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A Review of Soft Computing Advance in Genetics & Laser Biomedical Instrumentation

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ABSTRACT
Soft computing refers to a collection of computational techniques in computer science, artificial intelligence, machine learning, medical instrumentation which attempt to study, model and analyze very complex phenomena. The principal constituents of Soft Computing (SC) are Neural Networks, Fuzzy Systems, Evolutionary Computation, Machine Learning and Probabilistic Reasoning. The paper studies the biological background of cells, nucleic acids and terminologies in genetic algorithms and also uric acid metabolism with chemical tests and finally laser lithotripsy procedure.

Keywords:
DNA, RNA, SC, Laser, Genes, Chromosomes, Lithotripsy

I. INTRODUCTION:
Soft computing is a term applied to a field within computer science which is characterized by the use of inexact solutions to computationally hard tasks such as the solution of NP complete problems for which there is no known algorithm that can compute an exact solution in polynomial time and is tolerant of imprecision, uncertainty, partial truth and approximation and role model for soft computing is the human mind.

The evolutionary computing algorithms can be considered global optimization methods with a met heuristic or stochastic optimization character and are mostly applied for black box problems and uses iterative progress such as growth or development in a population and is selected in guided random search using parallel processing to achieve the desired end and processes are often inspired by biological mechanisms of evolution which produces highly optimized processes and networks it has many applications in computer science.

1.1 Extents
The soft computing approach provides problem solving techniques in genetics, biochemistry, genetic algorithms and neural networks. The nucleic acids studies DNA and RNA and genetic algorithms analyzes various algorithmic approaches in computer science. The uric acid metabolism and its chemical examination in kidney stone expanded for complex procedures. The laser lithotripsy is a surgical removal of kidney stones and powerful medical equipments are available.

1.2 Biological Environment
The science that deals with the mechanisms responsible for similarities and differences in a species is called genetics.

1.3 Terminologies Cell
Every animal / human cell is a complex of many small factories that work together. The center of all this is the cell nucleus. The genetic information is contained in the cell nucleus.

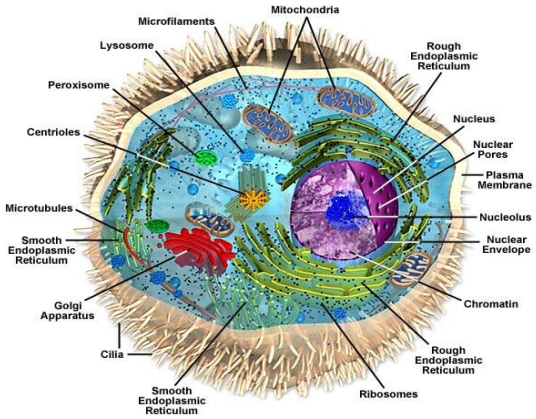


Fig.1 Terminologies Cell

II. CHROMOSOMES

All the genetic information gets stored in the chromosomes. Each chromosome is build of deoxyribonucleic acid (DNA). In humans the chromosomes exist in 23 pairs.

The chromosomes are divided into several parts called genes. Genes code the properties of species, i.e. the characteristics of an individual. The possibilities of combination of the genes for one property are called alleles and a gene can take different alleles. The size of the gene pool helps in determining the diversity of the individuals in the population and the set of all genes of a specific species is called genome. Each and every gene has a unique position on the genome called locus. The most living organisms store their genome on several chromosomes but in the GA all the genes are usually stored on the same chromosomes. Thus chromosomes and genomes are synonyms with one other in GA.

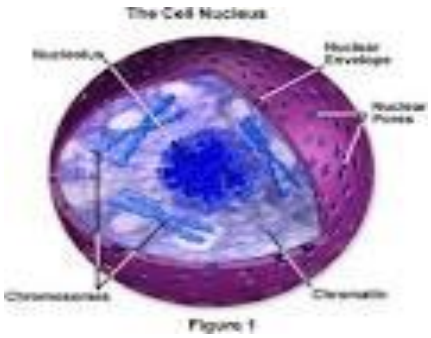


Fig .2 Chromosome

III. GENETICS

For a particular individual the entire combination of genes is called genotype. The phenotype describes the physical aspect of decoding a genotype to produce the phenotype also selection is always done on the phenotype whereas the reproduction recombines genotype.

