**Integrated databases:**

* RegulonDB (Escherichia coli K12 MG1655)
* Collectf (Several Bacteria)
* RegPrecise (Several Bacteria)
* DBTBS (Bacillus subtilis + Bacillus subtilis 168)
* Faria JP 2016 (Bacillus subtilis 168)
* Palsson 2017 (Escherichia coli K12 MG1655)
* Turkarslan 2015 (Mycobacterium tuberculosis H37Rv)
* Ortiz 2015 (Bacillus subtilis 168)
* Vásquez 2011 (Pseudomonas aeruginosa PAO1/ UCBPP-PA14/ PAK/ PA103)
* CoryneRegNet (Corynebacterium diphteriae NCTC 13129/ efficiens YS-314/ glutamicum ATCC 13032/ jeikeium K411)

**TRN Universal Graph Structure:**

**Nodes:**

* **Organism** – node representing a certain bacterial organism
* **Regulator** – node representing a certain regulator (there are many different regulatory mechanisms in the database such as Transcription Factors or RNA Riboswitches, but all this data is converged in the same “Regulator” entity)
* **Gene** – node representing a given gene
* **DNA\_Binding\_Site** - node representing the Binding Site at which a given “Regulator” binds to, to regulate a given “Gene”

**Edges:**

* **BELONGS\_TO** – relationship that connects “Regulator” nodes to “Organism” nodes. This a N:N relationship which conveys each regulator’s protein sequence and Uniprot Accession (if available) besides other informations. A given regulator may be found in several organisms, thus the existence of multiple “BELONGS\_TO” edges connecting the regulator to the organisms. An organism is expected to have multiple regulators. However, for a given “Regulator”-“Organism” pair, it is expected to exist only one “BELONGS\_TO” relationship, connecting both entities. Yet, it is possible to exist two “BELONGS\_TO” relationships, if the first time an “Regulator”-“Organism” pair is found, there is no Uniprot data, thus a connection is made without Uniprot Accession and Sequence. Later on, while exploring another external source, if the same “Regulator”-“Organism” pair is found, this time with Uniprot Data, a second connection will be made (with Uniprot Accession and Sequence).

* **BINDS\_TO** – relationship that connects “Regulator” nodes to “DNA\_Binding\_Site” nodes. This is a N:N relationship. A given “Regulator” may have multiple “DNA\_Binding\_Sites” and certain “DNA\_Binding\_Sites” may be shared by multiple “Regulators”. However, for a given “Regulator”-“DNA\_Binding\_Site” pair, there may only be one “BINDS\_TO” connecting both entities.
* **FORMS\_PROTEIN\_COMPLEX** – relationship that connects two “Regulator” nodes which may group together and form a protein complex. This a 1:1 relationship. One “regulator” may form a protein complex with one other “Regulator” (identified protein complexes included two regulators only). Neo4j does not support bidirectional edges thus, “Regulators” with a “FORMS\_PROTEIN\_COMPLEX” relationship have two edges, one for each direction, connecting the pair.
* **FROM\_ORGANISM** – relationship that connects “DNA\_Binding\_Site” nodes to “Organism” nodes. This is a N:1 relationship. One “DNA\_Binding\_Site” is associated with one “Organism” only but different “Organisms” are expected to have multiple “DNA\_Binding\_Sites”. This implies that there may be multiple “DNA\_Binding\_Site” nodes with the same structural data, such as nucleotide sequence, however these nodes are all connected to different organisms, thus being represented as different node entities. For a given “DNA\_Binding\_Site”-“Organism” pair, there may be multiple “FROM\_ORGANISM” edges. This happens when a given “DNA\_Binding\_Site”, associated with the same organism, is found in different external databases. Each “FROM\_ORGANISM” edge, connecting the same pair of “DNA\_Binding\_Site” and “Organism” nodes, provides information regarding the source and date of the interaction’s discovery.
* **GENE\_HAS\_BINDING\_SITE** – relationship that connects “Gene” nodes to “DNA\_Binding\_Site” nodes. This is a N:N relationship. A given “Gene” may have multiple “DNA\_Binding\_Sites” at which it is regulated, and a given “DNA\_Binding\_Site” may be shared by multiple genes (most likely belonging to the same operon). For a given “Gene”-“DNA\_Binding\_Site” pair, there may only be one “GENE\_HAS\_BINDING\_SITE” connecting both entities.
* **GENE\_IN\_ORGANISM** – relationship that connects “Gene” nodes to “Organism” nodes. This is a N:1 relationship. A given “Gene” is associated with a single “Organism” (genes with the same function and name across different organisms are treated as different entities due to different protein sequences and Uniprot Accessions) but an “Organism” is expected to have multiple “Genes”. For a given “Gene”-“Organism” pair, there may only be one “GENE\_IN\_ORGANISM” connecting both entities.
* **REGULATES** – relationship that connects “Regulator” nodes to “Gene” nodes. This is a N:N relationship. A given “Regulator” may regulate multiple “Genes”, and a “Gene” may be regulated by multiple “Regulators”. It is perfectly expected to have multiple “REGULATES” edges connecting a given “Regulator”-“Gene” pair, because, similarly to the “FROM\_ORGANISM” edges, each edge represents a regulation interaction found in a given external source, connecting the same pair of “Regulator” and “Gene” nodes. Even amongst the same external source, it is possible to have multiple “REGULATES” relationships connecting the same “Regulator”-“Gene” pair due to different experimental evidences or different regulatory effects. **Example:** Source Database “A” may have two entries portraying the following regulation interaction:
  + Regulator X –[ACTIVATES]-> Gene Y, with evidences 1,2,3
  + Regulator X –[REPRESSES]-> Gene Y, with evidences 1,4,5

