Dean&Francis
ISSN 2959-409X

Should CRISPR-Cas9 Be Used in Human Embryos to Eliminate Genetic Diseases? Public Attitudes and Benefit–Risk Analysis

Chengtai Li

Abstract:

CRISPR-Cas9 is one of the most extraordinary biotechnologies of the twenty-first century, and its possible application to editing human embryos to cure hereditary diseases still brings up some ethical, social, and technical questions. The current research examines the survey-based public perceptions and probabilistic benefits and risks trades-offs using a mixture of the primary survey data and mathematical model. A questionnaire that was structured and given to 320 participants; mostly students aged 16 and above, was used to measure demographic variables, risk perception, and trust in science and support of CRISPR in the event of severe disease, mild disease, and enhancement. It was found that there was high ranking of acceptance with the strongest support going to the severe cases of therapeutic application, moderate to mild disease cases having moderate and slight support respectively and enhancement hardly receiving support. The results of statistical testing proved the significant difference between severe disease and enhancement support. Contrary to the expectations, risk perception was not a significant predictor of support and such a result suggests that the aspect of humanitarian may override the aspect of technical in the sampled population. Probabilistic modelling of cystic fibrosis and Huntington's disease demonstrated that expected net benefits remained positive across reported ranges of editing efficiency and off-target probabilities, with high-burden diseases offering substantially greater margins of acceptable risk. Demographic variables, including age, field of study, and prior knowledge, were not significant predictors of support, suggesting that ethical reasoning exerts more influence than background characteristics. The findings provide evidence that therapeutic necessity dominates public acceptance of embryo editing among the sampled academic population and that quantitative models can reinforce the case for carefully regulated medical applications. Limitations include the use of a non-representative sample, primarily students, which may not fully reflect broader public attitudes.

Keywords: CRISPR-Cas9, human embryos, genetic disease, public opinion, probabilistic modelling, bioethics

ISSN 2959-409X

1. Introduction

Genetic editing has over the past decade shatters the limits of medical possibility not only by delivering the promise of curing an hereditary disease in the affected but also, in a highly contentious connection, has sown the possibility of genetic modification in the human germline that will in turn be passed on to subsequent generations (Montenegro de Wit, 2020). One of those tools has been CRISPR-Cas9; it is fairly easy, highly effective, and can be programmatically specific, making it raise the frequency of soliciting findings in laboratory research on monogenic ailments such as sickle cell disease, cystic fibrosis, and certain hereditary types of blindness (Konishi and Long, 2020).

Laboratory and preliminary clinical experiments have pushed both general and scientific minds beyond the imaginative possible to understand the practical safety, effectiveness, and ethical admissibility questions, when embryonic edits are performed, and the affects that organism and future generations. Embryonic genome editing as a discussion of ethics has a multidimensional aspect, including aspects of off-target sensitivity, mosaicism, a lack of consent by future generations and selectivity in access that enhances social inequalities and the shift to non-therapeutic regulation (Decker, 2025). According to a study by Nordberg et al., the international regulation procedures have been disproportionate' with a small proportion of regulatory authorities giving clearance to conditional studies on germline editing, others await clarity in regard to safety and social acceptance (Nordberg et al., 2020).

A conflict between therapeutic hope and the warning needed is the ethical and practical centre of the given study. In this research, primary data on attitudes is gathered using a structured survey that includes a sample of mostly students, with additions of a small proportion of teachers and adults, and a mathematical model is created to quantify the anticipated change in disease incidence as compared to the probabilistic burden of unintended genomic changes. It is theorized that an embryo modification support is positively correlated to the severity of a disease, and that the quantitative advantages of embryo modification, in specific circumstances, outweigh the estimated risks. The field of scope is limited to monogenic and early-onset disorders as well considering limitations of survey sampling as considered majorly representative of a younger, more academic population, and simplifications in probabilistic modelling.

2. Research Review

2.1 Mechanism and repair pathways

The CRISPR Cas9 system does this by utilizing a small programmable RNA section which triggers the Cas9 nuclease to target a complementary genomic sequence, at which point, the nuclease generates a double-strand break and, as such, transforms sequence recognition into actionable genomic alteration. (Konishi & Long, 2020). After the breakage event, cellular repair factors and experimental conditions determine what happens to the target locus, as non-homologous end joining that disorderly introduces cognizant factual and deletional corrections often form little downsizing or additions, whereas homology-regulated modification can decide the extent to which the sequence may be precisely fixed by means of a fitting template. The guided RNA design, local chromatin state, and biochemical state of editing complex are combined to determine on-target efficiency as well as the range of unintended outcomes, such that even small perturbations in protocol or delivery can cause large changes in outcome (Kim & Kim, 2025).

Efforts towards molecular optimization are focused, then, on better guiding selection algorithms, engineered high-fidelity Cas9 variants, and delivery strategies designed to coordinate the editing event with a compartment of the cell cycle that would be amenable to a successful repair. In early embryos, alleviation of bias in repair pathways and blastocystic cell divisions creates its own unresolved problems since partial editing of the blastomeres will result in mosaic creatures whose genomes differ by tissue and in its own phenotypic outcome, hard to anticipate. Sensitive methods of detection have improved conditions to catalogue low-frequency off-target events, although actual detection does not yet eradicate biological uncertainty regarding the downstream expression, the subsequent effects on the epigenome, and the survivors in the long term (Musson et al., 2022).

The post-modality aims to reduce the key liability of double-strand breaks, as base editors manipulate nucleotide conversions but do not nick both strands, and prime editors write short sequences in the form of reverse-transcriptase complexed to a nicking Cas9, yet each of these modalities comes with its own relative specificity business, which has to be individually characterized (Gowen et al., 2025). The technical image appearing here is thus one of gradual improvements in accuracy and control, along with inescapable and constant uncertainty, particularly when the target is an embryo whose reedited genome is destined to pass on to further generations.

2.2 Clinical progress and technical barriers

Genome editing applications in the clinic have to date been focused on somatic uses, where the patient cell is externally edited and then replenished, a strategy that dissociates risk with heredity of benefit and that has shown definite clinical improvements. Recent experiments of ex vivo editing to cure haemoglobinopathies indicated a sustained upsurge in foetal haemoglobin and significant clinical advantage in several patients, including transfusion independence and cutdown of vaso-occlusive crisis, results that show how stringent clinical protocols may guide CRISPR through to its safe therapeutic applications (Rosanwo & Bauer, 2021).