Thus morphogenesis plays a key role between selection and reproduction. In higher life forms chromosomes contain two sets of genes. These are known as diploids. In the case of conflicts between two values of the same pair of genes the dominant one will determine the phenotype whereas the other one called recessive will still be present and can be passed on to the offspring.

Diploid allows a wider diversity of alleles. This provides a useful memory mechanism in changing or noisy environment. The most GA concentrates on haploid chromosomes because they are much simple to construct. In haploid representation only one set of each gene is stored thus the process of determining which allele should be dominant and which one should be recessive is avoided.

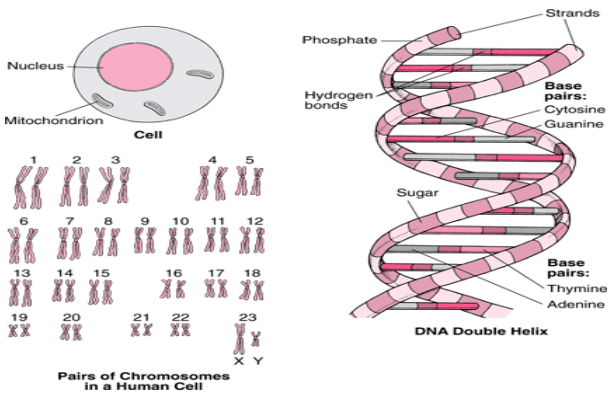


Fig.3 genes

3.1 REPRODUCTION

Reproduction of species via genetic information is carried out by the following

3.2 MITOSIS

In Mitosis the same genetic information is copied to new offspring. There is no exchange of information. This is a normal way of growing of multi cell structures such as organs.

3.3 MEIOSIS

Meiosis forms the basis of sexual reproduction. When meiotic division takes place two gametes appear in the process. Ehen reproduction occur these two gametes conjugate to a zygote which becomes the new individual. Thus in this case the genetic information is shared between the parents in order to create new offspring.

NATURAL EVOLUTION	GENETIC ALGORITHM
Chromosome	String
Gene	Feature or character
Allele	Feature value
Locus	String position
Genotype	Structure or Coded String
Phenotype	Parameter Set & Decoded Structure

3.4 NATURAL SELECTION

The origin of species is based on Preservation of favorable variations and rejection of unfavorable variations. The variation refers to the differences shown by the individual of a species and also by offspring's of the same parents. There are more individuals born than can survive so there is a continuous struggle for the individuals with an advantage have a greater chance of survival i.e. the survival of the fittest.

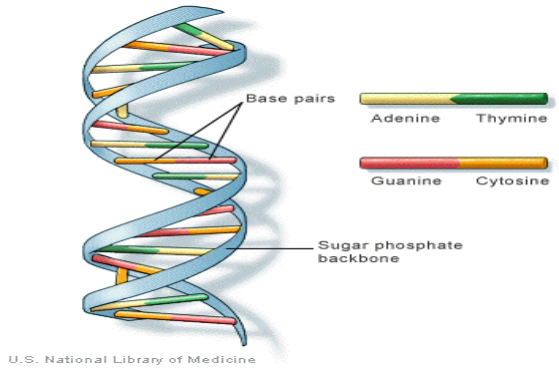


Fig. 4 Nature Selection

IV. NUCLEIC ACID

Nucleic acids fall into two principal classes according to the nature of the sugar they contain the deoxyribonucleic acids (DNA) and the ribose containing nucleic acids (RNA). DNA is found primarily in cell nuclei and certain viruses but it also occurs in other portions of cells such as mitochondria. It is associated with the storage and expression of genetic information and the primary processes of heredity.

The major types of nucleic acid are

1. Nuclear Deoxyribonucleic Acids
2. Messenger Ribonucleic Acids
3. Transfer or Soluble Ribonucleic Acids
4. Ribosomal Ribonucleic Acids
5. Vital Nucleic Acids
6.

4.1 DNA (DEOXYRIBONUCLEIC ACIDS)

DNA (a double stranded molecule) is present in the nucleus of eukaryotic organisms and it is also found in the mitochondria and chloroplasts. DNA is the chemical basis of heredity and may be regarded as the reserve source of genetic information.

DNA is exclusively responsible for maintaining the identity of different species of organisms. Every aspect of cellular function is under the control of DNA. Gene is a unit of heredity and it does not have

independent existence but it is a stretch of DNA.