This information will be stored as two different “REGULATES” edges, both connecting the same “Regulator X”-“Gene Y” pair.

**Directionality of Edges:**

Regulator –[:BELONGS\_TO]-> Organism

Regulator –[:BINDS\_TO]-> DNA\_Binding\_Site

Regulator –[:FORMS\_PROTEIN\_COMPLEX]-> Regulator

Regulator <–[:FORMS\_PROTEIN\_COMPLEX]- Regulator

DNA\_Binding\_Site –[:FROM\_ORGANISM]-> Organism

Gene –[:GENE\_HAS\_BINDING\_SITE]-> DNA\_Binding\_Site

Gene –[:GENE\_IN\_ORGANISM]-> Organism

Regulator –[:REGULATES]-> Gene

**Node properties and associated external sources:**

* **Organism**
  + **Name** - organism name as found in NCBI Taxonomy Database
    - Property of all “Organism” nodes
      * Example -> **Burkholderia pseudomallei 1026b**
  + **Taxonomy\_ID** – organism taxonomy identifier as found in NCBI Taxonomy Database
    - Property of all “Organism” nodes
      * Example -> **884204**
  + **Source\_Database** – external source where this organism was first analyzed
    - Property of all “Organism” nodes
      * Example -> **Collectf**
  + **timestamp** – time and date at which the organism was first analyzed
    - Property of all “Organism” nodes
      * Example -> **2019-06-13 19:02:48**
  + **Genome\_Accession** – Genome accession number of the organism in the external source where it was first analyzed
    - Exclusive property to “Organism” nodes created by RegulonDB and Collectf
      * Example -> **NC\_017832.1**
* **Regulator**
  + **Name** – name of the regulator entity as found in the external source
    - Property of all “Regulator” nodes
      * Example -> **beti**
  + **Mechanism­** – regulatory mechanism. The most common mechanisms are “Transcription Factor”, “RNA”, “Sigma Factor” and “Unknown” but other, under-represented mechanisms, are also present in the database
    - Property of all “Regulator” nodes
      * Example -> **Transcription Factor**
  + **Source\_Database** – external source where this regulator was first analyzed
    - Property of all “Regulator” nodes
      * Example -> **RegulonDB**
  + **timestamp** – time and date at which this regulator was first analyzed
    - Property of all “Regulator” nodes
      * Example -> **2019-06-13 19:01:15**
  + **Comment** – short sentence describing regulator’s function
    - Exclusive property to “Regulator” nodes found by Faria JP 2016
      * Example -> **senses the NADH:NAD ratio rather than the concentration of NADH**
  + **Locus\_Tag** – self-explanatory
    - Exclusive property to “Regulator” nodes found by Palsson 2017, RegulonDB, RegPrecise, Faria JP 2016, DBTBS, Collectf and CoryneRegNet
      * Example -> **b2707**
  + **Protein\_Complex** – Boolean flag (true/false) which is true for regulators which are protein complexes (and not a sole entity)
    - Exclusive property to “Regulator” nodes found by RegulonDB and Palsson 2017
      * Example -> **true**
  + **Name1/Name2, Locus\_Tag1/Locus\_Tag2, Uniprot\_Accession1/Uniprot\_Accession2, Sequence1/Sequence2, Sinonyms1/Sinonyms2** – data exclusive to “Regulator” nodes with “Protein\_Complex”=true. Properties with “1” and “2” are associated to the first and second elements of the protein complex, respectively.
