1. **Description of the cohort/biobank in which the algorithm was implemented**

|  |  |
| --- | --- |
| Total number of participants | Approx. 12300 |
| Source of recruitment  (e.g., community, clinic, hospital, healthcare system) | Healthcare system |
| Geographic region | Mid-atlantic |
| Phenotype(s) of interest (if not phenotype-driven, indicate None) | Approx. 3200 enriched for AAA, Obesity, Cardio |
| Number of adults (>18 years of age) with lipid profile in the cohort | Maybe 9000 |
| Number of children (less than 18 years) with lipid profile | Maybe 10 |
| Year biobank was initiated (when the first patient was enrolled) | 2012 |
| Year the database was frozen for the present analysis | 2017 |

1. **Overall time needed to implement the e-algorithm \_\_\_16, not including validation\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ hours**
2. **Describe the overall ease of implementing the FH algorithm at your site**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Very difficult | Somewhat difficult | Average (Acceptable) | Above Average | Excellent |
|  |  |  | X |  |

1. **Describe the ease of implementing structured data elements at your site**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Very difficult | Somewhat difficult | Average (Acceptable) | Above Average | Excellent |
|  |  |  |  | X |

1. **Describe the overall ease of implementing the NLP component at your site**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Very difficult | Somewhat difficult | Average (Acceptable) | Above Average | Excellent |
|  |  | X |  |  |

1. **Which NLP software did you use at your site?**

|  |  |  |
| --- | --- | --- |
| MedTagger  (It was part of the pseudocode) | Apache cTAKES | Other (Please describe) |
|  |  | KNIME, python |

1. **What EHR system is used at your site?**

|  |  |  |
| --- | --- | --- |
| GE Centricity (Synthesis) | EPIC | Other (indicate) |
|  | X |  |

1. **What hurdles did you encounter while implementing the FH e-algorithm**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Complexity of the phenotype *per se* | Features of the local EHR  (structured data were hard to implement due to …) | Features of the local EHR  (unstructured data were hard to implement due to …) | Difficulty in obtaining IT resources | Transitioning from one EHR system to another | Other (indicate) |
|  | X |  |  |  |  |

1. **Do you think a less complex phenotyping algorithm is needed to improve scalability and portability?**

|  |  |
| --- | --- |
| YES | NO |
|  | X |

1. **Did you find input description (structured and unstructured data elements) provided on PheKB similar to data elements at your site (e.g., family history was described as unstructured data element in the pseudocode)?**

|  |  |
| --- | --- |
| YES | NO |
|  | X |

1. **Did you need to modify the Mayo version of the FH e-algorithm (the PheKB version of the pseudocode)?**

|  |  |
| --- | --- |
| YES | NO |
| X |  |

1. **How easily would an automated algorithm for FH connection integrate in your EHR?**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Not probable (Very undesirable) | Somewhat improbable (Undesirable) | Neutral | Somewhat probable (Desirable) | Very probable (Very desirable) |
| X |  |  |  |  |

|  |
| --- |
| 1. **Suggestions to improve the electronic phenotyping algorithm for FH ascertainment (free text)** |

|  |
| --- |
| 1. **Other comments/feedback** |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| 1. **Number of people involved in implementation at your site** | 1 | 2 | 3 | >3 |
|  |  |  |  |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| 1. **Implementation Team (check all that apply)** | (Bio)informatician | Fellow / trainee | Clinician | IT specialist | Other (indicate) |
| X |  | X |  |  |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| 1. **Who completed this survey** | (Bio)informatician | Fellow/Trainee | Clinician | IT specialist | Other (indicate) |
| X |  |  |  |  |