【CLAIMS】

【Claim 1】

1. A process-implemented method for providing cancer diagnosis information using artificial intelligence-based liquid biopsy of exosome, the method comprising:

measuring, by Surface Enhanced Raman Spectroscopy (SERS) measurement device, cultured cell exosome SERS signals from cultured cancer cells and cultured normal cells;

training, by a processor, a deep learning model using the cultured cell exosome SERS signals, wherein the deep learning model comprises five convolutional layers and is configured to distinguish between cancer cell exosome signals and normal cell exosome signals, wherein the deep learning model includes a first convolutional layer configured to receive input data; a second to fifth convolutional layer, each comprising a plurality of sub-convolutional layers, wherein skip connections are inserted between every two of the sub-convolutional layers; and a fully connected layer connected sequentially after the fifth convolutional layer;

measuring, by the SERS measurement device, a blood exosome SERS signal from a subject's blood sample;

analyzing, by the processor, the blood exosome SERS signal using the deep learning model trained with the cultured cell exosome SERS signal to generate feature data, wherein analyzing comprises processing the blood exosome SERS signal through the five convolutional layers and a first fully connected layer; and

analyzing, by the processor, a similarity between blood exosome feature data and cultured cell exosome feature data analyzed using the deep learning model to generate cancer diagnosis information, wherein the similarity analysis comprises calculating a Mahalanobis distance, where D_{normal} is a Mahalanobis distance from the blood exosome data to normal cell exosome data, and D_{cancer} is a Mahalanobis distance from the blood exosome data to cancer cell exosome data.

【Claim 2】

The method of claim 1, wherein the cultured cell exosome comprises normal cell-derived exosome and cancer cell-derived exosome, and

wherein SERS signals include a normal cell exosome SERS signal and a cancer cell exosome SERS signal, each obtained by the SERS measurement device from exosomes derived from cultured normal cells and cultured cancer cells respectively.

【Claim 3】

The method of claim 2, wherein the fully connected layer includes:

a first fully connected layer configured to output 4096 feature values, and a second fully connected layer configured to output 10 feature values based on the output of the first fully connected layer.

【Claim 4】

The method of claim 3, wherein analyzing the similarity comprises comparing, by the processor, the 10 feature values output from the second fully connected layer based on the subject's blood exosome SERS signal with the

corresponding values derived from the cultured cancer cell exosome SERS signal.

【Claim 5】

The method of claim 4, wherein analyzing the similarity further comprises:

determining, by the processor, a relative similarity to cancer cell exosome data according to the following equation:

Relative similarity to cancer exosome=D_{normal}/D_{cancer}

where the D_{normal} is a Mahalanobis distance from the blood exosome data to the normal cell exosome data, and D_{cancer} is a Mahalanobis distance from the blood exosome data to the cancer cell exosome data.

【Claim 6】

A system implemented in a computing device comprising at least one processor capable of deep learning computation for providing cancer diagnosis information using artificial intelligence-based liquid biopsy of exosome, the at least one processor being configured to execute instructions stored in a non-transitory computer medium, thereby configuring the processor to:

measure a cultured cell exosome Surface Enhanced Raman Spectroscopy (SERS) signals from cultured cancer cells and cultured normal cells using a SERS measurement device;

train a deep learning model using the cultured cell exosome SERS signal, the deep learning model comprising five convolutional layers and a fully connected layer and being configured to distinguish between cancer cell exosome signals and normal cell exosome signals, wherein the deep learning

model includes a first convolutional layer configured to receive input data; a second to fifth convolutional layer, each comprising a plurality of sub-convolutional layers, wherein skip connections are inserted between every two of the sub-convolutional layers; and a fully connected layer connected sequentially after the fifth convolutional layer;

measure a blood exosome SERS signal from a subject's blood sample using the SERS measurement device;

analyze the blood exosome SERS signal using the deep learning model trained with the cultured cell exosome SERS signal to generate feature data, wherein analyzing comprises processing the blood exosome SERS signal through the five convolutional layers and a first fully connected layer; and

analyze a similarity between blood exosome feature data and cultured cell exosome feature data analyzed using the deep learning model to generate cancer diagnosis information, wherein the similarity analysis comprises calculating a Mahalanobis distance, where D_{normal} is a Mahalanobis distance from the blood exosome data to normal cell exosome data, and D_{cancer} is a Mahalanobis distance from the blood exosome data to cancer cell exosome data.