Germline editing intended to generate hereditary alteration has been under a very different clinical and normative calculus, as any off-target mutation or inconsequential genomic event will not be contained to the individual receiving the treatment and is subject to transmission through generations. The germline debate is dominated by two technical issues imposing practical constraints on clinical preparedness: off-target cleavages at off-match sequences would provide pathogenic alleles or perturbative changes in regulatory sequences, and mosaic in the developing embryo would lead to an organism with an uneven combination of edited and unedited cell lineage, and heterogeneous functional implications (Kansal, 2024).

The issues have been mitigated by laboratory research and design of fine guides, the creation of modified versions of Cas9, and the timeline of delivery, but the rest of the risk is still measurable despite the most favorable circumstances (Foley et al., 2022). Base and prime editing have provided opportunities to minimize the rate of double-strand break-induced indels, but the mechanism also has a different chemical footprint and is constrained in its specificity, which is currently only effectually studied in embryonic systems. According to the clinical record, careful design and monitoring of trials could reduce the level of safety in somatic CRISPR applications to acceptable levels, whereas germline applications remain in a state where technical barriers to their routine clinical application remain unaddressed.

2.3 Ethical dimensions and societal risks

With the focus on quantifiable laboratory hazard, the ethical negotiation surrounding the editing of embryos is an extremely difficult web of ethical concerns to evaluate, which include consent, justice, and the potential of improvement. Potential patients with edited genomes cannot issue their own consent and, therefore, a germline intervention creates special difficulties, regarding a place of the parent and place of society in decision-making regarding their further life (Hallerman et al., 2024)whether it is produced via conventional breeding methods or biotechnologies. While some countries have implemented animal biotechnology oversight policies, many countries have yet to develop theirs. Historically, regulatory approvals were required before products of biotechnology could enter the marketplace, and the high cost of the approval process limited the number and types of animal and plant products that sought approval. Only one biotech animal in the world that was developed for food production has reached the market under a GMO or rDNA approval process. The advent of genome editing techniques has revolutionized the scientific approach to introducing changes into DNA sequences and how biotechnology can be used to enhance agricultural breeding. Regulatory dialogs about biotechnology also have changed as a result of these new technologies. Regulatory agencies have begun to respond to these scientific advances, and a growing number of countries are looking to modernize regulatory approaches for these products, based on risk (or lack thereof. Equity considerations are also applicable, in the sense that the difference in access to future reproductive technologies has the capacity to contribute to the existing system of social stratification with therapeutic interventions being available to the already advantaged layers of the population, which is a distributional problem, overlapping more broadly with the discussion of medical entitlement and the design of health systems. Ethical considerations, slippery slope apprehensions are progressively more tense, as curative, and not cosmetic, motivation might remove the progress needed to achieve forms of demand, and social implications and outcomes of constructed heritable characteristics can possess a ripple effect on skill, diversity, and ignoring criteria (Wismayer, 2022).

Some of the odd peculiarities and controversial unlicensed clinical research into high-profile breaches of ethical conduct have been trial itself, trialing embryonic editing, and live births, which have spurred criminal and professional consequences such that it showing the detrimental effects of procedural obscureness and insufficient preclinical explanation (Gibelli et al., 2025). A cautious manner will be proposed by the regulatory commentators and moral philosophers, and according to them, laboratories would be left to continue with their business and all imaginings in society and anything that would be used in the germline would be regarded to be done first with special control measures and offering equal chance facilities and great protection against non-therapeutic escapes. Ethical modernity is therefore fragmented, negotiated, but a good concord can be found in the meaning of that it does not establish hereditary interventions, except across other social and distributive problems, in real life (Saul, 2025).

ISSN 2959-409X

2.4 Governance and candidate selection

The global governance context has responded with apprehensive structures that intend to discover an equilibrium between scientific development and the moral requirement of safeguarding future generations, and regulatory bodies have become templates of a combination of moratoria, registries, and guidelines provisions that preempt openness and controls. Registries and mechanisms of research governance, which would be drawn on to monitor human genome editing projects and which could yield a platform on which such projects are freely held accountable, have been encouraged by both international health agencies and national advisory organs (Nielsen et al., 2021). While the professional societies and at least declarations at summits have cautioned that clinical uses of germ line must not be implemented in the absence of closely regulated and democratically answerable systems and infrastructures. Practical advice arising out of these conferences may be rapidly narrow-seated on the criteria of candidate condition with severe monogenic early onset disorders where the genotype-phenotype associations are fully realized and where no other satisfactory alternative treatment exists.

Such prioritization is a pragmatically inclined ethic whereby the highest medical necessity and the most obvious causal pathway make the most warranted focus, whereas polygenic traits, disorders of late age, and cosmetic or enhancement purposes are generally viewed to be inappropriate defects in the germ line. Other alternatives like preimplantation genetic testing and somatic therapies are also considered as valuable comparators, as they may, in many cases, cut off the risk of diseases being transmitted, without adding any hereditary edits (Giuliano et al., 2023). California policy appraisal would therefore demand procedural disease selection, solid preclinical support, as well as clear disease follow-up pathways if any clinical program is even considered. Such gaps in knowledge encourage modelling and empiricism, as to transfer laboratory measurements of editing efficiency, and off-target frequency into population-level risk-benefit calculations, it is desirable to explicitly parameterize parameters in a precise way and have society enter them, which the current empirical and quantitative study aims to do.

3. Methodology

3.1 Hypotheses

H1: Support for CRISPR Cas9 embryo editing is higher when the purpose is the elimination of severe and early-onset genetic diseases compared with non-therapeutic enhancement.

H2: Perceived acceptance of embryo editing is negatively associated with perceived risk of off-target effects and mosaicism.

H3: A probabilistic model of gene editing demonstrates that, under current reported levels of editing efficiency and off-target probability, the expected reduction in disease incidence outweighs the expected burden of unintended mutations for selected monogenic diseases.

H4: Acceptance of embryo editing shows variation according to demographic factors such as age, field of study, and prior knowledge of genetics.

3.2 Primary data collection

3.2.1 Survey design

A structured questionnaire was designed to collect responses from a sample of 320 participants, primarily students aged 16 and above, with a smaller proportion of teachers and adults to provide comparison. The survey will contain three sections. The first section records demographic information such as age, gender, level of education, and subject background. The second section measures general attitudes toward CRISPR Cas9 using five-point Likert scale items that ask about trust in science, ethical acceptability, perceived safety, and willingness to permit use in embryos. The third section presents scenarios in which CRISPR is applied to severe genetic disease, mild genetic disease, or enhancement traits, and asks respondents to indicate their level of support. Additional items will measure perceived risks such as off-target mutations, mosaicism and long-term societal consequences.

