Having described the invention, we claim:

1. A method for fully automated screening for aneuploidy in a human embryo, comprising:

obtaining an image of the embryo at an associated imager;

providing the image of the embryo to a neural network to generate a first clinical parameter;

retrieving a set of at least one parameter representing one of a patient receiving the embryo, an egg utilized to produce the human embryo, a sperm used to create the embryo, a sperm donor who provided sperm used to create the embryo, and an egg donor who provided the egg;

generating a second clinical parameter from a set of classification parameters comprising the set of at least one parameter at a predictive model wherein none of the set of classification parameters are derived from imaging of the embryo; and

generating a composite parameter, representing a likelihood of aneuploidy in the embryo, from the first clinical parameter and the second clinical parameter.

2. The method of claim 1, wherein providing the image of the embryo to the neural network comprises providing the image of the embryo to a recurrent neural network.

3. The method of claim 1, wherein providing the image of the embryo to the neural network comprises providing the image of the embryo to a discriminative classifier trained as part of a generative adversarial network.

4. The method of claim 1, wherein providing the image of the embryo to the neural network comprises providing the image of the embryo to a convolutional neural network.

5. The method of claim 1, wherein the set of at least one parameter includes an age of the egg donor who provided the oocyte fertilized to produce the embryo.

6. The method of claim 1, wherein the set of at least one parameter includes a number of embryos that were normally fertilized from oocytes harvested with the oocyte fertilized to produce the embryo.

7. The method of claim 1, wherein the set of at least one parameter includes a value representing a quality of the sperm used to fertilize the embryo.

8. A system for fully automated screening for aneuploidy in a human embryo, the system comprising:

a processor; and

a non-transitory computer readable medium storing instructions executable by the processor, the machine executable instructions comprising:

an imager interface configured to receive an image of the embryo from an associated imager;

a neural network configured to generate a first clinical parameter from the image of the embryo;

a predictive model configured to generate a second clinical parameter from a set of classification parameters comprising a set of at least one parameter representing one of a patient receiving the embryo, an oocyte fertilized to produce the human embryo, a sperm used to create the embryo, a sperm donor who provided the sperm used to create the embryo, and an egg donor who provided the oocyte from an associated memory, wherein none of the set of classification parameters are derived from imaging of the embryo; and

an arbitrator configured to generate a composite parameter, representing a likelihood of aneuploidy in the embryo, from the first clinical parameter and the second clinical parameter.

9. The system of claim 8, wherein the arbitrator is configured to generate the composite parameter as a weighted linear combination of at least the first clinical parameter and the second clinical parameter.

10. The system of claim 8, wherein the arbitrator is configured to generate the composite parameter as an average of at least the first clinical parameter and the second clinical parameter.

11. The system of claim 8, wherein the predictive model is a first predictive model, the set of at least one parameter is a first set of at least one parameter, and the system further comprises a second predictive model configured to generate a third clinical parameter from a second set of at least one parameter, each of the first clinical parameter, the second clinical parameter, and the third clinical parameter being a categorical parameter and the arbitrator being configured to generate the composite parameter according to a majority vote among at least the first clinical parameter, the second clinical parameter, and the third clinical parameter.

12. The system of claim 8, wherein the predictive model is implemented as a support vector machine.

13. The system of claim 8, wherein the predictive model is implemented as a fully-connected feed-forward neural network.

14. The system of claim 8, wherein the set of at least one parameter includes at least one of an age of the egg, an age of an egg donor, an age of a sperm donor, a method of fertilization for the embryo, a hormonal profile of the egg donor, a past diagnosis of a condition of the egg donor, and a past diagnosis of a condition of the sperm donor.

15. A method for fully automated screening for aneuploidy in a human embryo, comprising:

obtaining an image of the embryo at an associated imager;

generating a first clinical parameter from the image of the embryo at a convolutional neural network;

retrieving a set of parameters from an associated memory, the set of parameters comprising an age of the egg donor who provided the oocyte fertilized to produce the embryo, a value representing a quality of the sperm used to create the embryo, and a number of embryos that were normally fertilized from oocytes harvested with the oocyte fertilized to produce the embryo;

generating a second clinical parameter at a first predictive model from a set of classification parameters comprising a first subset of the set of parameters, wherein none of the set of classification parameters are derived from imaging of the embryo;

generating a third clinical parameter at a second predictive model from a second subset of the set of parameters; and

generating a composite parameter, representing a likelihood of aneuploidy in the embryo, from the first clinical parameter, the second clinical parameter, and the third clinical parameter.

16. The method of claim 15, wherein generating the composite parameter from the first clinical parameter, the second clinical parameter, and the third clinical parameter comprises generating the composite parameter according to a majority vote among the first clinical parameter, the second clinical parameter, and the third clinical parameter.

17. The method of claim 15, wherein the first predictive model is implemented as a support vector machine, and the second predictive model is implemented as a fully-connected feedforward neural network.

18. The method of claim 15, wherein the set of classification parameters comprises the set of parameters, and generating the third clinical parameter at the second predictive model from the second subset of the set of parameters comprises generating the third clinical parameter at the second predictive model from the set of parameters.

19. The method of claim 15, wherein each of the first subset of the set of parameters and the second subset of the set of parameters are proper subsets of the set of parameters.