    - Exclusive property to “Regulator” nodes found by RegulonDB and Palsson 2017
      * Example -> **b3512/b2217**
  + **RegulonDB\_ID** – RegulonDB’s identifier of “Regulator” node.
    - Exclusive property to “Regulator” nodes created by RegulonDB
      * Example -> **ECK125257204**
  + **Module** – Divides regulators into groups by biological function.
    - Exclusive property to “Regulator” nodes created by CoryneRegNet
      * Example -> **Carbohydrate Metabolism**
* **Gene**
  + **Gene\_Name** – Self-explanatory
    - Property of all “Gene” nodes
      * Example -> **moeA**
  + **Source\_Database** - external source where this gene was first analyzed
    - Property of all “Gene” nodes
      * Example -> **RegPrecise**
  + **timestamp** – time and date at which this gene was first analyzed
    - Property of all “Gene” nodes
      * Example -> **2019-04-13 00:41:23**
  + **Is\_Regulator** – Boolean flag; true if the gene is also a regulator, false if not.
    - Property of all “Gene” nodes (except nodes created by Palsson 2017 that do not have Uniprot data)
      * Example -> **true**
  + **Gene\_Locus\_Tag** – Self-explanatory
    - Exclusive property of “Gene” nodes found in RegulonDB, Collectf, Faria JP 2016, Palsson 2017, Ortiz 2015 and CoryneRegNet
      * Example -> **BSU10300**
  + **Gene\_Uniprot\_Accession** – Gene’s Uniprot Accession number. Two similar genes, with the same function in two different organisms have two different Uniprot Accessions (unless they are equivalent strains)
    - Property of all “Gene” nodes for which we found Uniprot data
      * Example -> **P12281**
  + **Gene\_Sequence** – Gene’s protein sequence retrieved from Uniprot
    - Property of all “Gene” nodes for which we found Uniprot data
      * Example -> **MRSKKLWISLLFALTLIFTMAF…**
  + **Gene\_Sinonyms** – Gene’s multiple alias, as found in Uniprot
    - Property of all “Gene” nodes for which we found Uniprot data
      * Example -> **moeA bisB chlE narE b0827 JW081**
  + **Gene\_Annotation** – Self-explanatory
    - Exclusive property of “Gene” nodes found in Faria JP 2016
      * Example -> **DNA-3-methyladenine glycosylase**
  + **Gene\_Operon** – Gene is a part of this Operon
    - Property of all “Gene” nodes found in DBTBS, Faria JP 2016 and Vásquez 2011
      * Example -> **aprE**
  + **Gene\_Start\_Position** – Starting position of the gene in the genome
    - Exclusive property to “Gene” nodes created by RegulonDB
      * Example -> **3145143**
  + **Gene\_End\_Position** – Ending position of the gene in the genome
    - Exclusive property to “Gene” nodes created by RegulonDB
      * Example -> **3146261**
  + **Start\_Codon** – Self-explanatory
    - Exclusive property to “Gene” nodes created by RegulonDB
      * Example -> **ATG**
  + **Stop\_Codon** – Self-explanatory
    - Exclusive property to “Gene” nodes created by RegulonDB
      * Example -> **TAA**
  + **Product\_Type** – Self-explanatory
    - Exclusive property to “Gene” nodes created by RegulonDB
      * Example -> **small RNA**
