TABLE OF CONTENTS

| ACKNOWLEDGEMENTS | |
|--|----|
| ABSTRACT | ii |
| 1. INTRODUCTION | 1 |
| 1.1. OBJECTIVES | |
| 1.2. ELECTRICITY PYLONS | 2 |
| 1.3. STRUCTURE | |
| | |
| 2. DESIGN OF LATTICE TOWERS | 5 |
| 2.1. GENERAL PRINCIPLES | 5 |
| 2.2. DESIGN LOADS | 6 |
| 2.3. RESISTANCE VERIFICATION | |
| 2.3.1. IMPLEMENTATION NOTES | |
| 2.4. STABILITY VERIFICATION | 7 |
| 2.4.1. EFFECTIVE SLENDERNESS FACTOR - K | 7 |
| 2.4.1.1. Implementation notes – Leg members | 8 |
| 2.4.1.2. Implementation notes – Diagonal bracing members | |
| 2.4.1.3. Implementation notes – Horizontal bracing members | 10 |
| 2.4.2. Buckling Length | 10 |
| 2.5. CONNECTION DESIGN | 14 |
| | |
| 3. GENETIC ALGORITHM | 15 |
| 3.1. OVERVIEW | 15 |
| 3.2. FUNDAMENTAL ELEMENTS OF A GENETIC ALGORITHM | 16 |
| 3.2.1. INDIVIDUAL | 16 |
| 3.2.2. INITIAL POPULATION | 17 |
| 3.2.3. FITNESS FUNCTION | 18 |
| 3.2.4. SELECTION FUNCTION | 19 |
| 3.2.4.1. Roulette wheel | 19 |
| 3.2.4.2. Tournament selection | 20 |
| 2.2.5. CENETIC OPERATORS | 20 |

| 3.2.5.1. Crossover | 20 |
|----------------------------------|----|
| 3.2.5.2. Mutation | 21 |
| 3.2.6. Termination Criteria | 21 |
| | |
| 4. PROGRAM DESCRIPTION | 23 |
| 4.1. SUMMARY | 23 |
| 4.2. Program Flow | 23 |
| 4.3. BASE GENETIC CODE | 25 |
| 4.4. INITIAL POPULATION | 29 |
| 4.5. EVALUATE FUNCTION | 30 |
| 4.6. REPAIR FUNCTION | 33 |
| 4.7. SELECTION FUNCTION | 35 |
| 4.8. GENETIC OPERATORS | 35 |
| 4.8.1. Crossover | 35 |
| 4.8.2. GAUSSIAN MUTATION | 36 |
| | |
| 5. CASE STUDY | 39 |
| 5.1. BASE MODEL | 39 |
| 5.2. PROGRAM SETUP | 41 |
| 5.2.1. TEST RUNS AND CALIBRATION | 42 |
| 5.3. RESULTS | 44 |
| 5.3.1. Postprocessing | 44 |
| 5.3.2. ANALYSIS | 46 |
| 5.4. CONCLUDING REMARKS | 47 |
| 5.3.2. FUTURE WORK | 47 |
| REFERENCES | 40 |

LIST OF FIGURES

| Fig.1.1 – Power lines designed to withstand snow, Iceland | 2 |
|---|----|
| Fig.1.2 – Test bench – India | 3 |
| Fig.2.1 – Steel poles | 6 |
| Fig.2.2 – Lattice tower | 6 |
| Fig.2.3 – EC3-3-1 table G.1 from annex G | 8 |
| Fig.2.4 – EC3-3-1 table G.2 from annex G | 9 |
| Fig.2.5 – EC3-3-1 table G.3 from annex G | 10 |
| Fig.2.6 – EC3-3-1 Figure H.1 from annex H | 11 |
| Fig.2.7 – Increased number of horizontal divisions | 11 |
| Fig.2.8 – EC3-3-1 Figure H.3 from annex H | 12 |
| Fig.2.9 – EC3-3-1 Figure H.4 from annex H | 13 |
| Fig.3.1 – Flow of standard GA | 15 |
| Fig.3.2 – Chromosome structure and values | 16 |
| Fig.3.3 – Basic bit string chromosome | 17 |
| Fig.3.4 – More complex chromosome datatype | 17 |
| Fig.3.5 – Random vs Seeded population | 17 |
| Fig.3.6 – Roulette wheel: A is better than G, therefore selected more often | 19 |
| Fig.3.7 – Tournament selection | 20 |
| Fig.3.8 – Double and single point crossover | 21 |
| Fig.4.1 – User interface | 24 |
| Fig.4.2 – Interaction between key modules | 25 |
| Fig.4.3 – Grasshopper | 26 |
| Fig.4.4 – Grasshopper and rhino model | 27 |
| Fig.4.5 – IAM: Different bracing conditions | 31 |
| Fig.4.6 – Tapered normal distribution | 36 |
| Fig.5.1 – Base model | 39 |
| Fig.5.2 – Arm nodes | 40 |
| Fig.5.3 – Mutation adjustment trial | 43 |
| Fig.5.4 – Ideal mutation probability reached | 43 |
| Fig.5.5 – Final search | 43 |
| Fig.5.6 – Plan view of the tower | 44 |

| Fig.5.7 – Critical quadrant, front and side planes | .45 |
|--|-----|
| Fig.5.8 – Legs with secondary bracing added | .45 |

TABLE LIST

| Table 4.1 – DNA definition | 28 |
|---|----|
| Table 4.2 – Initial mutation implementation | 29 |
| Table 4.3 – Evaluate function call | 30 |
| Table 4.4 – IAM scan (leg scan excerpt) | 30 |
| Table 4.5 – EC3 verification for leg members | 32 |
| Table 4.6 –Repair function excerpt | 34 |
| Table 4.7 – Tournament selection | 35 |
| Table 4.8 – Crossover function applied to the bar array | 35 |
| Table 4.9 – Gaussian mutation algorithm | 37 |
| Table 4.10 – Clamp function | 37 |
| Table 4.11 – Mutation function | 37 |
| Table 5.1 – Base model weight distribution | 40 |
| Table 5.2 – Load cases | 41 |
| Table 5.3 – Final structure weight distribution | 46 |