3.2.2 Sampling and procedure

Participants were recruited through convenience sampling in schools and local community settings. Anonymity will be guaranteed, and informed consent will be obtained before participation. The questionnaire will be distributed in both digital and paper formats to maximise accessibility. Responses will be coded numerically for statistical analysis. Descriptive statistics will be used to summarise levels of support across scenarios. Chi-square tests were used to examine associations between categorical demographic factors and acceptance of embryo editing. Correlation analysis will measure the relationship between perceived risk scores and acceptance levels. Graphical presentation of distributions will aid interpretation.

3.3 Mathematical modelling

A simplified probabilistic model is constructed to evaluate the expected benefit and risk of CRISPR Cas9 embryo editing for monogenic disorders. Let d represent the baseline probability of disease inheritance in the absence of

intervention, p represent the editing success rate, and q represent the probability of off-target mutation that results in a harmful outcome. The expected probability of disease after editing can be modelled as:

$$P_{\text{diseaseafteredit}} = d \times (1 - p) + q$$

The net benefit of CRISPR intervention is then:

$$\text{NetBenefit} = d - P_{\text{diseaseafteredit}}$$

Values of **p** and **q** will be drawn from current published estimates, such as success rates of 70 to 90% and off-target probabilities between one and ten percent. Sensitivity analysis will be performed by varying these parameters within their reported ranges, allowing the model to identify thresholds at which benefits exceed risks. Disease burden will be quantified by applying the model to examples such as cystic fibrosis and Huntington's disease, where inheritance probabilities and severity are well documented.

4. Data Analysis

4.1 Data preparation and cleaning

The first step of the analysis process is to describe the respondents of the survey, which is depicted in Table 1, providing a demographic picture.

Table 1: Demographics summary

n	female_pct	mean_prior_knowledge	mean_trust_science
320	63.4375	2.2875	3.5375

Among 320 people, 63.44% were female, the average score of genetics knowledge acquired in the past was 2.29 regarding the 5-point Likert, and the average score of general analysis of science was 3.54. The result of these baseline measures is that the sample is characterized by female preponderance, little subject-specific knowledge, and moderate trust toward science, which underlies the latter attitudinal results.

4.2 Descriptive statistics

When central tendencies are tested, patterns of acceptance start to appear, and Table 2 shows that there is a startling gradient in the public support in different scenarios. Interventions to avoid severe disease in embryos yielded the highest mean support (3.78), unemployment in mild disease intervention produced a lower average (2.61), and weakness in enhancement application received the least support at 1.73, and all were distinctly differentiated. This gradual deterioration through conditions indicates the ability of therapeutic necessity to have an influence on endorsement.

Table 2: Scenario support summary

mean_severe	sd_severe	mean_mild	sd_mild	mean_enhance	sd_enhance
3.778125	1.093221	2.60625	1.086231	1.725	1.088267

Figure 1 presents the entire distribution of support scores of enhancement, mild disease, and severe diseases in a manner that strengthens the validity of the same. Unlike for severe disease, the little severe disease induces a sharp response of higher endorsements, enhancement responses appear accumulated at the lowest end of the scale, and mild disease exhibited a scattered response. The figure so impressively reflects in graphic terms the comparative readiness to accept CRISPR interventions based on situations.

ISSN 2959-409X

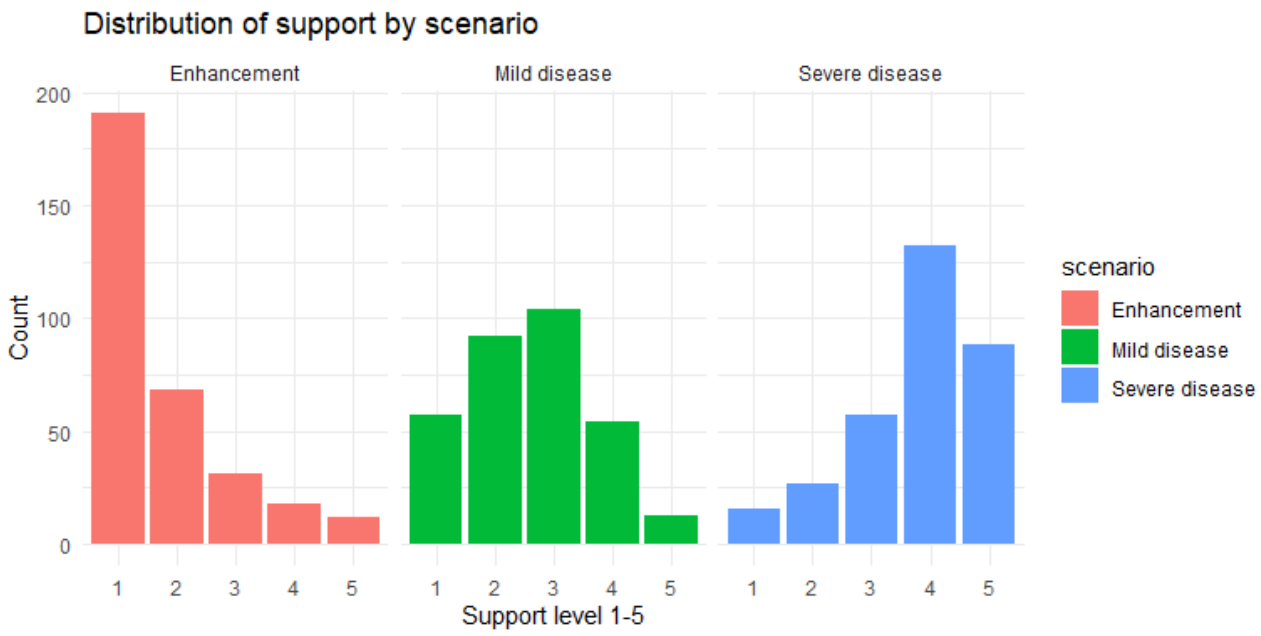

Figure 1: Distribution of Support by Scenario

4.3 Hypothesis Tests: Public Attitudes

4.3.1 H1: Severe Disease versus Enhancement

A rigorous paired test of differences confirms what descriptive statistics suggest. Table 3 presents the Wilcoxon signed-rank result comparing support for severe disease editing and enhancement, yielding a statistic of 40,696 with a p-value smaller than 1.3×10^{-44}. This overwhelming level of significance demonstrates that respondents consistently prefer therapeutic applications for severe disease over enhancement, lending strong support to Hypothesis 1.

Table 3: H1 Wilcoxon test

Statistic	P value	Method	Alternative
40696	1.27E-44	Wilcoxon signed rank test with continuity correction	Two sided

4.3.2 H2: Perceived Risk and Support

Exploring whether heightened perceptions of risk dampen enthusiasm, Table 4 summarizes the Spearman correlation between the perceived risk index and support for severe disease editing. The estimated correlation is only 0.045 with a p-value of 0.421, showing no meaningful relationship. This low correlation indicates that perceptions of risk by themselves fail to account for the differences in the levels of support.