  + **Gene\_Strand** – Self-explanatory
    - Exclusive property to “Gene” nodes created by RegulonDB
      * Example -> **forward**
  + **Gene\_RegulonDB\_ID** – RegulonDB’s identifier of the “Gene” node
    - Exclusive property to “Gene” nodes created by RegulonDB
      * Example -> **ECK120000149**
  + **Product\_Name** – Self-explanatory
    - Exclusive property to “Gene” nodes created by RegulonDB
      * Example -> **L-lactate dehydrogenase**
  + **Gene\_Nucleotide\_Sequence** – Gene nucleotide sequence as found in RegulonDB
    - Exclusive property to “Gene” nodes created by RegulonDB
      * Example -> **ATGACTGGAGATAACACCCTCAT…**
  + **Module** – Divides genes into groups by biological function.
    - Exclusive property to “Gene” nodes created by CoryneRegNet
      * Example -> **Carbohydrate Metabolism**
* **DNA\_Binding\_Site**
  + **Sequence** – Nucleotide sequence of the genome, at which the Regulator binds to regulate a given gene/s (binding site sequence)
    - Property of all “DNA\_Binding\_Site” nodes
      * Example -> **TACATACATTCACAAATGTATGTA**
  + **Start** – Starting position of the binding site in the genome
    - Property of all “DNA\_Binding\_Site” nodes except RegPrecise
      * Example -> **485709**
  + **End** – Ending position of the binding site in the genome
    - Property of all “DNA\_Binding\_Site” nodes except RegPrecise
      * Example -> **485732**
  + **Strand** – Strand of the binding site in the genome
    - Property of all “DNA\_Binding\_Site” nodes except RegPrecise
      * Example -> **reverse**
  + **Evidence** – Experimental evidence which provided the binding site data
    - Property of “DNA\_Binding\_Site” nodes found in RegulonDB
      * Example -> **[BCE|W|Binding of cellular extracts]**
  + **timestamp** time and date at which this binding site was first analyzed
    - Property of all “DNA\_Binding\_Site” nodes
      * Example -> **2019-06-13 19:01:15**
  + **Source\_Database** - external source where this binding site was first analyzed
    - Property of all “DNA\_Binding\_Site” nodes
      * Example -> **DBTBS**
  + **Evidence1/Evidence2/Evidence3/Evidence4** – Experimental evidence which provided the binding site data
    - Property of “DNA\_Binding\_Site” nodes found in DBTBS
      * Example -> **DB RG FT**
  + **Evidence\_Confidence\_Level** – Degree of confidence regarding the Evidence. Possible values are “Strong” or “Weak”.
    - Property of “DNA\_Binding\_Site” nodes found in RegulonDB
      * Example -> **Strong**
  + **TFBS\_Center\_Position** – Center position of binding site regarding the Transcription Start Site
    - Property of “DNA\_Binding\_Site” nodes found in RegulonDB
      * Example -> **22.5**
  + **TFBS\_RegulonDB\_ID** – RegulonDB’s identifier of the binding site
    - Property of “DNA\_Binding\_Site” nodes found in RegulonDB
      * Example -> **ECK125258528**
  + **Protein\_Complex** – Boolean flag equivalent to the one for the “Regulator” nodes. True when the binding site is associated with a Protein Complex Regulator
    - Property of “DNA\_Binding\_Site” nodes found in RegulonDB
      * Example -> **true**