4.2 Nucleotides

Nucleotides are composed of a nitrogenous base, a pentose sugar and a phosphate.

4.3 Nucleosides

Nucleosides are composed of a nitrogenous base and a pentose sugar.

4.4 Nitrogenous Bases

Nitrogenous bases are mainly Purines and Pyrimidines found in nucleic acid.

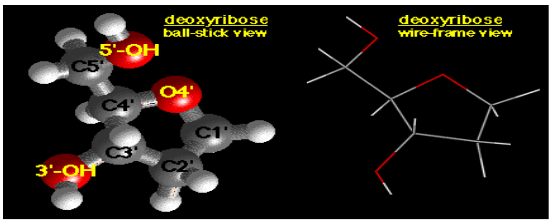
Purines are Adenine (A) and Guanine (G)

Pyrimidines are Cytosine (C), Thymine (T) and Uracil (U)

The two sugars are D - Ribose and 2 – Deoxy – D – Ribose

V. DEOXYRIBOSE SUGAR:

The deoxyribose sugar of the DNA backbone has 5 carbons and 3 oxygen. The carbon atoms are numbered 1', 2', 3', 4' and 5' to distinguish from the numbering of the atoms of the purines and pyrimidines rings.



The hydroxyl groups on the 5'- and 3'- carbons link to the phosphate groups to form the DNA backbone. Deoxyribose lacks hydroxyl group at the 2'-position when compared to ribose and sugar component of RNA

5.1 PURINES

Purine is a heterocyclic aromatic organic compound. It consists of a pyrimidine ring fused to an imidazole ring. Purines including substituted purines and their tautomers are the most widely occurring nitrogen containing heterocycle in nature.

Purines and Pyrimidines make up the two groups of nitrogenous bases including the two groups of nucleotide bases. Two of the four de-oxyribonucleotides and two of the four ribo nucleotides, the respective building blocks of DNA and RNA are pureness.

There are many naturally occurring purines and two of the four bases in nucleic acids are Adenine and Guanine which are purines. In DNA these bases form hydrogen bonds with their complementary pyrimidines like thymine and cytosine. This is called complementary base pairing. In RNA the complement of adenine is uracil instead of thymine. The other notable purines are Hypoxanthine, Xathine, Theobromine, Caffeine, Uric acid and Isoguanine

5.2 ADENINE

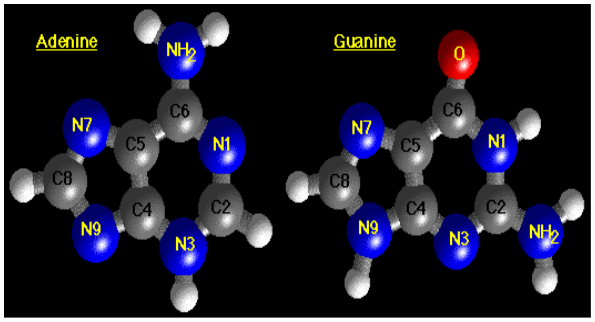
Adenine is a nucleobase (a purine derivative) with a variety of roles in biochemistry including cellular respiration in the form of both the energy rich adenosine triphosphate (ATP) and the cofactors nicotinamide adenine dinucleotide (NAD) and flavin adenine dinucleotide (FAD) and protein synthesis as a chemical component of DNA and RNA. Adenine is one of the two purine nucleobases (guanine) used in forming nucleotides of the nucleic acids. In DNA adenine binds to thymine via two hydrogen bonds to assist in stabilizing the nucleic acid structures and RNA which is used for protein synthesis and also binds to uracil Adenine formed adenosine, a nucleoside when attached to ribose and deoxyadenosine when attached to deoxyribose. It forms adenosine triphosphate (ATP), nucleotide when three phosphate groups are added to adenosine. Adenosine triphosphate is used in cellular metabolism as one of the basic methods of transferring chemical energy between chemical reactions.

The shape of adenine is complementary to either thymine in DNA or uracil in RNA.

5.3 GUANINE

Guanine is one of the four main nucleobase found in the nucleic acids DNA and RNA also the others being adenine, cytosine and

thymine (uracil in RNA). In DNA guanine is paired with cytosine. With the formula $C_5H_5N_5O$, guanine is a derivative of purine consisting of a fused pyrimidine imidazole ring system with conjugated double bonds. Being unsaturated the bicyclic molecule is planar. The guanine nucleoside is called guanosine.