Table 4: H2 Spearman correlation

Estimate	Statistic	P value	Method	Alternative
0.045135	5214784	0.421019	Spearman's rank correlation rho	Two sided

Figure 2 further develops that finding by showing how the perceived risk varies with the scores of supports, which can be seen through the wide range of responses, and how the roughly linear fit line indicates that high-risk perceivers may still support therapeutic editing and some individuals with low risk may be reluctant. The figure, thus, demonstrates the reason why the correlation is inconsequential as support is influenced by other factors other than just risk perception.

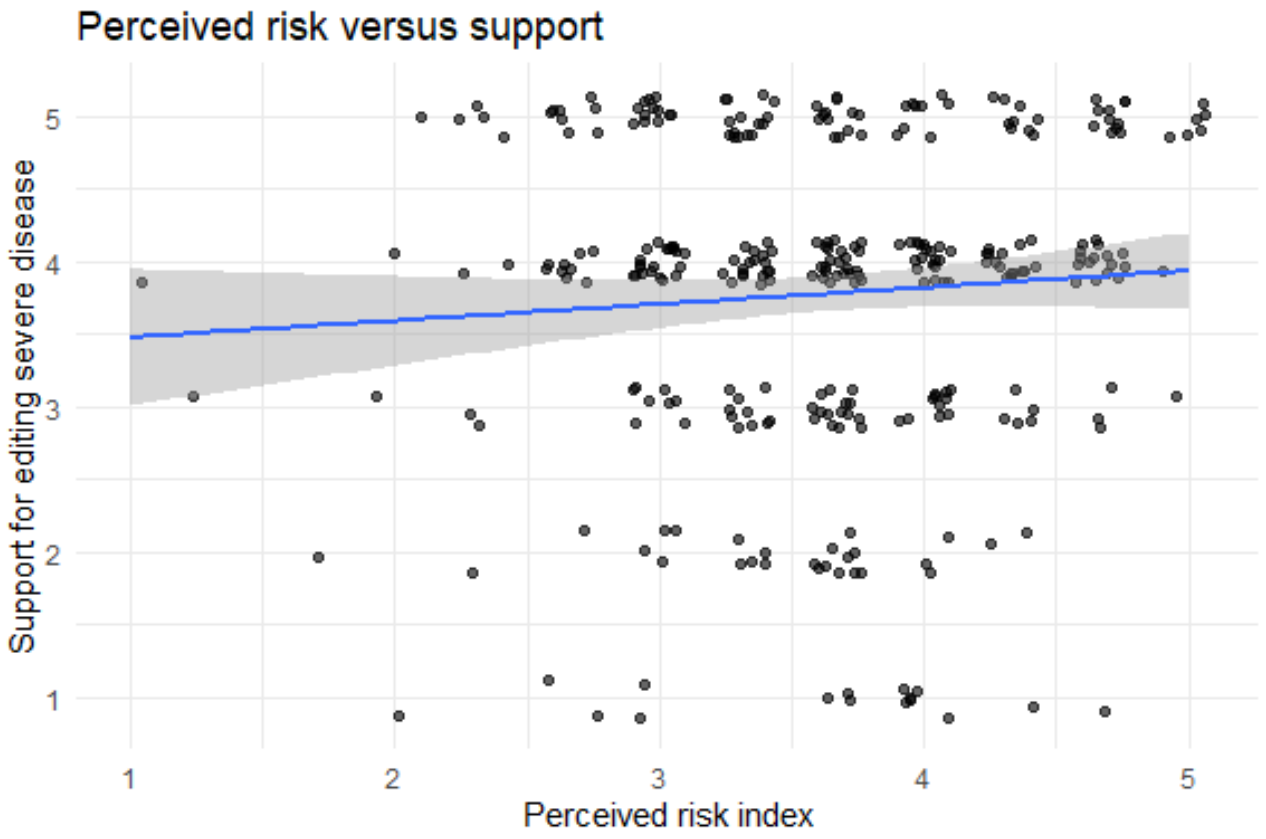

Figure 2: Perceived Risk versus Support

4.3.3 H3: Probabilistic Model Validation and Threshold Analysis

Using the mathematical model, Table 5 is a summary of the sensitivity grid of cystic fibrosis with d = 0.25 as the probability of inheritance. At the most unfavourable point (p = 0.70, q = 0.12), the model indicates a positive net benefit of 0.055 although the highest benefit is 0.2275 at large editing efficiency and low off-target risk. The analysis showed that the net benefit of cystic fibrosis interventions, on average of 0.1412 over the grid, is positive in all the conditions in which it was tested.

Table 5: Summary of sensitivity grid for cystic fibrosis (baseline inheritance probability d = 0.25)

d	p range	q range	p mean	q mean	min net	p at min net	q at min net	mean net	max net	p at max net	q at max net	break-even q at p mean
0.25	0.70 – 0.95	0.010 – 0.120	0.825	0.065	0.0550	0.70	0.12	0.1412	0.2275	0.95	0.01	0.2062

These results are converted into a parameter space gradient of benefit in the corresponding heatmap shown in Figure 3. The warmer colours indicate the conditions of high efficiency and low off target risk and the cooler colours indicate where the benefit margin is thinner, but still positive. The figure therefore shows how improvement in efficiency can be added into in a small way to gain more health.