**Edge properties and associated external sources:**

* **BELONGS\_TO**
  + **Source\_Database** – External source, where the presence of a given “Regulator” in a given “Organism” was first analyzed.
    - Property of all “BELONGS\_TO” edges
      * Example -> **Turkarslan 2015**
  + **timestamp** – time and date, associated to the first analysis of a given “Regulator” in a given “Organism”
    - Property of all “BELONGS\_TO” edges
      * Example -> **2019-06-13 19:01:15**
  + **Uniprot\_Accession** - Uniprot Accession number of the regulator (origin node) in a given organism (target node)
    - Property of all “BELONGS\_TO” edges for regulators which we found Uniprot data
      * Example -> **P0ACF8**
  + **Sequence** – Protein sequence of the regulator (origin node) in a given organism (target node)
    - Property of all “BELONGS\_TO” edges for regulators which we found Uniprot data
      * Example -> **MDALSRLLMLNAPQGTIDKNCVL…**
  + **Locus\_Tag ­­**– Gene locus tag of the regulator (origin node) in a given organism (target node)
    - Property of “BELONGS\_TO” edges found by Faria JP 2016 or Palsson 2017
      * Example -> **b2163**
  + **Sinonyms** – Collection of possible aliases for a regulator (origin node) in a given organism (target node)
    - Property of “BELONGS\_TO” edges found by Faria JP 2016, Palsson 2017, Turkarslan 2015 or Ortiz 2015
      * Example -> **srlR gutR b2707 JW2676**
  + **Swissprot** – Swissprot identifier of a regulator in a given organism
    - Property of “BELONGS\_TO” edges found by DBTBS
      * Example -> **O34723**
  + **Factor\_Type** – Ontology of a regulator in a given organism
    - Property of “BELONGS\_TO” edges found by DBTBS
      * Example -> **TetR family**
  + **Consensus\_Sequence** – Consensus sequence of a regulator’s (origin node) binding site in a given organism (target node)
    - Property of “BELONGS\_TO” edges found by DBTBS
      * Example -> **TTAT(C/A)CACA**
  + **Subtilist** – Subtilist identifier of the regulator in a given organism (Subtilist is another resource for Bacillus subtilis regulatory data)
    - Property of “BELONGS\_TO” edges found by DBTBS
      * Example -> **BG14133**
  + **Comment** – Further description of the regulator’s biological functions in a given organism
    - Property of “BELONGS\_TO” edges found by DBTBS
      * Example -> **regulation of manganese transport (repression of mntH in high Mn(II) conditions, activation of mntABCD under low Mn(II) conditions)**
  + **Complete\_Name** – Regulator name + locus tag
    - Property of “BELONGS\_TO” edges found by RegPrecise
      * Example -> **ydcr: b1439**
* **BINDS\_TO**
  + No properties. The purpose of this relationship is merely to associate “Regulator” nodes to its respective “DNA\_Binding\_Site” nodes
* **FORMS\_PROTEIN\_COMPLEX**
  + No properties. The purpose of this relationship is merely to connect “Regulator” nodes that may form a protein complex
* **FROM\_ORGANISM**
  + **Source\_Database** – External source where a binding site (origin node) was found in a given organism (target node).
    - Property of all “FROM\_ORGANISM” edges
      * Example -> **Ortiz 2015**
  + **Timestamp** – Time and date, when a binding site (origin node) was found in a given organism (target node) in an external source
    - Property of all “FROM\_ORGANISM” edges
      * Example -> **2019-06-13 19:59:35**
* **GENE\_HAS\_BINDING\_SITE**
  + No properties. The purpose of this relationship is merely to connect “Gene” nodes to its associated “DNA\_Binding\_Site” nodes.
* **GENE\_IN\_ORGANISM**
  + No properties. The purpose of this relationship is merely to connect “Gene” nodes to its associated “Organism” node.
* **REGULATES**
  + **Source\_Database** – External source, where a regulatory interaction was found between a regulator (origin node) and a gene (target node)
    - Property of all “REGULATES” edges
      * Example -> **Palsson 2017**
  + **timestamp** – Time and date, where a regulatory interaction was found between a regulator and a gene
    - Property of all “REGULATES” edges
      * Example -> **2019-06-13 19:44:07**
  + **Regulatory\_Effect** – The effect a regulator has in a given gene. There are four possible values; “Activation” or “Repression” in a scenario where a regulator promotes or inhibits a given gene’s expression, respectively; “Dual” when a regulator both activates and represses a gene, depending on certain stimuli, and “Unknown” when it is inferred that a certain regulator regulates a given gene, but there is no evidence that proves the regulatory effect.
    - Property of all “REGULATES” edges
      * Example -> **Repression**
  + **Condition** -Condition further explaining the regulatory effect
    - Property of “REGULATES” edges found by DBTBS
      * Example -> **Positive at low Mn(II) concentration**
  + **Sigma\_Factor** – Sigma factor involved in the regulatory interaction
    - Property of “REGULATES” edges found by DBTBS and Faria JP 2016
      * Example -> **SigA**
  + **Involved\_Effectors** – Effectors (metabolites or stimuli) involved in the regulatory interaction
