2004**, use the **full sample MEC weights** (since Glycohemoglobin was measured in all participants).
* Drop rows with **zero or missing weights**.

**3. Keep Raw HbA1c Values**

* Do **not apply cross-over regression** adjustments between 2003-2004 and 2005-2006.
* Retain **LBXGH (Glycohemoglobin %)** values as recorded.

**4. Merge with Demographics (Optional)**

* Use **SEQN** to merge with **age, BMI, ethnicity, diabetes status** (if needed).
* Helps in **stratified analysis** (e.g., age groups, BMI categories).

**5. Convert HbA1c to Diagnostic Categories (Optional)**

If you need classification:

* **Normal:** HbA1c < 5.7%
* **Prediabetes:** 5.7% ≤ HbA1c < 6.5%
* **Diabetes:** HbA1c ≥ 6.5%

**6. Handle Missing Data**

* Remove or impute missing values in **LBXGH**.
* Ensure proper handling of **outliers** (e.g., extremely high values).

**7. Analyze Trends**

* If comparing HbA1c across years, **normalize with proper survey weights**.
* Use **boxplots, histograms, or trend lines** to inspect shifts over time.