ISSN 2959-409X

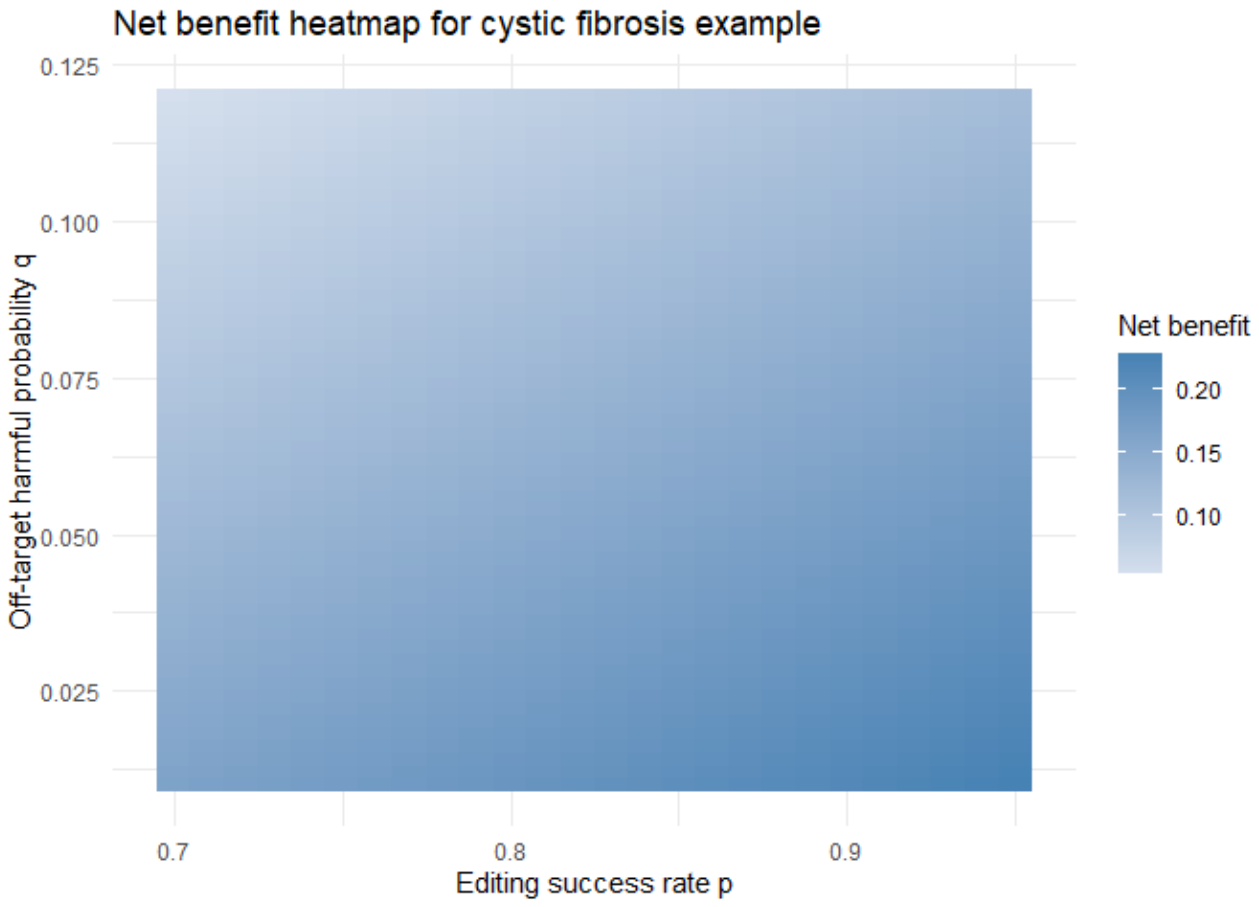

Figure 3: Net Benefit Heatmap for Cystic Fibrosis

The results are even stronger in the case of Huntington disease whose probability of inheriting is higher (d = 0.5). Table 6 indicates a net benefit of 0.230, 0.3475 on average and a net benefit of 0.465. Such numbers highlight the importance of the beneficial power of disease burden boosting the success of editing.

Table 6: Summary of sensitivity grid for Huntington's disease with baseline inheritance probability d equals 0.5.

d	p range	q range	p mean	q mean	min net	p at min net	q at min net	mean net	max net	p at max net	q at max net	break-even q at p mean
0.5	0.70 – 0.95	0.010 – 0.120	0.825	0.065	0.2300	0.70	0.12	0.3475	0.4650	0.95	0.01	0.4125

Figure 4 plots the net benefit surface of Huntington, and it is clear that Huntington has a higher value of the net benefit throughout the grid as compared to the cystic fibrosis scenario. The difference between Figure 3 and Figure 4 shows that the probability of the disease occurring at the base causes a critical shift in the balance between benefit and risk.