    - Property of “REGULATES” edges found by Faria JP 2016
      * Example -> **Galacturonate**
  + **Effector\_Effect** – The effect an effector has on a given regulatory interaction. There are three possible values, “Activation”, “Inactivation” and “Unknown”. This property is strictly related to the “Regulatory\_Effect” property. “Activation” with “Activation” means that the presence of the effector, activates the regulator’s activation of a given gene. “Activation” with “Repression” means that the presence of the effector, activates the regulator’s repression of a given gene. This process can be summarized as follows:
    - Effector activation + Regulator Activation = Gene Activation
    - Effector activation + Regulator Repression = Gene Repression
    - Effector inactivation + Regulator Activation = Gene Repression
    - Effector inactivation + Regulator Repression = Gene Activation
    - Property of “REGULATES” edges found by Faria JP 2016
      * Example -> **Inactivation**
  + **Conditioned\_rules** – Rules for a certain regulatory interaction to occur (simultaneous activity of two different regulators for example)
    - Property of “REGULATES” edges found by Faria JP 2016
      * Example -> **LexA + RecA**
  + **Regulatory\_Mechanism ­**– Additional information regarding the regulatory mechanism between a regulator and a given gene
    - Property of “REGULATES” edges found by Faria JP 2016
      * Example -> **Transcription factor conditioned by a metabolite**
  + **Prior\_Interaction** – Information regarding the external source discovery of the regulatory interaction. “Recovered Prior Activation” and “Recovered Prior Repression” means that a given regulatory interaction was previously discovered in other studies. “Novel Interaction” means that the associated regulatory interaction was found in the study corresponding to its external “Source\_Database”
    - Property of “REGULATES” edges found by Ortiz 2015
      * Example -> **Novel Interaction**
  + **Beta\_Score**  - Beta score metric representing the variation in gene expression. Positive values stand for gene activations, negative values on the other hand, stand for gene repressions.
    - Property of “REGULATES” edges found by Ortiz 2015
      * Example -> **-0.975**
  + **Var\_Exp\_Rank\_Mean** – Metric used to evaluate a given regulatory interaction
    - Property of “REGULATES” edges found by Ortiz 2015
      * Example -> **138.34**
  + **Evidence** – Experimental (or in silico) evidence for a given regulatory interaction
    - Property of “REGULATES” edges found by RegulonDB, Palsson 2017, Vásquez 2011 and CoryneRegNet
      * Example -> **[GEA, HIBSCS]**
  + **Evidence\_Confidence** – Confidence level of the evidence. May vary between “Weak”, “Strong” or “Inferred”
    - Property of “REGULATES” edges found by RegulonDB and Palsson 2017
      * Example -> **Strong**
  + **Regulator\_Biological\_Process** – Biological function of the Regulator associated with a given regulatory interaction
    - Property of “REGULATES” edges found by RegPrecise
      * Example -> **Arginine biosynthesis; Arginine degradation**
  + **Regulator\_Effector** – Effector related to a regulator’s activity associated with a given regulatory interaction
    - Property of “REGULATES” edges found by RegPrecise
      * Example -> **Arabinose**
  + **Expression\_log2**  - Log2 value of differential gene expression in a given regulatory interaction after induction of the regulator
    - Property of “REGULATES” edges found by Turkarslan 2015
      * Example -> **-1.63**
  + **Distance\_to\_nearest\_Start** – Distance of the chip center to the nearest gene’s transcription start site
    - Property of “REGULATES” edges found by Turkarslan 2015
      * Example -> -**40**
  + **Strand ­**– Strand where the regulated gene was identified
    - Property of “REGULATES” edges found by Turkarslan 2015
      * Example -> **reverse**
  + **Chip\_Center** – Center position (nucleotide) of the chip
    - Property of “REGULATES” edges found by Turkarslan 2015
      * Example -> **1561401**
  + **Relative\_Regulatory\_Effect** – Relative regulatory effect based on the percentile distribution of gene expression values. Possible values are; “Strong Activation”, “Activation” and “Weak Activation”, in addition to “Strong Repression”, “Repression” and “Weak Repression”.
    - Property of “REGULATES” edges found by Turkarslan 2015
      * Example -> **Strong Activation**
  + **Expression\_pvalue** – pValue associated with the variation of gene expression in a regulatory interaction
    - Property of “REGULATES” edges found by Turkarslan 2015
      * Example -> **1.05495e-14**
  + **Genomic\_Position** – Nucleotide position of the nearest gene’s transcription start site in the genome
    - Property of “REGULATES” edges found by Turkarslan 2015
      * Example -> **339322**
  + **PubMed\_Reference** – PubMed identifier of the study detailing the regulatory interaction
    - Property of “REGULATES” edges found by Vásquez 2011 and CoryneRegNet
      * Example -> **19930444**