Client Consultation Report

Project: Parkinson's Disease Prediction using AI/ML

Project Goal: To develop an AI/ML-powered system that accurately predicts Parkinson's Disease in its early stages using biometric and voice-based features, while also integrating 3D protein structure visualization (e.g., alpha-synuclein) to enhance understanding of disease progression and aid in potential drug target identification.

Client Meetings and Questions

This report consists of four meetings with the client, each addressing specific objectives. Below are the questions posed to the client and their responses.

Meeting 1: Understanding Parkinson's Disease Prediction Goals

Objectives:

1. Understand the client's vision and primary goals for Parkinson's detection.
2. Discuss expected use cases and beneficiaries (doctors, researchers, etc.).
3. Clarify scope, dataset needs, and model expectations.

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Q: What is the goal of using SVM with PDB data?
A: To classify alpha-synuclein variants as aggregation-prone or stable based on structural features.

Q: Who uses this system?
A: Researchers, bioinformaticians, and drug developers.

Q: What features are used for prediction?
A: Amino acid composition, secondary structure, hydrophobicity, and aggregation scores from PDB files.

Q: Is it for research or clinical use?
A: Mainly research, with future clinical potential.

Q: What data is needed?
A: PDB structures of alpha-synuclein and its mutants.

Q: What does the system output?
A: Aggregation risk (Yes/No), confidence score, and structural visualization.

Q: How fast is the prediction?
A: Around 5–15 seconds per structure.

Q: What does the MVP include?
A: Upload PDB → Feature extraction → SVM prediction → 3D result view.

Q: Does it suggest treatments?
A: No, only predictive support.

Q: What challenge does it solve?
A: Detecting misfolding patterns and classifying structural risks efficiently.

Meeting 2: Technical Design for Parkinson's Prediction System

Objectives:

1. Define technical and model requirements.
2. Discuss feature engineering, algorithms, and training strategies.
3. Clarify deployment and data handling needs.

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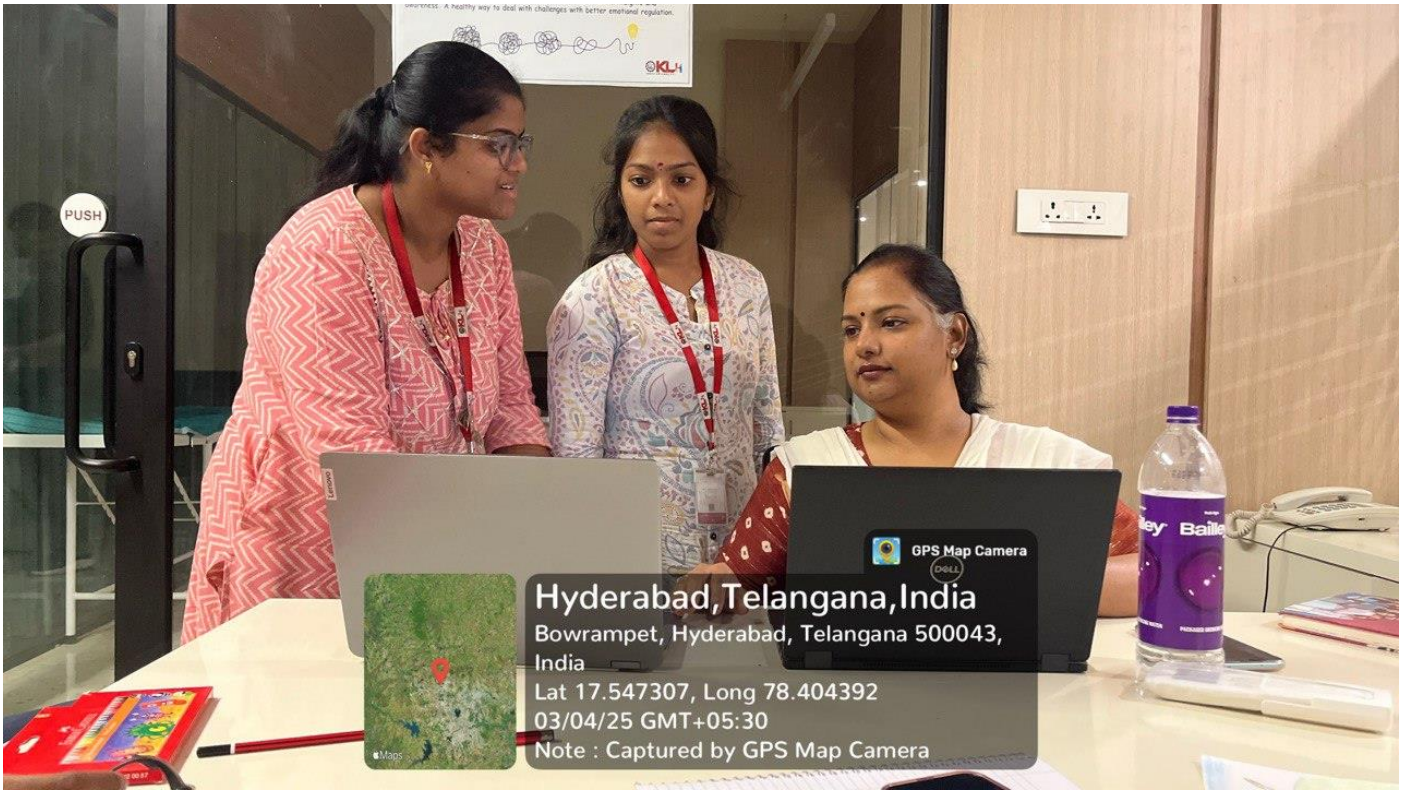

