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BEFORE THE PATENT TRIAL AND APPEAL BOARD

Ex parte CHARLES J. VASKE, STEPHEN C. BENZ, JOSHUA M. STUART, and DAVID HAUSSLER

Appeal 2017-006005
Application 13/068,002[1]
Technology Center 1600

Before DONALD E. ADAMS, ULRIKE W. JENKS, and TIMOTHY G. MAJORS, *Administrative Patent Judges*.

ADAMS, *Administrative Patent Judge*.

DECISION ON APPEAL

This Appeal[2] under 35 U.S.C. § 134(a) involves claims 1–5, 7, and 10–13 (App. Br. 1).[3] Examiner entered rejections under 35 U.S.C. § 112, second paragraph, 35 U.S.C. § 101, and obviousness-type double patenting. We have jurisdiction under 35 U.S.C. § 6(b).

We AFFIRM.

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[1] Appellants identify the real party in interest as "the Regents of the University of California" (App. Br. 1).
[2] This Appeal is related to co-pending Appeal 2017-006133, Application 13/317,769.
[3] Pending "[c]laims 8, 9 and 14-32 [stand] withdrawn" from consideration (App. Br. 1).

STATEMENT OF THE CASE

> A central premise in modern cancer treatment is that patient diagnosis, prognosis, risk assessment, and treatment response prediction can be improved by stratification of cancers based on genomic, transcriptional and epigenomic characteristics of the tumor alongside relevant clinical information gathered at the time of diagnosis (for example, patient history, tumor histology and stage) as well as subsequent clinical follow-up data (for example, treatment regimens and disease recurrence events).

(Spec. ¶ 2.) Appellants disclose, however, that "the challenges of integrating multiple data sources to identify reproducible and interpretable molecular signatures of tumorigenesis and progression remain elusive" (Spec. ¶ 7). In this regard, Appellants disclose that although "[a]pproaches for interpreting genome-wide cancer data have focused on identifying gene expression profiles that are highly correlated with a particular phenotype or disease state, and have led to promising results" (Spec. ¶ 8),

> [n]ew computational approaches are needed to connect multiple genomic alterations such as copy number, DNA methylation, somatic mutations, mRNA expression and microRNA expression. Integrated pathway analysis is expected to increase the precision and sensitivity of causal interpretations for large sets of observations since no single data source is likely to provide a complete picture on its own.

(Spec. ¶ 14; *see also id.* ¶ 19 ("There is currently a need to provide methods that can be used in characterization, diagnosis, prevention, treatment, and determining outcome of diseases and disorders")). Therefore, Appellants disclose and claim "[a] method of generating a dynamic pathway map (DPM)" (*see* App. Br. 24–25; Spec. ¶ 20).

Appellants' disclose, "[i]n one embodiment, . . . a method of generating a dynamic pathway map (DPM), [wherein] the method compris[es]" the following steps (*see* Spec. ¶ 20):

(A) "providing access to a pathway element[4] database storing a plurality of pathway elements, each pathway element being characterized by its involvement in at least one pathway[5]" (*id.*);

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[4] Appellants disclose that a pathway element may be (i) a protein, "selected from the group consisting of a receptor, a hormone binding protein, a kinase, a transcription factor, a methylase, a histone acetylase, and a histone deacetylase" or (ii) nucleic acid, "selected from the group consisting of a protein coding sequence, a genomic regulatory sequence, a regulatory RNA, and a trans-activating sequence" (Spec. ¶ 20).

[5] "In a preferred embodiment, the pathway is within a regulatory pathway network" (Spec. ¶ 20). In this regard, Appellants disclose:

> In a more preferred embodiment, the regulatory pathway network is selected from the group consisting of an ageing pathway network, an apoptosis pathway network, a homeostasis pathway network, a *metabolic pathway network*, a replication pathway network, and an immune response pathway network. In a yet more preferred embodiment, the pathway is within a signaling pathway network. In an alternative yet more preferred embodiment, the pathway is within a network of distinct pathway networks. In a most preferred embodiment, the signaling pathway network is selected from the group consisting of a calcium/calmodulin dependent signaling pathway network, a cytokine mediated signaling pathway network, a chemokine mediated signaling pathway network, a growth factor signaling pathway network, a hormone signaling pathway network, a MAP kinase signaling pathway network, a phosphatase mediated signaling pathway network, a Ras superfamily mediated signaling pathway network, and a transcription factor mediated signaling pathway network.

