found that KBD in the Zamtang County has a less obvious relationship both with trace elements and organic stuff respectively. Through the analysis of hydrogeochemical factors affecting KBD, the obviously negative correlation between KBD and constant index represented by TDS is obtained. Therefore, low TDS plays an essential role in KBD, but the trace elements and organic stuff has on unremarkable influence on KBD. (3) A hydrogeochemical influence model of KBD in Zamtang County is designed, taking mineralization and logarithm of constant ions as independent variables, and disease index as dependent variables. Simulation effect of the influence model is good. The influence model of Zequ River is y=149.687-23.852lnx, and the model of Duke River is y=104.478-16.592lnx (y stands for disease index; x stands for TDS); on the contrary, simulating effects of county structure is unsatisfying, indicating TDS is the main but not only factor of KBD, other geological environment factors or life-style can also have some impacts on KBD.

**B018**

**LATEX IMMUNOAGGLUTINATION ASSAY FOR RHEUMATOID FACTOR IN A MICROFLUIDIC DEVICE BASED ON LIGHT SCATTERING DETECTION**

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**Background:** Rheumatoid factor is often evaluated in patients suspected of having any form of arthritis. Therefore, a sensitive and selective method for an accurate assay is essential.

**Methods:** An immunoassay performed on a portable microfluidic device based on light scattering detection was evaluated for the determination of rheumatoid factor. The microfluidic device consisted of injector, micromixer, reaction chamber, and detection chamber. The average size parameter of immunoagglutinated particles was obtained from microscope images, and the parameters of detection point and wavelength were optimized by regression analysis to build an light scattering detection mathematical model.

**Results:** A series of microscope images were taken for the immunoagglutinated particles to evaluate the average particle agglutinate size. It is found that the average particle agglutinate size is about 550nm. We used rheumatoid factor positive serum with different titers to react with sensitized latex reagent. From the absorption spectrum, we found that the curve of the absorption spectrum correspondingly uplifts with the increase of titer, when the wavelength of light is smaller than the average particle agglutinate size. So we filter the characteristic absorption wavelength within the range of 250nm to 450nm. After regression analysis, we found that the parameters of detection point and wavelength are 60° and 380 nm respectively. The experimental results are in conformance with the results calculated by mathematical model in the titers range of 5 to 60 IU/mL, and the correlation coefficient between them is up to 0.996.

**Conclusion:** An effective on-chip immunoassay with an light scattering detection mathematical model for the determination of rheumatoid factor was proposed in this article. The high correlation coefficient between experimental results and results calculated by mathematical model in the titers range of 5 to 60 IU/mL shows this method is suitable for low levels of rheumatoid factor high precision detection.

**B019**

**CORRELATION BETWEEN MONOUNCLEOTIDE POLYMORPHISMS IN THE TOLL-LIKE RECEPTOR 9 GENE PROMOTER AND ALLERGIC ASTHMA IN CHILDREN**

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**Background:** Toll-like receptors (TLRs) are a key set of sensors of the immune system that recognize the presence of bacterial and viral infections. Toll-like receptor 9 (TLR9) binds bacterial DNA and prepares the immune system for a counter attack, thereby inducing an anti-microbial immune reaction of the “normal” T helper type 1. Type 2 responses that lead to asthma and allergies are in turn suppressed. The aim of this study was to investigate the distribution characteristics of single nucleotide polymorphisms (SNPs) in the promoter region of TLR9 in asthmatic children and analyze their associations with asthma susceptibility and phenotypes.

**Methods:** Single nucleotide polymorphisms (SNPs) of TLR9 -1486 C/T (rs1797804) and -1237 C/T (rs751338) were genotyped by direct DNA sequencing of the PCR products in 183 asthmatic children (asthma group) and 191 healthy children (control group). Serum levels of IFN-γ, IL-12 and IL-4 were detected by ELISA method, and serum levels of total IgE (TgE) were detected by chemiluminescence.

**Results:** The genotype frequencies of TT, TC, CC at -1486 C/T were 39.9%, 48.1%, and 12.0% in the asthma group and 40.3%, 51.8%, and 7.9% in the control group. There was no statistical significance between the two groups (P > 0.05). The -1237 C/T polymorphism was not detected in either the asthma or the control group. There were significant differences in serum IFN-γ and IL-4 levels among the three -1486 C/T genotypes in asthmatic children (P < 0.05). The CC genotype had the lowest serum IFN-γ and the highest IL-4 level. There were significant differences in serum IFN-γ and IL-4 levels among the three -1486 C/T genotypes in asthmatic children (P < 0.05). There were no significant differences in serum IL-12 and TgE levels among the three -1486 C/T genotypes in the control group (P > 0.05).

**Conclusion:** The -1237C/T polymorphism of the TLR9 gene was not detected in children in this study. The -1486C/T polymorphism was associated with serum IFN-γ and IL-4 in asthmatic children. However, there were no correlations between the -1486C/T polymorphism and serum IL-12, TgE levels, or asthmatic susceptibility.

**B020**

**A LIFECYCLE MODEL FOR SIMULATING BACTERIAL COLONY EVOLUTION**

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**Background:** Bacteria have developed many intricate capabilities (e.g. chemotaxis, quorum-sensing, elimination and dispersal) to cooperatively self-organize into highly structured colonies with elevated environmental adaptability. Escherichia coli, or E. coli bacterium is probably the best-understood microorganism, and well studied in various aspects of microbiology science. Pattern formation in populations of E. coli has been studied since the 1960s, mostly by differential equations.

**Methods:** In this work we propose a model for simulating the lifecycle of an E. coli colony. That is, the proposed bacterial lifecycle model (BLM) can simulate bacterial evolution from a finite population of E. coli bacteria. The potential of this method is in relating the microscopic behaviors of single bacterial cell to the macroscopic effects of bacterial colonies. This can be accomplished via use of an individual-based modeling method under the framework of agent-environment rule (AER).

**Results:** The simulation results through a environment with varying food source demonstrates that our model can be used to study under which circumstances a certain collective bacterial pattern emerges, and also gives an inspiration to design a new biological optimization model being used for optimization problems.

**Conclusion:** In the proposed BLM model, each E. coli agent could split, die, or migrate dynamically in the foraging processes, and population size varies as the bacterial colony evolves. Quorum-sensing based communication is also introduced so that the bacteria will tumble towards better directions in the chemotactic steps. In the future work, our study will focuses on investigating the colony dynamics at different developmental stages in E. coli lifecycle and developing a efficient biologically inspired methodology for static or dynamic optimization systems.

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**B021**

**TRI-TIER MODEL OF IMMUNE SYSTEM AGAINST INFECTIOUS HEPATITIS B DISEASE**

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