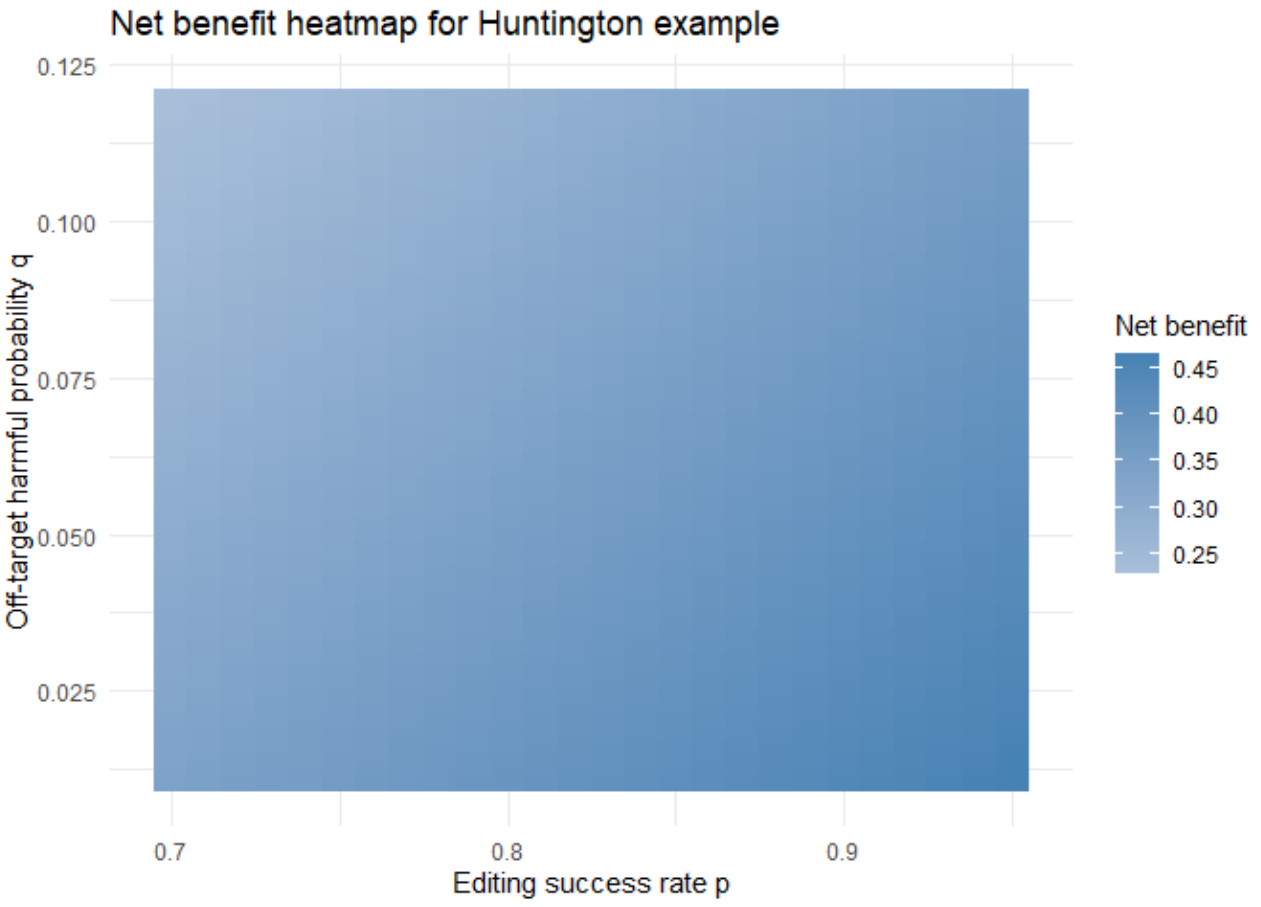

Figure 4: Net Benefit Heatmap for Huntington

The traces of Figure 5 follow interest in following the theoretical levels at which net benefit would be reduced to zero, with possible values of allowable q being plotted against editing efficiency p. The curves rise due to the fact that increased efficiency allows increased tolerable off-target risk, and the disease with more serious likelihoods of occurrence, like Huntington, can give a broader scope of allowed error.

ISSN 2959-409X

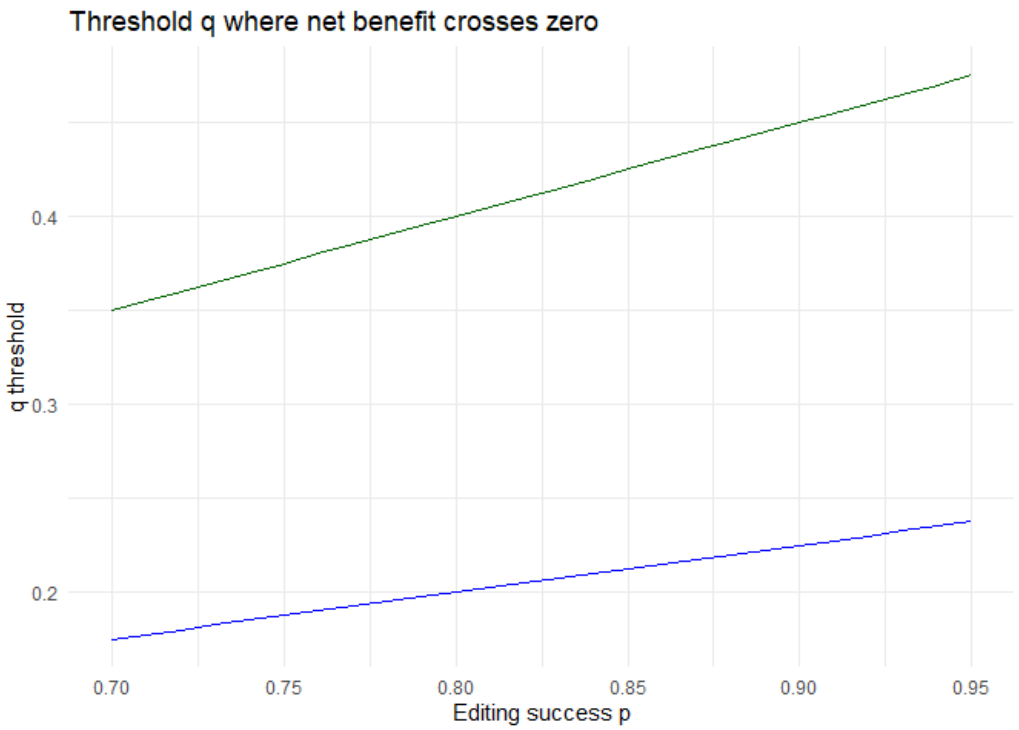

Figure 5: Threshold plot showing q thresholds as a function

4.3.4 H4: Demographic Variation and Multivariable Models

The differences between the support of CRISPR embryo editing in various academic domains can be seen when the raw frequencies are inspected, and Table 7 demonstrates that the representatives of life sciences are the most numerous groups of their supporters, and the participants of the engineering, social humanities, and other fields demonstrate more humble and unequal percentages. These variations in numbers are interesting descriptively, but not very strong to define whether the academic background has a real effect on the support, yet still, they form the pre-condition under which the formal statistical tests can be conducted to define whether the observed variation is more than a product of sampling fluctuation.

Table 7: Crosstab Field vs Support

Var1	Var2	Freq
Engineering	0	25
Life Sciences	0	18
Other	0	17
Other Science	0	21
Social Hum	0	19
Engineering	1	42
Life Sciences	1	53
Other	1	36
Other Science	1	45
Social Hum	1	44

A Pearson chi-square test applied to these raw differences shows that the relationship between field of study and support is not statistically significant, with χ^2 equal to 2.36 and a p-value of 0.67, which is strongly suggestive of the fact that the distribution of support across academic categories is not statistically different than what would be obtained with the influence of chance alone (Table 8). As much as life sciences respondents seem numerically

more supportive, when the overall sample structure is considered, the trend falls below the level at which statistically significant discernibility is increasing the rigor of the argument that disciplinary training influences levels of acceptance in some systematic fashion.

Table 8: Chi-square

Statistic	P value	Parameter	method
2.357739	0.670278	4	Pearson‘s Chi-squared test

Table 9 further extends by modelling the study and adjusting prior knowledge, field, age group, and perceived risk using a logistic regression model. All the coefficients are not statistically significant, with confidence intervals that are greater than one, and p-values that are significantly more than 0.05. The adjusted model thus suggests that the demographic and knowledge variables in this group of data do not have a strong predictive statement, meaning that there are other unmeasured attitudinal or situational determinants of acceptance.

Table 9: Adjusted logistic regression

term	estimate	std. error	statistic	p. value	conf. low	conf. high
(Intercept)	0.910867	0.727291	-0.12836	0.897861	0.219092	3.832878
prior_knowledge	0.883934	0.132067	-0.93417	0.350219	0.68147	1.145081
fieldLifeSciences	1.695323	0.374503	1.409529	0.158679	0.817411	3.569466
fieldOther	1.257262	0.391034	0.585465	0.558235	0.586448	2.733196
fieldOtherScience	1.225049	0.370553	0.547779	0.583844	0.592803	2.546598
fieldSocialHum	1.354247	0.37541	0.807771	0.419222	0.650572	2.849864
age_group19-24	1.092184	0.313988	0.280836	0.778836	0.592133	2.0349
age_group25-34	1.11002	0.347245	0.300588	0.763729	0.566485	2.222401
age_group35+	1.060696	0.349975	0.16837	0.866292	0.537933	2.133255
perceived_risk	1.270649	0.176647	1.355971	0.175108	0.899035	1.801082

4.4 Discussion

The attitude of the population to CRISPR-Cas9 gene editing continues to be greatly determined by the perceived intention of the intervention, and the current results demonstrate a clear and solid moral and practical distinction between treatment and improvement cases. There was significantly more support in preventing severe genetic diseases as compared to non-therapeutic traits, which also reflects the trends in previous surveys with respondents being always open to medical necessity more than enhancement (Himes, 2025). These findings indicate that the therapeutic imperative is the hub around which the opinion is structured and that there is the possibility of ranking abstract technical aspects and more on the perceived humanitarian value to be promoted by the people.