Q: What ML models fit this use case?
A: SVM for structural classification, Random Forest for feature selection, and CNNs for 3D pattern learning.

Q: What preprocessing is needed?
A: Structure cleaning, feature extraction (e.g., hydrophobicity, RMSD), and scaling.

Q: Should the model be explainable?
A: Yes, using SHAP/LIME to highlight influential structural features.

Q: Is 3D protein visualization required?
A: Yes, using PyMOL or Chimera to visualize alpha-synuclein aggregation zones.

Q: Which backend is preferred?
A: Flask, for a lightweight API and easy integration.

Q: Real-time or batch predictions?
A: Real-time for single PDB input; batch mode for multiple structures.

Q: What is the target accuracy?
A: Minimum 90%, with high precision to ensure structural prediction reliability.

Q: Will the model be built from scratch or fine-tuned?
A: Initially from scratch; later versions may use pre-trained structural models.

Q: What deployment platform is preferred?
A: AWS or Heroku for cloud hosting; GitHub for collaboration and versioning.

Q: Can users upload PDB or sequence files?
A: Yes, with clear file format instructions and data privacy measures.

Meeting 3: User Experience and Model Interaction for Parkinson's Prediction

- **Objectives:**
  1. Finalize how users interact with the system.
  2. Design feedback, explanation, and error handling flow.
  3. Improve accessibility for healthcare professionals.