The 9 atoms that make up the fused rings (5 carbons, 4 nitrogen) are numbered 1-9. All rings Atoms lie in the same plane.

5.4 PYRIMIDINE

Pyrimidine is an aromatic heterocyclic organic compound similar to pyridine. One of the three diazines (6 membered heterocyclics with two nitrogen atoms in the ring) as it has the nitrogen at positions 1 and 3 in the ring. The other diazines are pyrazine (nitrogens 1 and 4) and pyridazine (nitrogens 1 and 2).

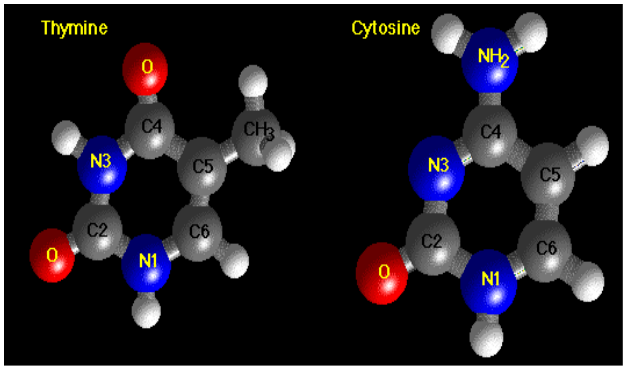
5.5 CYTOSINE

Cytosine is one of the four main bases found in DNA and RNA along with adenine, guanine and thymine (uracil in RNA). It is a pyrimidine derivative with a heterocyclic aromatic ring and two substituent attached (an amine group at position 4 and a keto group at position 2). The nucleoside of cytosine is cytidine.

5.6 THYMINE

Thymine is one of the four nucleobase in the nucleic acid of DNA that are represented by the letters G–C–A–T. The others are adenine, guanine and cytosine. Thymine is also known as 5-methyluracil a pyrimidine nucleobase.

The thymine may be derived by methylation of uracil at the 5th carbon. In RNA thymine is replaced with uracil in most cases. In DNA thymine (T) binds to adenine (A) via two hydrogen bonds thus stabilizing the nucleic acid structures



Cytosine and thymine are pyrimidines. The 6 atoms (4 carbons, 2 nitrogen) are numbered 1-6. Like purines all pyrimidines ring atoms lie in the same plane.

5.7 FORMATION OF NUCLEOSID

The pentoses are bound to nitrogenous bases by Beta – N - glycosidic bounds. The N9 of a purine ring binds with C1 of a pentose sugar to form a covalent bold in purine nucleoside.

VI. FORMATION OF A NUCLEOTIDE

The hydroxyl group of the pentose of a nucleotide is esterified with phosphate to form 5’ monophosphate

6.1 STRUCTURE OF DNA

DNA is a polymer made up of deoxynucleotides and is composed of monomeric units. The monomeric deoxynucleotides in DNA are held together by 3’, 5’ – phosphodiester bridges. The DNA is a right handed double helix. It consists of two anti parallel right handed double helix in which one strand runs in 5’ to 3’ direction while the other in 3’ to 5’ direction.

The two strands are held together by hydrogen bonds formed by complementary base pairs. The A-T pair has 2 hydrogen

bonds while G-C pair has 3 hydrogen bonds. In all the species the DNA has equal numbers of adenine and thymine residues (A=T) and equal numbers of guanine and cytosine residues (G = C). DNA double helix is the most predominant form under physiological conditions and known as B – form.

In a human cell there are 46 chromosomes (23 pairs) which contain about 100,000 genes. A Total length of DNA per cell of 1 – 2 meters is packed in to a nucleus millions of times smaller in diameter. An adult human body has about 10^{14} cells. Thus the total length of DNA in the human body is about 2×10^{10} km i.e. 20 billion km.

6.2 BASIC TERMINOLOGIES IN GENETIC ALGORITHM

The two distinct elements in the GA are individuals and populations. An individual is a single solution while the population is the set of individuals currently involved in the search process.

6.3 INDIVIDUALS

An individual is a single solution and groups together two forms of solutions. The chromosome is raw generic information (genotype) that GA deals and phenotype which is the expressive of the chromosome in the terms of the model. A chromosome is sub divided into genes. A gene is the GA's representation of a single factor for a control factor. Each factor in the solution set corresponds to a gene in the chromosome.

