

10. The system according to claim 8, wherein the fine needle aspiration biopsy results include an inadequate score, indeterminate score, negative score, and positive score; wherein the ultrasound data include a complex cyst score, mixed score, simple cyst score, and solid score; and wherein the lymph node size includes a less than 18 centimeters score, 18-31 centimeters score, and greater than 31 centimeters score.

11. The system according to claim 8, wherein the imaging data includes results from electrical impedance scanning.

12. The system according to claim 11, wherein the results from the electrical impedance scanning include a definitely benign score, probably benign score, suspicious for cancer score, probably cancer score, and definitely cancer score.

13. The system according to claim 8, wherein said fully unsupervised Bayesian Belief Network model lacks human-developed decision support rules.

14. The system according to claim 8, wherein said graphic user interface further outputs an estimated accuracy of the patient-specific probability of malignancy in the thyroid nodule, the estimated accuracy including at least one of model sensitivity, model specificity, positive and negative predictive values, and overall accuracy.

15. A computer program product for determining a patient-specific probability of malignancy in a thyroid nodule, said computer program product including:

a computer readable storage medium;

first program instructions to collect clinical parameters from a plurality of patients to create a training database, the clinical parameters including fine needle aspiration biopsy results, ultrasound data, lymph node size, and imaging data;

second program instructions to create a fully unsupervised Bayesian Belief Network model using data from the training database;

third program instructions to validate the fully unsupervised Bayesian Belief Network model;

fourth program instructions to collect the clinical parameters for an individual patient;

fifth program instructions to input the clinical parameters for the individual patient into the fully unsupervised Bayesian Belief Network model via a graphical user interface;

sixth program instructions to output the patient-specific probability of malignancy in the thyroid nodule from the fully unsupervised Bayesian Belief Network model to the graphical user interface for use by a clinician; and

seventh program instructions to update the fully unsupervised Bayesian Belief Network model using the clinical parameters for the individual patient and the patient-specific probability of malignancy in the thyroid nodule, the first program instructions, the second program instructions, the third program instructions, the fourth program instructions, the fifth program instructions, the sixth program instructions, and the seventh program instructions are stored on the computer readable storage medium.

16. A method for determining a patient-specific probability of transplant glomerulopathy, said method including:

collecting clinical parameters from a plurality of patients to create a training database, the clinical parameters including biomarker levels from biopsy tissue;

creating a fully unsupervised Bayesian Belief Network model using data from the training database;

validating the fully unsupervised Bayesian Belief Network model;

collecting the clinical parameters for an individual patient; receiving the clinical parameters for the individual patient into the fully unsupervised Bayesian Belief Network model;

outputting the patient-specific probability of transplant glomerulopathy from the fully unsupervised Bayesian Belief Network model to a graphical user interface for use by a clinician; and

updating the fully unsupervised Bayesian Belief Network model using the clinical parameters for the individual patient and the patient-specific probability of transplant glomerulopathy.

17. The method according to claim 16, wherein the biomarker levels include gene expression levels for an ICAM-1 gene, IL-10 gene, CCL-3 gene, CD-86 gene, CCL-2 gene, CXCL-11 gene, CD-80 gene, GNLY gene, and PRF-1 gene.

18. The method according to claim 17, wherein the biomarker levels further include gene expression levels for a CD40LG gene, IFNG gene, CD-28 gene, CXCL-10 gene, CCR-5 gene, CD-40 gene, CTLA-4 gene, TNF gene, CXCL-9 gene, CX3CR-1 gene, FOXP-3 gene, EDN-1 gene, CD-4 gene, TBX-21 gene, FASLG gene, C-3 gene, CD3E gene, CXCR-3 gene, and CCL-5 gene.

19. The method according to claim 16, wherein the biomarker levels include gene expression levels for the VCAM1 gene, MMP9 gene, Banff C4d gene, MMP7 gene, and LAMC2 gene.

20. The method according to claim 20, wherein the biomarker levels further include gene expression levels for a TNC gene, S100A4 gene, NPHS1 gene, NPHS2 gene, AFAP gene, PDGF8 gene, SERPINH1 gene, TIMP4 gene, TIMP3 gene, VIM gene, SERPINE1 gene, TIMP1 gene, FN1 gene, ANGPT2 gene, TGFB1 gene, ACTA2 gene, TIMP2 gene, COL4A2 gene, MMP2 gene, COL1A1 gene, COL3A1 gene, GREM1_2 gene, SPARC gene, IGF1 gene, SMAD3 gene, HSPG2 gene, FN1 gene, ANGPT2 gene, TGFB1 gene, ACTA2 gene, THBS1 gene, CTNBN1 gene, FGF2 gene, TJP1 gene, FAT gene, CDH1 gene, SMAD7 gene, CD2AP gene, CDH3 gene, CTGF gene, ACTN4 gene, SPP1 gene, AGRN gene, VEGF gene, and BMP7 gene.

21. The method according to claim 16, wherein said creating of the fully unsupervised Bayesian Belief Network model includes creating the fully unsupervised Bayesian Belief Network model without human-developed decision support rules.

22. The method according to claim 16, further including estimating an accuracy of the patient-specific probability of transplant glomerulopathy, the accuracy including at least one of model sensitivity, model specificity, positive and negative predictive values, and overall accuracy.

23. A method for determining a patient-specific probability of impaired wound healing, said method including:

collecting clinical parameters from a plurality of patients to create a training database, the clinical parameters including biomarker levels from at least one of serum, wound effluent and biopsy tissue, the biomarker levels including gene expression levels for an IP-10 gene, IL-6 gene, MCP-1 gene, IL-5 gene, and RANTES gene;

creating a fully unsupervised Bayesian Belief Network model using data from the training database;

validating the fully unsupervised Bayesian Belief Network model;