(*Id.* (emphasis added).)

(B) "providing access to a modification engine coupled to the pathway element database" (*id.*);

(C) "using the modification engine to associate a first pathway element with at least one *a priori* known attribute[6]" (*id.*);

(D) "using the modification engine to associate a second pathway element with at least one assumed attribute[7]" (*id.*);

(E) "using the modification engine to cross-correlate and assign an influence level of the first and second pathway elements for at least one pathway using the known and assumed attributes, respectively, to form a probabilistic pathway model" (*id.*);

(F) "and using the probabilistic pathway model, via an analysis engine, to derive from a plurality of measured attributes[8] for a plurality of elements of a patient sample the DPM having reference pathway activity information[9] for a particular pathway" (*id.*).

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[6] "In a preferred embodiment, the known attribute is selected from the group consisting of a compound attribute, a class attribute, a gene copy number, a transcription level, a translation level, and a protein activity" (Spec. ¶ 20).
[7] "In another preferred embodiment, the assumed attribute is selected from the group consisting of a compound attribute, a class attribute, a gene copy number, a transcription level, a translation level, and a protein activity" (Spec. ¶ 20).
[8] "In another alternative embodiment, the measured attributes are selected from the group consisting of a mutation, a differential genetic sequence object, a gene copy number, a transcription level, a translation level, a protein activity, and a protein interaction" (Spec. ¶ 20).
[9] Appellants disclose that "the reference pathway activity information is specific with respect to a normal tissue, a diseased tissue, an ageing tissue, or a recovering tissue" (Spec. ¶ 20).

Appellants' claim 1 representative and reproduced below:

1. A method of generating a dynamic pathway map (DPM), comprising:

accessing a pathway element database storing a plurality of pathway elements relating to gene expressions, activities or products, the pathway elements comprising proteins;

associating a first pathway element of the pathway element database with at least one a priori known attribute relating to gene expressions, activities or products;

associating a second pathway element of the pathway element database with at least one assumed attribute relating to gene expressions, activities or products;

cross-correlating the first pathway element, the second pathway element and at least one pathway;

assigning an influence level of the first and second pathway elements for the at least one pathway using the known attribute and the assumed attribute, based on the cross-correlating;

converting each pathway of the at least one pathway, and the influence level of the first and second pathway elements for the at least one pathway, to a probabilistic model having each interaction in each pathway represented as an edge in a factor graph of a probabilistic pathway model, with the influence level of the first and second pathway elements comprising one of a negative value or a positive value, the negative value and the positive value correlated to the corresponding edge of the factor graph associated with the at least one pathway; and

deriving the DPM from expectation maximization of the probabilistic pathway model and a plurality of measured attributes for a plurality of elements based on a genome-scale assay of a biological sample, the DPM inferring probabilistic reference pathway activity information for a particular pathway; and

> identifying an altered pathway based on pathway inferences in the DPM, wherein at least one method operation is executed by a processor.

(App. Br. 24–25.)

The claims stand rejected as follows:

Claims 1–5, 7, and 10–13 stand provisionally rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over the claims of copending Application 13/317,769.

Claims 1–5, 7, and 10–13 stand rejected under 35 U.S.C. § 112, second paragraph.

Claims 1–5, 7, and 10–13 stand rejected under 35 U.S.C. § 101.

Obviousness-type Double Patenting:

Appellants do not contest and, thereby, waived appeal of the provisional obviousness-type double patenting rejection on this record (*see generally* Ans. 14; *cf.* Final Act.[10] 8). Therefore, we summarily affirm the provisional rejection of claim 1 under the judicially created doctrine of obviousness-type double patenting as being unpatentable over the claims of copending Application No. 13/317,769.

[10] Office Action mailed April 14, 2016.

Definiteness:[11]

ISSUE

Does the preponderance of evidence support Examiner's conclusion that Appellants' claim 1 is indefinite?

ANALYSIS

Pathway elements relating to gene expressions, activities, or products:

The method of Appellants' claim 1 comprises, *inter alia*,

> accessing a pathway element database storing a plurality of *pathway elements relating to gene expressions, activities or products*, the pathway elements comprising proteins;
>
> associating *a first pathway element* of the pathway element database with at least one a priori known attribute *relating to gene expressions, activities or products*;
>
> associating *a second pathway element* of the pathway element database with at least one assumed attribute *relating to gene expressions, activities or products*;

(App. Br. 24 (emphasis added).)