A chromosome should in some way contain information about the solution that it represents. The morphogenesis function associates each genotype with its phenotype. It simply means that each chromosome must define one unique solution but it does not mean that each solution is encoded by exactly one chromosome.

The morphogenesis function should at least be subjective. The candidate solutions of the problem must correspond to at least one possible chromosome to be sure that the whole search space can be explored. Thus when the morphogenesis function that associates each chromosome to one solution is not injective i.e. different chromosomes can encode the same solution the representation is said to be degenerated.

A slight degeneracy is not so worrying even if the space where the algorithm is looking for the optional solution is inevitably enlarged. But a too important degeneracy could be a more serious problem. It can badly affect the behavior of the GA mostly because if several chromosomes can represent the same phenotype the meaning of each gene will obviously not correspond to a specific characteristic of the solution. It may add some kind of confusion in the search.

6.4 GENES

Genes are the basic instructions for building a GA. A chromosome is a sequence of genes. Genes may describe a possible solution to a problem without actually being the solution. A gene is a bit string of arbitrary lengths.

The bit string is a binary representation of number of intervals from a lower bound. A gene is the GA's representation of a single factor value for a control factor where control factor must have an upper bound and a lower bound. This range can be divided into the number of intervals that can be expressed by the gene's bit string. A bit string of length n can represent (2 – 1) intervals. The size of the interval would be (range) / (2 – 1).

The structure of each gene is defined in a record of phenotype parameters. The phenotype parameters are instructions for mapping between genotype and phenotype. It can also be said as encoding a solution set in to a chromosome and decoding a chromosome to a solution set.

The mapping between genotype and phenotype is necessary to convert solution sets from the model into a form that the GA

can work with and for converting new individuals from the GA in to a form that the model can evaluate.

6.5 FITNESS

The fitness of an individual in a GA is the value of an objective function for its phenotype. For calculating fitness the chromosome has to be first decoded and the objective function has to be evaluated. The fitness not only indicates how good the solution is but also corresponds to how close the chromosome is to the optimal one.

In the case of multi criterion optimization the fitness function is definitely more difficult to determine to multi criterion optimization problems there is often a dilemma as how to determine if one solution is better than another.

6.6 URIC ACID

Dietary nucleic acids are digested in the small intestine as follows. The enzyme polynucleotidase acts on nucleic acids to form nucleotides Nucleotides act on nucleotides to form nucleosides and phosphates Nucleosidase splits nucleosides in to purine or pyrimidines base and ribose or 2 – Deoxy – D -Ribose molecules After absorption it is the small intestine where purine and pyrimidines reach liver through portal circulation. In liver both exogenous and endogenous purines are degraded to the excretory end product uric acid.

6.7 URIC ACID METABOLISM

Uric acid is the end product of purine metabolism. The two purines found in RNA & DNA are adenine and guanine. The first step in the catabolism of purines is their hydrolytic deamination to form xanthine and hypoxanthine. These are then oxidized to uric acid. The chemical reactions involved in the formation of uric acid are

Adenosine in presence of Adenosine deaminase gives inosine in presence of nucleoside phosphorylase gives hypoxanthine gives xanthine and in presence of xanthine oxidase produces uric acid. The guinosine in presence of nucleoside phosphorylase gives guanine in presence of guanase gives xanthine and in presence of xanthine oxidase produces uric acid.

Uric Acid is filtered in the glomeruli and partially reabsorbed by the tubules and then it is excreted in urine. The quantity excreted in urine depends to a large extent on the purine content of the diet and normally the excretion rate is 0.5 – 2.0 g / 24 hrs. The normal plasma uric acid level is 2.0 – 7.0 mg / dl.

The uric acid concentration in erythrocytes is lower than in plasma so that the normal range in whole blood is 1.4 mg / dl. The plasma uric acid level is little affected by variation in the purine content of the diet and maintains a steady state between endogenous synthesis and urinary excretion.

A raised plasma uric acid may be found in the following conditions like Hyperuricemia, Gout,Primary Gout and Secondary Gout

6.8 CHEMICAL EXAMINATION OF URIC ACID IN KIDNEY STONE MUREXIDE TEST

One milligram or more of the powder is treated with 2 or 3 drops of concentrated nitric acid in a

Porcelain dish. The mixture is carefully evaporated to dryness and heating continued until the colour change is complete. If the test is carried out on the water bath uric acid gives first a lemon yellow colour and if heating is continued for few minutes longer the colour changes to orange and finally to scarlet. Now on adding of a drop of ammonia the uric acid oxidation product assumes a brilliant purple colour.