The statistically insignificant marginal correlation between risk perception and support of therapeutic applications provides a significant point of departure in comparison with the existing literature. Surveys at an international scale, such as European-wide ones, have indicated that the reasons for opposition were mostly safety-related, off-target and long-term outcomes (Lopes & Prasad, 2024). However, the current analysis showed that those who said they were more concerned with the matter were not systematically less supportive of editing embryos in case of severe disease. It is possible to attribute this to the fact that younger students (the respondents being mostly younger in age) consider potential advantages more than risks, which is expressed in younger age categories who tend to be more optimistic about biotechnology (Tasnim, 2024).

The justification of therapeutic use was further supported by mathematical modelling of expected benefit or risk. In both cystic fibrosis and Huntington disease, the benefit to risk ratio was highly favourable even at pessimistic assumptions regarding efficiency and off-target mutations. Diseases with higher baseline inheritance probabilities, such as Huntington’s, provided substantially larger margins of acceptable risk, a finding that corresponds with Evans and Steven’s and Gilbert’s (2022) argument that disease severity should guide regulatory thresholds. Quantitative validation, therefore, supports the intuition re-

ISSN 2959-409X

vealed in survey responses that therapeutic contexts carry greater legitimacy (Stevens & Gilbert, 2022).

Demographic and educational predictors, including age, field of study, and prior knowledge, did not significantly explain variation in support. While earlier studies often emphasised the role of scientific literacy in shaping biotechnology attitudes (Li & Ma, 2024), the present results point to a more complex interplay where ethical reasoning and broader cultural factors may outweigh demographic determinants. The implication is that public debate should not narrowly focus on technical expertise but instead acknowledge shared moral concerns about suffering, fairness, and social implications. When the empirical attitudes are merged with the probabilistic modelling, the project helps to promote the argument, that there should be a close regulation of the therapeutic uses and the scepticism persists regarding the concept of enhancement.

5. Conclusion

This study reveals strong support among a primarily academic sample for CRISPR-Cas9 embryo editing to address severe genetic diseases, with minimal support for enhancement. Risk perceptions had little impact, suggesting humanitarian motives dominate. Probabilistic models confirm positive benefits, particularly for high-burden diseases. The academic skew of the sample limits generalizability, but findings align with therapeutic necessity driving acceptance.

In this dataset, risk perceptions that numerous previous studies reported to constrain the acceptance were not significantly correlated with support of severe disease editing. The observation indicates that, at any rates at least of this younger and, mostly, academic population, the humanitarian case of minimizing suffering could prevail over the feelings of technical doubt. Probabilistic models also supported such conclusion by showing positive net benefits expected throughout both realistic efficiency and off-target ranges, especially large-burden conditions where the allowance to acceptable risk is wide.

Demographical variables could not provide much predictive power since all the three groups of people (age, field of study, and prior knowledge) failed to indicate a significant variance in attitudes. Although this is contrary to previous accounts of support based on scientific literacy, it assumes that support is mediated in more by joint discussions of ethics rather than college degree. The work offers evidence that people might approve the editing of CRISPR embryos only under therapeutic necessity, and probabilistic modelling can predict the possibility of such procedures in serious monogenic pathologies.

6. Evaluation

The project was educational and was used to bring out the significance of empirical research in addressing complex bioethical questions. Incorporating data into systematically addressing these questions by modelling our bodies with mathematical elements and data as an information base, data and mathematical model studies were unified. The formulation of the questionnaire in a manner that they received other answers other than socially beneficial was one of the issues. Although the method of recruitment of the respondents was the convenience sampling, we were fortunate to discover very strong patterns that were consistent with the international discussion. This showed that a sample is effective with a small sample as long as one critically analyses the data.

The modelling section was especially interesting because it translated probabilities identified in the literature into reality-readable terms of net benefit and risk which could be deciphered by stakeholders. These sensitivity analyses proved helpful in determining how the calculations of benefit might be varied when there were technical uncertainties, e.g., how did editing efficiency vary, or when there were off-target rates. They also made themselves see the reason why high hereditability diseases may warrant a higher tolerance of residual risk. We put our findings to test critically against what is in the existing literature particularly where we discovered that our findings were not matching with what is known to be true that it is so.

I could not find a clear connection between the perception of risk and the support, and thus, I was not disposed to think that the characteristics of the samples and the cultural background were at work. These contradictions were the greatest intellectual delights of the work as they demonstrate that it is more critical to observe the data in broader social and ethical pictures. The critical and reflective practice skills developed significantly over the course of the project, which helped substantiate the idea that studies of recently emerging technologies require a balance between a quantitative rigor approach and an ethical sensitivity. The experience has inspired me to not only look beyond the timeframes of the disciplinary prerogatives but also to utilize an integrated toolkit in the future unanswered problems with the same sort of questions.

References

Decker, S. S. (2025). *Navigating the ethical implications of human gene editing technology: A comparative, multi-perspective approach.* [PhD Thesis]. https://baylor-ir.tdl.org/items/acb12778-d2da-4040-81e8-7baf69e1addc

Foley, R. A., Sims, R. A., Duggan, E. C., Olmedo, J. K., Ma, R., & Jonas, S. J. (2022). Delivering the CRISPR/Cas9 system for engineering gene therapies: Recent cargo and delivery approaches for clinical translation. *Frontiers in Bioengineering and Biotechnology*, *10*, 973326.

Gibelli, F., Ricci, G., & Bailo, P. (2025). Genome Editing in Medicine: A Scoping Review of Ethical, Bioethical, and Medico-Legal Implications. *Journal of Law, Medicine & Ethics*, 1–9.

Giuliano, R., Maione, A., Vallefuoco, A., Sorrentino, U., & Zuccarello, D. (2023). Preimplantation genetic testing for genetic diseases: Limits and review of current literature. *Genes*, *14*(11), 2095.

Gowen, B. G., Melton, K., Leong, W. I., Khekare, P., McCawley, S., Chan, J., Boivin, P., Jani, V., Cantor, A. J., & Tambe, A. (2025). Systematic identification and characterization of high efficiency Cas9 guide RNAs for therapeutic targeting of ADAR. *PloS One*, *20*(2), e0317745.