Examiner finds the terms "activities" and "products," as recited in Appellants' claim 1, unclear. In this regard, Examiner finds "the terms 'activities' and 'products' . . . are not defined in [Appellants'] [S]pecification and clearly encompass multiple plausible interpretations, e.g., gene activities and gene products, *metabolism*, proteins, enzymes, etc." (Final Act. 6 (emphasis added)). In addition, Examiner finds that although

[11] Examiner found the phrase "cross-correlating the first pathway element, the second pathway element, and at least one pathway" indefinite in the recitation of the phrase "one pathway" (Final Act. 7). Appellants provided arguments addressing Examiner's rejection (App. Br. 19–20). Thereafter, Examiner did not repeat or address this indefiniteness issue in the Answer (*see generally* Ans. 10–14). Therefore, we find that Examiner withdrew this ground of rejection.

paragraphs 20 and 83 of Appellants' Specification "provide[] examples of pathway elements (e.g. as proteins and nucleic acids)," Appellants' Specification "does not provide any limiting definitions that would serve to clarify the scope of the claimed 'activities' and 'products'" (Ans. 11).

According to Appellants' Specification a pathway element may be (i) a protein, "selected from the group consisting of a receptor, a hormone binding protein, a kinase, a transcription factor, a methylase, a histone acetylase, and a histone deacetylase" or (ii) nucleic acid, "selected from the group consisting of a protein coding sequence, a genomic regulatory sequence, a regulatory RNA, and a trans-activating sequence" (Spec. ¶ 20). Appellants further disclose that "[m]ultiple genome-scale measurements on a single patient sample are combined to infer the activities of genes, products, and abstract process inputs and outputs for a single national Cancer Institute (NCI) pathway" (*id.* ¶ 83).

Thus, Appellants contend that the phrase "pathway elements relating to gene expressions, activities or products," as recited in Appellants' claim 1, refers to pathway elements relating to gene expressions, gene activities, or gene products and agree with Examiner's finding that the scope of the phrase "'pathway elements relating to gene expressions, activities, or products' in claim 1, . . . includes gene activities and gene products, metabolism, proteins, and enzymes" (*see* App. Br. 19 (citing Spec. ¶¶ 20 and 83); Reply Br. 7 (emphasis added); *cf.* App. Br. 24–25;). Stated differently, in the context of Appellants' claim 1, gene expression, gene activity, or a gene product represent an element of pathway, such as a metabolic pathway (*see* Spec. ¶¶ 20). More than one element of a pathway, as recited in Appellants' claim 1, through the use of the plural "pathway elements"

would, as both Examiner and Appellants agree, read on a pathway, such as metabolism, i.e., a metabolic pathway (*see* Final Act. 6; Reply Br. 7).

Thus, although we agree with Examiner's intimation that the phrase "pathway elements relating to gene expressions, activities or products" is broad, "breadth is not to be equated with indefiniteness." *In re Miller*, 441 F.2d 689, 693 (CCPA 1971).

The influence level of the first and second pathway elements:

> The method of Appellants' claim 1 requires, *inter alia*,
>
> > assigning an *influence level* of the first and second pathway elements for the at least one pathway using the known attribute and the assumed attribute, based on the cross-correlating; [and]
> >
> > converting each pathway of the at least one pathway, and *the influence level* of the first and second pathway elements for the at least one pathway, to a probabilistic model having each interaction in each pathway represented as an edge in a factor graph of a probabilistic pathway model, with *the influence level* of the first and second pathway elements comprising one of a negative value or a positive value, the negative value and the positive value correlated to the corresponding edge of the factor graph associated with the at least one pathway.

(App. Br. 24.)

Examiner finds that "the meaning of the term 'influence level' is unknown as this is a relative term" and Appellants' "[S]pecification does not provide any limiting definitions, specific properties, or scoring criteria indicating the scope of this term, i.e. the result is subjective and imperceptible" (Final Act. 7). In this regard, Examiner finds that Appellants' Brief fails to address this issue (*see* Ans. 11–12; *cf.* App. Br. 19–23). We agree.