6.9 PHOSPHOTUNGSTIC ACID TEST

A pinch of powder is treated with 1 drop of 20 g/dl sodium carbonate and added 2 drops of phosphotungstic acid reagent. A deep blue colouration is produced.

VII. LASER LITHOTRIPSY

The urinary system removes a type of waste called urea from our blood. This urea is produced when foods containing protein such as meat, poultry and certain vegetables are broken down in the body. Urea is carried in the bloodstream to the kidneys.

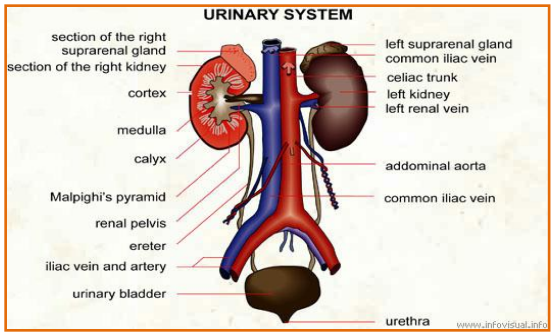
The main function of the kidneys is to filter out impurities and add them to the urine. These impurities usually dissolve in the urine and are flushed out naturally.

The urine then trickles down the ureter into the bladder as shown in figure. The undissolved waste materials remain in the kidneys and form small crystals. These crystals stick together creating kidney stones. This condition is termed renal stone disease. The size of a kidney stone may vary from a few mm to several cm. Many stones pass naturally through urination however some stones due to their size remain in either the kidney or the ureter. Stones that remain in the ureter are termed ureteral stones.

If a patient shows symptoms of a urinary stone the physician will diagnose the problem using either x ray or ultrasound imaging. To know the precise size and location of the stones the doctor may use a cystoscope to see the inside of the bladder and urethra. Lithotripsy is a technique for breaking up these stones. There are several ways of performing lithotripsy depending upon the size and location of the stone as well as patient's history. The most common treatment for urinary stones is extracorporeal shock wave lithotripsy (ESWL). Extracorporeal means outside the body. High energy shock waves also called sound waves pass through the body to the area on the kidney stones.

The waves break the stones into tiny pieces. It is easier for smaller pieces to pass out of the body during urination. This type of lithotripsy must not be performed during pregnancy. Moreover not all stones can be treated using this method and alternative to ESWL is laser lithotripsy. This treatment too breaks down kidney stones without making any incisions.

Laser lithotripsy is generally performed under general anaesthesia and is considered minimally invasive. A urologist inserts a cystoscope into the patient's urethra either



directly or over a guide wire and proceeds visually up the urinary tract to locate the target kidney or bladder stone. To monitor the procedure an endoscope is used which has a camera on the end of a long flexible tube.

The endoscope is inserted into the body through the urinary tract and advanced to the location of the stone. Once the stone is located a thin fibre optic is introduced into the working channel of the endoscope which acts as a light guide and advanced until it comes in contact with the stone.

Light from a holmium laser is directed through the fibre optic and the stone disintegrates or fragments. The Holmium laser fibre can be placed in contact with the stone or adjacent to it. Short Holmium laser pulses create a shockwave that causes fragmentation of the stone. Smaller stones can be fragmented directly whereas with larger ones holes are punched in the centre after which the edges are chiselled away with the Holmium laser. The Holmium laser has a wavelength of 2100 nm which is in the infrared spectrum. This wavelength is ideal for treating stones.

The Holmium laser energy is absorbed by the stone creating cracks within the stone. This laser energy is sufficient to break even the hardest stone. The high absorption of the holmium laser light by the kidney stones leads to the fragmentation of the stone regardless of its chemical composition. The smaller fragments can be removed with a basket tool or left or flush out with normal urinary function.

Conclusion:

The soft computing approach solves various biological aspects of computing and evolutionary computation uses iterative progress such as growth or development in a population. The DNA is unique for each individual. The qualitative chemical test for uric acid is normally done for kidney stone disease and laser lithotripsy is the procedure for surgical removal of kidney stones in medical instrumentation.

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