Hallerman, E., Bredlau, J., Camargo, L. S. A., Dagli, M. L. Z., Karembu, M., Kovich, D., Muia, A. N., Murrone, M. L., Rocha-Salavarrieta, P. J., Romero-Aldemita, R., Tizard, M., Walton, M., & Wray-Cahen, D. (2024). Enabling regulatory policy globally will promote realization of the potential of animal biotechnology. *CABI Agriculture and Bioscience*, 25. https://doi.org/10.1186/s43170-024-00221-6

Himes, D. (2025). *Ethical Leadership in the Development and Integration of AI Implants for Human Enhancement* [PhD Thesis, Alliant International University]. https://search.proquest.com/openview/2c6278aeebbfd6ef70020f6ecd04dc03/1?pq-origsite=gscholar&cbl=18750&diss=y

Kansal, R. (2024). The CRISPR-Cas system and clinical applications of CRISPR-based gene editing in hematology with a focus on inherited germline predisposition to hematologic malignancies. *Genes*, *15*(7), 863.

Kim, H. K., & Kim, H. H. (2025). Evaluation and prediction of guide RNA activities in genome-editing tools. *Nature Reviews Bioengineering*, 1–16.

Konishi, C. T., & Long, C. (2020). Progress and challenges in CRISPR-mediated therapeutic genome editing for monogenic diseases. *Journal of Biomedical Research*, *35*(2), 148.

Li, R.-Y., & Ma, Y.-Y. (2024). Knowledge and Attitudes toward Biotechnology in STEM Education as an Indicator of Scientific Literacy. *Journal of Baltic Science Education*, *23*(1), 76–89.

Lopes, R., & Prasad, M. K. (2024). Beyond the promise: Evaluating and mitigating off-target effects in CRISPR gene editing for safer therapeutics. *Frontiers in Bioengineering and Biotechnology*, *11*, 1339189.

Montenegro de Wit, M. (2020). Democratizing CRISPR? Stories, practices, and politics of science and governance on the agricultural gene editing frontier. *Elem Sci Anth*, *8*, 9.

Musson, R., Gąsior, Ł., Bisogno, S., & Ptak, G. E. (2022). DNA damage in preimplantation embryos and gametes: Specification, clinical relevance and repair strategies. *Human Reproduction Update*, *28*(3), 376–399.

Nielsen, J., Eckstein, L., Nicol, D., & Stewart, C. (2021). Integrating public participation, transparency and accountability into governance of marketing authorisation for genome editing products. *Frontiers in Political Science*, *3*, 747838.

Nordberg, A., Minssen, T., Feeney, O., De Miguel Beriain, I., Galvagni, L., & Wartiovaara, K. (2020). Regulating germline editing in assisted reproductive technology: An EU cross-disciplinary perspective. *Bioethics*, *34*(1), 16–32. https://doi.org/10.1111/bioe.12705

Rosanwo, T. O., & Bauer, D. E. (2021). Editing outside the body: Ex vivo gene-modification for β-hemoglobinopathy cellular therapy. *Molecular Therapy*, *29*(11), 3163–3178.

Saul, N. (2025). Anthropotechnik? Ernst Jünger's Organic Constructions, Self-Optimization and Modernity. *Self-Optimization in Modernist Culture*, *9*, 328.

Stevens, I., & Gilbert, F. (2022). International Regulatory Standards for the Qualitative Measurement of Deep Brain Stimulation in Clinical Research. *Journal of Empirical Research on Human Research Ethics*, *17*(3), 228–241. https://doi.org/10.1177/15562646221094922

Tasnim, N. (2024). *Understanding the impacts of biotechnology: A survey among the university students in chittagong* [PhD Thesis, Brac University]. https://dspace.bracu.ac.bd/xmlui/handle/10361/23987

Wismayer, H. (2022). *A Heuristic Inquiry in Two Parts Exploring Experiences of Silence Described by Novice and Clinically-experienced Psychotherapists and Any Implications for the Therapeutic Encounter* [PhD Thesis, University of Roehampton]. https://pure.roehampton.ac.uk/ws/portalfiles/portal/8557828/Wismayer_Hildegard_Final_Thesis.pdf

Appendix

Survey Instrument

Use this verbatim survey text for both paper and the online form. code for response coding is indicated in brackets.

Section A Personal and demographic information

A1 Age group

· 16 to 18 [code 1]
· 19 to 24 [2]
· 25 to 34 [3]
· 35 and above [4]

ISSN 2959-409X

A2 Gender
· Female [1]
· Male [2]
· Prefer not to say [3]
· Other specify [4]
A3 Highest education level currently studied or completed
· Secondary school [1]
· College or diploma [2]
· Undergraduate degree [3]
· Postgraduate degree [4]
A4 Field of study or profession
· Life sciences or medicine [1]
· Natural sciences not life sciences [2]
· Social sciences or humanities [3]
· Engineering or computing [4]
· Other specify [5]
A5 Prior knowledge of genetics and gene editing
· None [1]
· Basic school level [2]
· Moderate, some university or independent study [3]
· Advanced, formal training or work experience [4]
Section B General attitudes and perception scales
Instructions: mark one number for each statement where 1 means strongly disagree and 5 means strongly agree
B1 I trust scientific research to produce safe gene therapies [1 to 5]
B2 Using CRISPR Cas9 to eliminate serious inherited diseases in embryos is ethically acceptable [1 to 5]
B3 I believe CRISPR Cas9 is currently safe enough for use in embryos to eliminate disease [1 to 5]
B4 I would personally approve use of CRISPR Cas9 on embryos to prevent a severe early onset disease in my family [1 to 5]
B5 I would approve use of CRISPR Cas9 on embryos to produce non therapeutic enhancements such as increased height or eye colour [1 to 5]
Section C Perceived risks and consequences
C1 How likely do you think a harmful off target mutation is when editing embryos today
· Very unlikely [1] to Very likely [5]
C2 How likely do you think mosaicism is after embryo editing today
· Very unlikely [1] to Very likely [5]
C3 How concerned are you about long term societal harms from germline editing
· Not concerned [1] to Extremely concerned [5]
C4 Overall perceived risk index will be calculated later as the mean of C1 through C3
Section D Scenario support
For each scenario mark level of support from 1 strongly oppose to 5 strongly support
D1 Scenario one severe early onset monogenic disease with no effective therapy for which embryos would be edited to correct the causal mutation [1 to 5]
D2 Scenario two mild monogenic disease where quality of life effect is minor and alternatives exist [1 to 5]
D3 Scenario three non therapeutic enhancement such as increased height or cosmetic traits [1 to 5]