Although Appellant appears to address this issue in Appellants' Reply Brief, Appellants failed to "explain what 'good cause' there might be to consider the new argument. On this record, Appellant's new argument is belated." *See Ex parte Borden*, 93 USPQ2d 1473, 1474 (BPAI 2010) (informative); *see also In re Berger*, 279 F.3d 975, 984 (Fed. Cir. 2002).

Accordingly, we are compelled to affirm this ground of rejection.

Converting:

The method of Appellants' claim 1 requires, *inter alia*,

> *converting* each pathway of the at least one pathway, and the influence level of the first and second pathway elements for the at least one pathway, to a probabilistic model having each interaction in each pathway represented as an edge in a factor graph of a probabilistic pathway model, with the influence level of the first and second pathway elements comprising one of a negative value or a positive value, the negative value and the positive value correlated to the corresponding edge of the factor graph associated with the at least one pathway.

(App. Br. 24.)

Examiner finds:

> The meaning of the term "converting" is unknown because after interpreting the claim in view of the specification, one of ordinary skill in the art would not understand the boundary of mathematical or computational operations required to achieve the claimed result. Such generic functional claim language amounts to descriptions of problems to be solved and/or functions, and covers all means or methods of performing the claimed functions.

(Final Act. 7.) Examiner recognizes that Appellants' Specification "generically describe[s] an approach to infer genetic pathways called PARADIGM and the use of variables to 'describe states in a cell'" but

"fail[s] to provide any limiting definitions or clarifying examples of 'converting' pathways to a model that would serve to clarify the scope of the mathematical or computational operations required to achieve the claimed result" (Ans. 12). In this regard, Examiner finds:

> Such generic functional claim language amounts to descriptions of problems to be solved and/or functions, and covers all means or methods of performing the claimed functions, i.e. doing math, drawing (which is a means of converting ideas or information into graphs, etc. Therefore, the examiner maintains that the claim(s) is/are indefinite for failing to point out the requisite computational techniques that are included or excluded by the claim language, such that the artisan would know how to avoid infringement.

(Ans. 12–13.)

Appellants contend that, notwithstanding Examiner's assertion to the contrary, their Specification provides a description of the converting step, such "one skilled in the art would understand the bounds of the claim when read in light of [their] [S]pecification." *See Miles Laboratories Inc. v. Shandon Inc.*, 997 F.2d 870, 875 (Fed. Cir. 1993); *see generally* App. Br. 21 (citing Spec. ¶¶ 83–85, 146–150, and 153–155). More specifically, Appellants contend that their Specification provides, *inter alia*, "a mathematical description of how the entire graph of entities and factors encodes the joint probability distribution over all of the entities," a description of how "[s]tates are encoded in 1, 0 or -1," "the process of converting a pathway into a directed graph," a description of "variables and relationships among the variables," and provides additional "mathematical relations" (App. Br. 21 (citing, *inter alia*, Spec. ¶¶ 149, 150, and 153–155)).

In sum, we find the evidence on this record favors Appellants. Claims are not indefinite simply because they do not describe the invention using numerical values. *See In re Mattison*, 509 F.2d 563, 565 (CCPA 1975). As Appellants make clear, notwithstanding Examiner's assertion to the contrary, their Specification provides the computation techniques that Examiner finds "are included or excluded by [Appellants'] claim language" (App. Br. 21; *cf.* Ans. 12–13). Thus, on this record, Examiner failed to explain why a person of ordinary skill in this art would not have reasonably understood the bounds of Appellants' claimed invention when Appellants' claim 1 is read in light of Appellants' Specification. *See Miles Laboratories Inc.*, 997 F.2d at 875.

Deriving the DPM from a plurality of measured attributes . . . based on a genome-scale assay:

> The method of Appellants' claim 1 requires, *inter alia*,
>
> > deriving the DPM from expectation maximization of the probabilistic pathway model and a plurality of measured attributes for a plurality of elements *based on a genome-scale assay of a biological sample*, the DPM inferring probabilistic reference pathway activity information for a particular pathway.

(App. Br. 24–25.)

Examiner finds the phrase "based on a genome scale assay" indefinite because Appellants' claim does "not require any positive process limitation for performing any genomic assays" (Final Act. 7–8; *see* Ans. 13 ("the claim was rejected for being indefinite because of the phrase '*based on a genome-scale assay*'")). According to Examiner, "[s]uch generic functional claim language amounts to descriptions of problems to be solved and/or functions, and covers all means or methods of performing the claimed functions, i.e.

the claims generically read on 'doing math'" (Final Act. 8; *see* Ans. 13). We are not persuaded.