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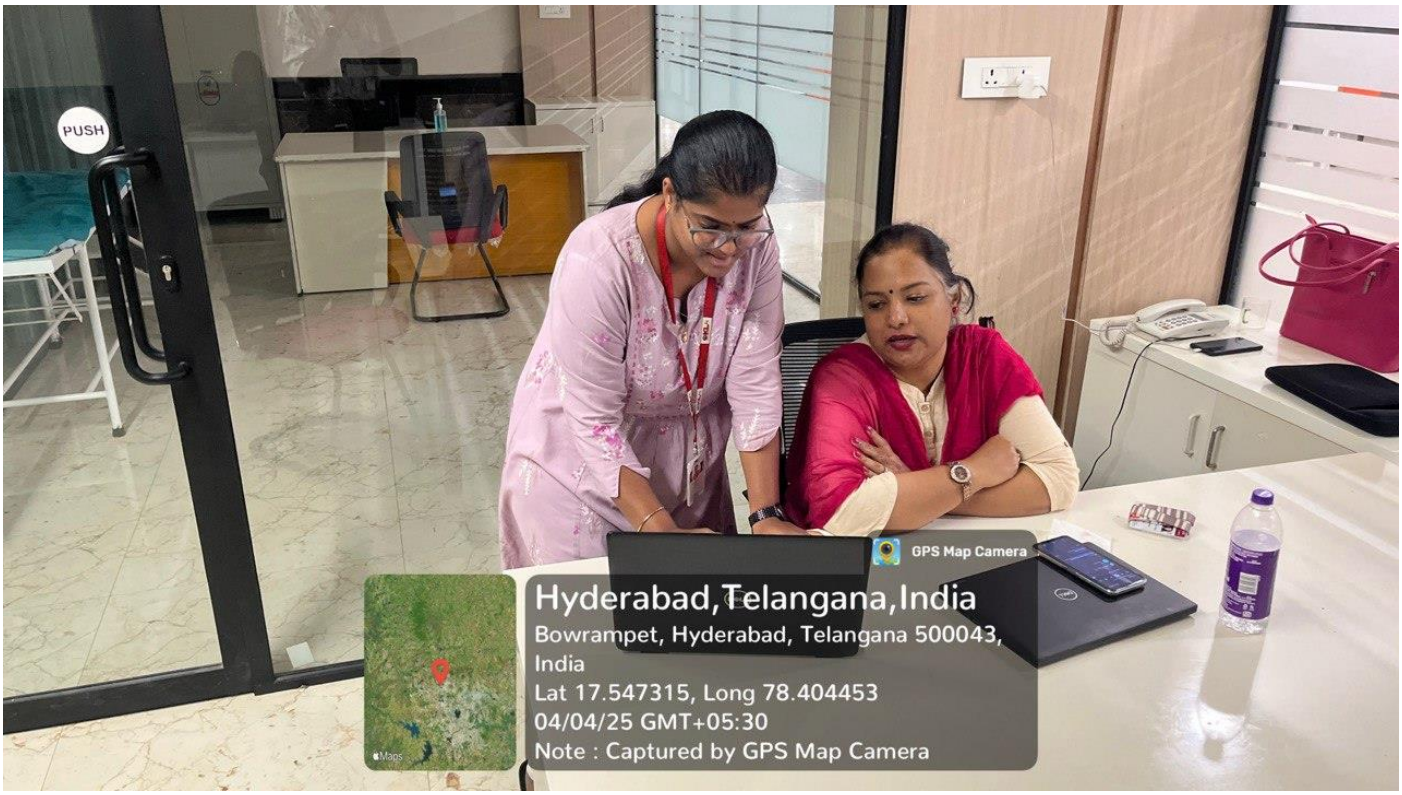

Q: How should prediction results be shown?
A: As "Aggregation Likely" or "Stable Structure", with confidence score and feature explanation.

Q: Should users get post-result suggestions?
A: Yes, like "Review with Structural Biologist" or "Analyze Additional Variants."

Q: Will the system support PDB uploads only, or allow sequence input too?
A: Initially PDB uploads; future versions may support raw sequence input.

Q: How to handle invalid or unsupported files?
A: Show an error message with accepted formats (.pdb) and retry option.

Q: Is the UI designed for accessibility?
A: Yes, with readable fonts, simple layout, and keyboard-friendly design.

Q: Can users download their results?
A: Yes, a PDF report with prediction, visual highlights, and key structural features.

Q: What if model confidence is low?
A: Return an “Inconclusive” message and suggest manual structural review.

Q: Will structural data visualization be available?
A: Yes, with basic charts and interactive 3D model views (e.g., PyMOL snapshots).

Q: Will language support be limited?
A: Start with English; other languages can be added later.

Q: Can users give feedback to improve predictions?
A: Yes, with consent, user feedback will help retrain and refine the model.

Meeting 4: Deployment, Validation, and Final Checklist

Objectives:

1. Confirm final deployment plans and hosting platform.
2. Discuss testing, security, and release timeline.
3. Final QA checks and go-live readiness.

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Q: What is the target launch timeline?
A: Within 2 months after testing and model validation.

Q: What types of testing will be done?
A: Unit, functional, and structural prediction accuracy testing using real-world protein data.

Q: How will clinical validation be handled?
A: Using expert-reviewed predictions on anonymized research datasets.

Q: What privacy standards are followed?
A: GDPR-compliant storage, anonymized inputs, and encryption.

Q: Will user documentation be provided?
A: Yes, with a guide and demo video for onboarding.

Q: What happens if the system fails?
A: Auto-restart, failover backup, and crash notifications.

Q: Will the model be updated regularly?
A: Yes, retrained biannually with new structural or clinical data.

Q: Can system usage be monitored?
A: Yes, through an integrated analytics dashboard.

Q: Will users get update notifications?
A: Yes, through email or in-app alerts.

Q: Who handles support after deployment?
A: A dedicated technical team for maintenance and issue resolution.

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