As Appellants' explain, their "claims are not limited to any specific manner of performing genomic assays in and of themselves" (App. Br. 22). Stated differently, Appellants' claims are open to include obtaining "a plurality of measured attributes for a plurality of elements based on [any] genome-scale assay of a biological sample," available to a person of ordinary skill in this art (*see* App. Br. 24–25). Thus, although Appellants' claims is broadly written, "breadth is not to be equated with indefiniteness." *In re Miller*, 441 F.2d at 693.

CONCLUSION

The preponderance of evidence supports Examiner's conclusion that Appellants' claim 1 is indefinite with respect to "the meaning of the term 'influence level'" (Final Act. 7). The rejection of claim 1 under 35 U.S.C. § 112, second paragraph, is affirmed. Claims 2–5, 7, and 10–13 are not separately argued and fall with claim 1.

Subject Matter Eligibility:

ISSUE

Does the evidence of record support Examiner's finding that Appellants' claimed invention is directed to patent ineligible subject matter?

ANALYSIS

The scope of 35 U.S.C. § 101 "is subject to an implicit exception for 'laws of nature, natural phenomena, and abstract ideas,' which are not patentable." *Intellectual Ventures I LLC v. Capital One Financial Corp.*, 850 F.3d 1332, 1338 (Fed. Cir. 2017), citing *Alice Corp. Pty. Ltd. v. CLS*

Bank Int'l., 134 S. Ct. 2347, 2355 (2014); *see also Mayo Collaborative Services v. Prometheus Labs., Inc.*, 566 U.S. 66, 70 (2012) ("'[L]aws of nature, natural phenomena, and abstract ideas' are not patentable" (citation omitted, alteration original)).

Alice, sets forth the following two-step analysis for determining patent eligibility under Section 101:

> First, we determine whether the claims at issue are directed to one of those patent-ineligible concepts [e.g., a law of nature, natural phenomenon, or abstract idea]. If so, we then ask, what else is there in the claims before us? . . . We have described step two of this analysis as a search for an inventive concept—i.e., an element or combination of elements that is sufficient to ensure that the patent in practice amounts to significantly more than a patent upon the ineligible concept itself.

Alice, 134 S. Ct. at 2355 (alterations, citations, and quotation marks omitted).

With respect to *Alice*'s first step, Examiner finds that, when considered as a whole, Appellants' claimed invention is "directed to gathering data (using routine and conventional techniques and/or instrumentations), and mathematically manipulating the data (using a general purpose computer) to generate additional data" (Final Act. 3; *see* Ans. 2–3 and 9). Thus, Examiner finds that Appellants' claimed invention is directed to an abstract idea, specifically "algorithmic concepts involving the mathematical manipulation of data" (Final Act. 3; *see* Ans. 8). Thus, Appellants' claimed invention comprises, at best, the steps of collecting, manipulating, and displaying data. "[A]n invention directed to collection, manipulation, and display of data [is] an abstract process." *Intellectual Ventures*, 850 F.3d at 1340; *see generally id.* at 1340–41.

> Without additional limitations, a process that employs mathematical algorithms to manipulate existing information to generate additional information is not patent eligible. "If a claim is directed essentially to a method of calculating, using a mathematical formula, even if the solution is for a specific purpose, the claimed method is nonstatutory." *Parker v. Flook*, 437 U.S. 584, 595[] (1978) (internal quotations omitted).

Digitech Image Techs., LLC v. Elecs. For Imaging, Inc., 758 F.3d 1344, 1351 (Fed. Cir. 2014). *See also FairWarning IP, LLC v. Iatric Systems, Inc.*, 839 F.3d 1089, 1093 (Fed. Cir. 2016) ("analyzing information by steps people go through in their minds, or by mathematical algorithms, without more," are "essentially mental processes within the abstract-idea category).

With respect to *Alice*'s second step, the search for an inventive concept, Examiner finds that Appellants' "claims do not include additional elements/steps appended to the abstract idea that are sufficient to amount to significantly more than the judicial exception" (Final Act. 4; *see* Ans. 3–4). In this regard, Examiner finds that the additional elements/steps appended to the abstract idea set forth in Appellants' claimed invention are "routine and conventional techniques for collecting data" (*id.*; *see* Ans. 6 ("high-throughput technologies [] are well-known in the art"); *see also* Ans. 8–9 (citing Spec. ¶¶ 12–13) (Appellants' Specification "provides evidence that pathway databases were routine and conventional in the art")). *See Genetic Techs. Ltd. v. Merial L.L.C.*, 818 F.3d 1369, 1376 (Fed. Cir. 2016) (Appellants "must provide something inventive, beyond mere well-understood, routine, conventional activity") (quotation omitted).

Examiner finds that the "processor" limitation set forth in Appellants' claimed invention "amount[s] to nothing more than a general purpose computer and/or general instructions for applying or using the judicial

exception(s)" (Final Act. 4; *see* Ans. 8). *See Mayo*, 566 U.S. at 84–86 ("simply implementing a mathematical principle on a physical machine, namely a computer, [is] not a patentable application of that principle"); *Alice*, 134 S. Ct. at 2360 ("none of the hardware recited by the [] claims 'offers a meaningful limitation beyond generally linking 'the use of the [method] to a particular technological environment,' that is, implementation via computers" (alteration original)).

In addition, Examiner finds that Appellants' "claims fail to recite any limitations that purport to improve the functioning of a specific claimed device, effect an improvement to the technology or technical field, or provide meaningful limitations beyond generally linking the use of an abstract idea to a particular technological environment" (Final Act. 4; *see* Ans. 6–7). *See Enfish LLC v. Microsoft Corp.*, 822 F.3d 1327, 1335–6 (Fed. Cir. 2016).

Examiner finds that the requirements of Appellants' dependent claims 2–5, 7, and 10–13 "do nothing more than further limit the type of pathway, the type of protein data, and the type of attributes being used in [the] judicial exception, and therefore do not add significantly more to the judicial exception" (Ans. 10).

For the foregoing reasons, we find no error in Examiner's finding that Appellants' claimed invention is directed to patent ineligible subject matter.

For the foregoing reasons, we are not persuaded by Appellants' contention that Examiner failed to "identify[] the alleged abstract idea" (App. Br. 4; *see id.* at 5 and 7–8; *cf.* Final Act. 3–4; Ans. 2–4).

For the foregoing reasons, we are not persuaded by Appellants' contention that "Examiner has not analyzed the additional elements in the

claim, and has not explained why the additional elements in combination, i.e. the claim as a whole, is not significantly more than the exception" (App. Br. 5; *see also id.* at 6–7 and 13–14; *cf.* Final Act. 4; Ans. 4–7 and 8–9).

For the foregoing reasons, we are not persuaded by Appellants' contention that Examiner gave "no weight to the improvement in computing technology evidenced in the claims" (App. Br. 8; *see id.* at 8–11; *cf.* Final Act. 4; Ans. 6–7). Similarly, we are not persuaded by Appellants' contention that Examiner "erred by ignoring the size and complexity of the pathway element database and the plurality of elements based on a genome-scale assay of a biological sample, and the necessity of performing the claimed method on a processor, as recited in the claims" (App. Br. 13–14; *cf.* Final Act. 4; Ans. 8–9). *See Mayo*, 566 U.S. at 84–86 ("simply implementing a mathematical principle on a physical machine, namely a computer, [is] not a patentable application of that principle");

For the foregoing reasons, we are not persuaded by Appellants' contentions that Examiner "erred by ignoring the withdrawal of the rejection of the claims under 35 USC § 103" and Examiner's rejection is counter to legal precedent (App. Br. 11–12 and 15–17; *see generally* Ans. 7–8).

For the reasons set forth by Examiner, we are not persuaded by Appellants' contention that Examiner "erred by rejecting claims 2-5, 7 and 10-13 under 35 USC §101 without analysis of the limitation of claims 2-5, 7 and 10-13" (App. Br. 17–18; *cf.* Ans. 10).

CONCLUSION

The evidence of record supports Examiner's finding that Appellants' claimed invention is directed to patent ineligible subject matter. The rejection of claims 1–5, 7, and 10–13 under 35 U.S.C. § 101 is affirmed.

TIME PERIOD FOR RESPONSE

No time period for taking any subsequent action in connection with this appeal may be extended under 37 C.F.R. § 1.136(a).

AFFIRMED